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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) Internati nal Patent Classification 7 : C07H

A2

(11) International Publicati n Number: WO 00/09525

(43) International Publication Date: 24 February 2000 (24.02.00)

(21) International Application Number: PCT/US99/17712

(22) International Filing Date: 3 August 1999 (03.08.99)

(30) Priority Data:
60/095,212 3 August 1998 (03.08.98) US

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(81) Designated States: AU, CA, CN, MX, RU, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).

Published
Without international search report and to be republished upon receipt of that report.

(54) Title: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE AGENT, COMPOSITION, KIT AND TREATMENTS

(57) Abstract

A composition comprises a nucleic acid comprising an oligo anti-sense to a target such as polypeptide(s) associated with an ailment afflicting lung airways, genes and mRNAs encoding them, genomic and mRNA flanking regions, intron and exon borders and all regulatory and functionally related segments of the genes and mRNAs encoding the polypeptides, their salts and mixtures. Various formulations contain a requisite carrier, and optionally other additives and biologically active agents. The agent of the invention may be prepared by selecting a target gene(s), genomic flanking region(s), RNA(s) and/or polypeptide(s) associated with a disease(s) or condition(s) afflicting lung airways, obtaining the sequence of the mRNA(s) corresponding to the target gene(s) and/or genomic flanking region(s), and/or RNAs encoding the target polypeptide(s), selecting at least one segment of the mRNA which may be up to 60 % free of thymidine (T) and synthesizing one or more anti-sense oligonucleotide(s) to the mRNA segments which are free of adenosine (A) by substituting a universal base for A when present in the oligonucleotide. The agent may be prepared by selection of target nucleic acid sequences with GC running stretches, which have low T content, and by optionally replacing A in the anti-sense oligonucleotides with a AUniversal base@. The agent, composition and formulations are used for prophylactic, preventive and therapeutic treatment of ailments associated with impaired respiration, allergy(ies) and/or inflammation, such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, lung pain, cystic fibrosis, bronchoconstriction, pulmonary hypertension and bronchoconstriction, chronic bronchitis, emphysema, chronic obstructive pulmonary disease (COPD), acute respiratory distress syndrome (ARDS), ischemic conditions including ischemia itself, and cancers such as leukemias, lymphomas, carcinomas, and the like, e.g. colon cancer, breast cancer, pancreatic cancer, lung cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastasis, etc., as well as all types of cancers with may metastasize or have metastasized to the lung(s), including breast and prostate cancer. The present treatment is suitable for administration in combination with other treatments, e.g. before, during and after other treatments, including radiation, chemotherapy, antibody therapy and surgery, among others. The present agent is effectively administered preventatively, prophylactically or therapeutically by itself for conditions without known therapies, or as a substitute for, or in conjunction with, other therapies exhibiting undesirable side effects. The treatment of this invention may be administered directly into the respiratory system of a subject, so that the agent has direct access to the airways and the lungs.

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LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE AGENT, COMPOSITION, KIT & TREATMENTS

BACKGROUND OF THE INVENTION

Field of the Invention

This application relates to an agent comprising anti-sense oligonucleotides of low or no adenosine content. These agents are suitable for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. Examples of these diseases are allergies, asthma, impeded respiration, pain, cystic fibrosis, and cancers such as leukemias, e.g. colon cancer, and the like. The present agent may be administered prophylactically or therapeutically in conjunction with other therapies, or may be utilized as a substitute for therapies that have significant, negative side effects.

Background of the Invention

Respiratory ailments, associated with a variety of diseases and conditions, are extremely common in the general population, and more so in certain ethnic groups, such as African Americans. In some cases they are accompanied by inflammation, which aggravates the condition of the lungs. Asthma, for example, is one of the most common diseases in industrialized countries. In the United States it accounts for about 1% of all health care costs. An alarming increase in both the prevalence and mortality of asthma over the past decade has been reported, and asthma is predicted to be the preeminent occupational lung disease in the next decade. While the increasing mortality of asthma in industrialized countries could be attributable to the increased reliance upon beta agonists in the treatment of this disease, the underlying causes of asthma remain poorly understood.

Anti-sense oligonucleotides have received considerable theoretical consideration as potential useful pharmacological agents in human disease. Their practical application in actual models of human disease, however, has been somewhat elusive. One important impediment to their effective application has been a difficulty in finding an appropriate route of administration to deliver them to their site of action. Many in viv experiments were conducted by administering anti-sense oligonucleotides directly to specific regions of the brain. These applications, however, necessarily have limited clinical utility due to their invasive nature.

The systemic administration of anti-sense oligonucleotides also presents significant problems, not the least being an inherent difficulty in targeting disease-involved tissues. In contrast, the lung is an excellent target for the direct administration of anti-sense oligonucleotides, and provides a non-invasive and a tissue-specific route. The delivery of anti-sense agents to the lung has been relatively undeveloped.

Adenosine may constitute an important mediator in the lung for various diseases, including bronchial asthma. Its potential role was suggested by the finding that asthmatics respond favorably to aerosolized adenosine with marked bronchoconstriction whereas normal individuals do not. An asthmatic rabbit animal model, the dust mite allergic rabbit model for human asthma, responded in a similar fashion to aerosolized adenosine with marked bronchoconstriction whereas non-asthmatic rabbits showed no response. More recent work with this animal model suggested that adenosine-induced bronchoconstriction and bronchial hyperresponsiveness in asthma may be mediated primarily through the stimulation of adenosine receptors. Adenosine has also been shown to cause adverse effects, including death, when administered therapeutically for other diseases and conditions in subjects with previously undiagnosed hyper reactive airways.

A handful of medicaments have been available for the treatment of respiratory diseases and conditions, although in general they all have limitations. Theophylline, an important drug in the treatment of asthma, is a known adenosine receptor antagonist which was reported to eliminate adenosine-mediated bronchoconstriction in asthmatic rabbits. A selective adenosine A_1 receptor antagonist, 8-cyclopentyl-1, 3-dipropylxanthine (DPCPX) was also reported to inhibit adenosine-mediated bronchoconstriction and bronchial hyperresponsiveness in allergic rabbits. The therapeutic and preventative applications of currently available adenosine A_1 receptor-specific antagonists are, nevertheless, limited by their toxicity. Theophylline, for example, has been widely used in the treatment of asthma, but is associated with frequent, significant toxicity resulting from its narrow therapeutic dose range. DPCPX is far too toxic to be useful clinically. The fact that, despite decades of extensive research, no specific adenosine receptor antagonist is available for clinical use attests to the general toxicity of these agents.

Anti-sense oligonucleotides have received considerable theoretical consideration for their potential use as

pharmacological agents in human disease. Finding practical and effective applications of these agents in actual models of human disease, however, have been few and far between, particularly because they had to be administered in large doses. Another important consideration in the pharmacologic application of these molecules is their route of administration. Many in vivo applications have involved the direct administration of anti-sense oligonucleotides to limited regions of the brain. Such applications, however, have limited clinical utility due to their invasive nature.

The systemic administration of anti-sense oligonucleotides as pharmacological agents has been found to have also significant problems, not the least of which being a difficulty in targeting disease-involved tissues. That is, the necessary dilution of the anti-sense oligonucleotide in the circulatory system makes extremely difficult to attain a therapeutic dose at the target tissue by intravenous or oral administration. The bioavailability of orally administered anti-sense oligonucleotides is very low, of the order of less than about 5%.

There are presently no effective therapies for treating these ailments, or at least no therapies which are effective and devoid of significant detrimental side effects. Accordingly, there is still a need for an agent for the treatment of ailments afflicting the lung airways, including respiratory problems and inflammation, which is highly effective and producing minimal, or entirely devoid of, side effects.

SUMMARY OF THE INVENTION

This invention relates to an agent which comprises an oligonucleotide (oligo) consisting essentially of less than about 15% adenosine (A), which is selected from the group consisting of anti-sense oligonucleotides to mRNAs corresponding to target genes, to genomic flanking regions selected from the group consisting of intron and exon borders, such as the 5' end, the 3' end and the juxta-section between coding and non-coding regions, and to all segments of mRNAs encoding polypeptides associated with ailments afflicting lung airways, combinations thereof, pharmaceutically acceptable salts thereof, and mixtures thereof. The mRNA(s), for example, encode polypeptide(s) such as transcription factors, stimulating and activating factors, interleukins, interleukin receptors, chemokines, chemokine receptors, endogenously produced specific and non-specific enzymes, immunoglobulins, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules, defensines, growth factors, vasoactive peptides and receptors, and binding proteins; or those mRNA which correspond to an oncogene. The agents is are provided in the form of specific compositions and formulations, with a carrier, and optionally with other therapeutic agents and additives which are typically used for administration by a specific route, e.g. into the respiratory system. The agent is also provided as a capsule or cartridge, and in the form of a kit.

This agent is suitable for the treatment of diseases and conditions associated with impaired respiration and inflammation, including lung diseases, ailments and conditions that have a negative effect on the lungs of a subject. Examples of diseases and conditions, which may be treated preventively, prophylactically and therapeutically with the agent of this invention, are pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas, and the like, e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, etc., as well as all types of cancers which may metastasize or have metastasized to the lung(s), including breast and prostate cancer. The present agent(s) is (are) also suitable for administration before, during and after other treatments, including radiation, chemotherapy, antibody therapy, phototherapy and cancer, and other types of surgery. Alternatively, the present agent may be effectively administered preventively, prophylactically or therapeutically, and in conjunction with other therapies, or by itself for conditions without known therapies or as a substitute for therapies that have significant negative side effects.

The composition of this invention may be administered by transdermal or systemic routes, including by, but not exclusively, oral, intracavitary, intranasal, intraanal, intravaginal, transdermal, intradermal, intrabuccal, intravenous, subcutaneous, intramuscular, intratumor, intraglandular, by inhalation, intraarterial, intravascular in general, into the ear, intracranial, intrathecal, intraorgan including via a shunt to, for example, the liver or other organs, by implantation and intraocular administration to a human or any other animal, including vertebrates, such as mammals. In a preferred embodiment, the present agents are administered directly into the respiratory

system of a subject, so that the agent has direct access to the lungs, in an amount effective to reduce or inhibit the effect in the lung of the targeted diseases or conditions.

Also part of this invention is a method of producing an anti-sense oligonucleotide consisting essentially of less than about 15% adenosine (A), by selecting a target including genes, genomic flanking regions, RNAs and polypeptide associated with an ailment afflicting the lung airways, obtaining the sequence of a mRNA(s) corresponding to the target gene(s) and/or their genomic flanking region(s) and/or the juxta-membrane regions thereof, and mRNA(s) encoding the target polypeptide(s), selecting at least one segment of the mRNA(s), and synthesizing one or more anti-sense oligonucleotide(s) to the selected mRNA segment(s), and substituting, if necessary, a universal base(s) for one or more A to reduce the proportion of A present in the oligonucleotide to less than 15%.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

This invention arose from a desire by the inventor to improve on his own prior discovery that anti-sense oligonucleotides (oligos) may be utilized therapeutically in the treatment of diseases or conditions which impair respiration, cause inflammation, constrict bronchial tissue or the lung airways, or otherwise impede normal breathing. The inventor reasoned that he could improve on his prior discovery that anti-sense oligos targeted to genes associated with such ailments could effectively treat and prevent the effects and symptomatology of such disease(s) or condition(s). The present invention is premised on the recent discovery by the inventor that oligonucleotides are metabolized in vivo to their deoxynucleotides. In the case of adenosine (A)-containing oligonucleotides, there is break down with release of deoxyadenosine which, in turn, activates adenosine receptors causing bronchoconstriction, inflammation and the like.

The present technology relies on the design of anti-sense oligos targeted to mRNAs associated with ailments involving lung airway pathology(ies), and on their modification to reduce the occurrence of undesirable side effects caused by their release of adenosine upon breakdown, while preserving their activity and efficacy for their intended purpose. In this manner, the inventor targets a specific gene to design one or more anti-sense oligonucleotide(s) (oligos) that selectively bind(s) to the corresponding mRNA, and then reduces, if necessary, their content of adenosine via substitution with universal base or an adenosine analog incapable of activating adenosine A_1, A_{2b} or A_3 receptors. Based on his prior experience in the field, the inventor reasoned that in addition to Adownregulating@ specific genes, he could increase the effect of the agent(s) administered by either selecting segments of RNA that are devoid, or have a low content, of thymidine (T) or, alternatively, substitute one or more adenosine(s) present in the designed oligonucleotide(s) with other nucleotide bases, so called universal bases, which bind to thymidine but lack the ability to activate adenosine receptors and otherwise exercise the constricting effect of adenosine in the lungs, etc. Given that adenosine (A) is a nucleotide base complementary to thymidine (T), when a T appears in the RNA, the anti-sense oligo will have an A at the same position. For consistency's sake, all RNAs and oligonucleotides are represented in this patent by a single strand in the 5' to 3' direction, when read from left to right, although their complementary sequence(s) is (are) also encompassed within the four corners of the invention. In addition, all nucleotide bases and amino acids are represented utilizing the recommendations of the IUPAC-IUB Biochemical Nomenclature Commission, or by the known 3-letter code (for amino acids).

The method of the present invention may be used to treat ailments associated with reduced airway function in a subject, whatever its cause. The adenosine content of the anti-sense agent(s) of the invention have a reduced A content to prevent its liberation upon in vivo degradation of the agent(s). Examples of airway diseases that may be treated by the method of the present invention include cystic fibrosis, asthma, pulmonary hypertension and vasoconstriction, chronic obstructive pulmonary disease (COPD), chronic bronchitis, respiratory distress syndrome, lung cancer and lung metastatic cancers and other airway diseases, including those with inflammatory response.

Anti-sense oligos to the aden-sine A_1, A_{2a}, A_{2b}, and A_3 receptors, CCR3 (chemokine receptors), bradykinin 2B, CAM (vascular cell adhesion molecule), and eosinophil receptors, among others, have been shown to be effective in down-regulating the expression of their genes. Some of these act to alleviate the symptoms or reduce respiratory ailments and/or inflammation, for example, by Adown regulation@ of the adenosine A_1, A_{2a}, A_{2b}, and/or A_3 receptors and CCR3, bradykinin 2B, VCAM (vascular cell adhesion molecule) and eosinophil receptors. These agents are preferably administered directly into the respiratory system, e.g., by

inhalation or other means, so that they may reach the lungs without widespread systemic dissemination. This permits the use of substantially lower doses of the agent of the invention as compared with those administered by the prior art, systemically or by other generalized routes and, consequently, reduce undesirable side effects resulting from the agent's widespread distribution in the body. The agent(s) of this invention has (have) been shown to reduce the amount of receptor protein expressed by the tissue. These agents, thus, rather than merely interacting with their targets, e.g. a receptor, lower the number of target proteins that other drugs may interact with. In this manner, the present agent(s) afford(s) extremely high efficacy with low toxicity.

The adenosine receptors discussed above are mere examples of the high power of the inventor's technology. In fact, a large number of genes may be targeted in a similar manner by the present agent(s), to reduce or down-regulate protein expression. By means of example, if the target disease or condition is one associated with impeded or reduced breathing, bronchoconstriction, chronic bronchitis, pulmonary bronchoconstriction and/or hypertension, chronic obstructive pulmonary disease (COPD), allergy, asthma, cystic fibrosis, respiratory distress syndrome, cancers, which either directly or by metastasis afflict the lung, the present method may be applied to a list of potential target mRNAs, which includes the targets listed in Table 1 below, among others.

Table 1: Pulmonary Disease or Condition (Asthma/Inflammation) Targets

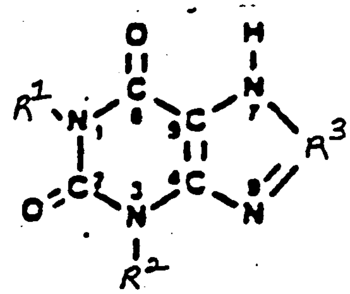
Nf6B Transcription Factor	Interleukin-8 Receptor (IL-8 R)
Interleukin-5 Receptor (IL-5R)	Interleukin-4 Receptor (IL-4R)
Interleukin-3 Receptor (IL-3R)	Interleukin-1beta (IL-1beta)
Interleukin-1β Receptor (IL-1beta R)	Eotaxin
Tryptase	Major Basic Protein
β2-adrenergic Receptor Kinase	Endothelin Receptor A
Endothelin Receptor B	Preproendothelin
Bradykinin B2 Receptor (B2BR)	IgE (High Affinity Receptor)
Interleukin-1 (IL-1)	Interleukin 1 Receptor (IL-1 R)
Interleukin-9 (IL-9)	Interleukin-9 Receptor (IL-9 R)
Interleukin-11 (IL-11)	Interleukin-11 Receptor (IL-11 R)
Inducible Nitric Oxide Synthase	Cyclooxygenase (COX)
Intracellular Adhesion Molecule 1 (ICAM-1)	Vascular Cellular Adhesion Molecule (VCAM)
Rantes	Endothelial Leukocyte Adhesion Molecule (ELAM-1)
Cyclooxygenase-2 (COX-2)	GM-CSF, Endothelin-1
Monocyte Activating Factor	Neutrophil Chemotactic Factor
Neutrophil Elastase	Defensin 1,2,3
Muscarinic Acetylcholine Receptors	Platelet Activating Factor
Tumor Necrosis Factor α	5-lipoxygenase
Phosphodiesterase IV	Substance P
Substance P Receptor	Histamine Receptor
Chymase	CCR-1 CC Chemokine Receptor
Interleukin-2 (IL-2)	Interleukin-4 (IL-4)
Interleukin-12 (IL-12)	Interleukin-5 (IL-5)
Interleukin-6 (IL-6)	Interleukin-7 (IL-7)
Interleukin-8 (IL-8)	Interleukin-12 Receptor (IL-12R)
Interleukin-7 Receptor (IL-7R)	Interleukin-1 (IL-1)
Interleukin-14 Receptor (IL-14R)	Interleukin-14
CCR-2 CC Chemokine Receptor	CCR-3 CC Chemokine Receptor
CCR-4 CC Chemokine Receptor	CCR-5 CC Chemokine Receptor
Prostanoid Receptors	GATA-3 Transcription Factor
Neutrophil Adherence Receptor	MAP Kinase
Interleukin-15 (IL-15)	Interleukin-15 Receptor (IL-15R)
Interleukin-11 (IL-11)	Interleukin-11 Receptor (IL-11R)
NFAT Transcription Factors	STAT 4
MIP-1α	MCP-2
MCP-3	MCP-4
Cyclophillin (A, B, etc.)	Phospholipase A2
Basic Fibroblast Growth Factor	Metalloproteinase

CSBP/p38 MAP Kinase	Tryptase Receptor
PDG2	Interleukin-3 (IL-3)
Interleukin-10 (IL-10)	Cyclosporin A - Binding Protein
FK506-Binding Protein	α4β1 Selectin
Fibronectin	α4β7 Selectin
cMad CAM-1	LFA-1 (CD11a/CD18)
PECAM-1	LFA-1 Selectin
C3bi	PSGL-1
E-Selectin	P-Selectin
CD-34	L-Selectin
p150,95	Mac-1 (CD11b/CD18)
Fucosyl transferase	VLA-4
CD-18/CD11a	CD11b/CD18
ICAM2 and ICAM3	C5a
CCR3 (Eotaxin Receptor)	CCR1, CCR2, CCR4, CCR5
LTB-4	AP-1 Transcription Factor
Protein kinase C	Cysteinyl Leukotriene Receptor
Tachykinnen Receptors (tach R)	IκB Kinase 1 & 2
Interleukin-2 Receptor (IL-2R)	(e.g., Substance P, NK-1 & NK-3 Receptors)
STAT 6	c-mas
NF-Interleukin-6 (NF-IL-6)	Interleukin-10 Receptor (IL-10R)
Interleukin-3 (IL-3)	Interleukin-2 Receptor (IL-2R)
Interleukin-13 (IL-13)	Interleukin-12 Receptor (IL-12R)
Interleukin-14 (IL-14)	Interleukin-6 Receptor (IL-6R)
Interleukin-16 (IL-16)	Interleukin-13 Receptor (IL-13R)
Medullasin	Interleukin-16 Receptor (IL-16R)
Adenosine A_1 Receptor (A_1 R)	Tryptase-I
Adenosine A_{2b} Receptor (A_{2b} R)	Adenosine A_3 Receptor (A_3 R)
β Tryptase	
Adenosine A_{2a} Receptor (A_{2a} R)	IgE Receptor β Subunit (IgE R β)
Fc-epsilon receptor CD23 antigen	IgE Receptor α Subunit (IgE R α)
IgE Receptor Fc Epsilon Receptor (IgERFc ζ R)	Substance P Receptor
Histidine decarboxylase	Tryptase-1
Prostaglandin D Synthase	Eosinophil Cationic Protein
Eosinophil Derived Neurotoxin	Eosinophil Peroxidase
Endothelial Nitric Oxide Synthase	Endothelial Monocyte Activating Factor
Neutrophil Oxidase Factor	Cathepsin G
Macrophage Inflammatory Protein-1-Alpha/Rantes Receptor	Interleukin-8 Receptor α Subunit (IL-8 R α)
	Substance P
Endothelin Receptor ET-B	Endothelin ETA Receptor

Examples of other targets are 5-lipoxygenase, α-Rantes receptor, Cathepsin G, CCR-1 CC Chemokine receptor, CCR-1 CC Chemokine receptor, CCCR-5 CC Chemokine receptor,, CD-11-CD11a, c-Mas, Endothelial Nitric Oxide Synthase, Endothelial receptor ET-B, Endothelin 1, Eosinophil Cationic Proetin, Eosinophil Derived Neurotoxin, Fc-e receptor II (CD 23 Antigen), Histidine Decarboxylase, Interleukin 10 (IL-10), IL-10 receptor, IL-11 receptor, IL-12, IL-12 receptor, IL-13, IL-13 receptor, IL-14 and its receptor, IL-15 and its receptor, IL-16 and its receptor, IL-6 and its receptor, IL-7 and its receptor, Intracellular Adhesion Molecule -2 (ICAM-2), ICAM-3, Medullasin, Neurokinin-3 receptor (NK-3 R), Neutrophil Oxidase Factor, Platelet Activating Factor receptor, Prostaglandin D Synthase, Protein Kinase c, P-Selectin Glycoprotein Ligand 1 (PSGL-1), Tryptase Activated receptor, IL-2 and its receptor, IL-3 and its receptor, IL-4 and its receptor, IL-5 and its receptor, IL-8 and its receptor, IL-9 and its receptor, Intracellular adhesion Molecule-1, Leukocyte Adhesion Glycoprotein, Leukotriene C-4 Synthase, Major Basic Protein, MCP-3, Monocyte Asctuating Factor, Muscarinic Acetylcholine receptors, Neurokinin-1 Receptor, Neutrophil Chemotactic Factor, Neutrophil Elastase, NfKB, Phosphodiesterase IV, Prostaglandin Receptor, P-selectin, Rantes, Stat-1, Stat-2, Stat-3, Substance P and its receptor, Tryptase, Tumor Necrosis Factor A, Vascular Cellular Adhesion Molecule, AP-1 Transcription Factor, Basic Fibroblast Growth Factor, C5a, CCR-2 CC Chemokine Receptor, CSBP-p38 MAP Kinase,

Cyclooxygenase-2 (COX-2), Cyclophilin (A, B, C, and the rest), Cyclosporin A Binding Protein, Cysteinyl Leukotriene Receptor, E-Selectin, Fibronectin, Fusosyl Transferase, GATAS-3 Transcription Factor, Granulocyte-Macrophage Stimulating Factor (GM-CSF), Histamine Receptor, IKB Kinase 1 and 2, nterleukin 7, L-Selectin, Mac-1 (CD11b and CD18), Mad CAM-1, Map Kinase, MCP-4, Metalloproteinase, MIP-1a, Neutrophil Adherence Receptors, NFAT Transcription Factors, NF-Interleukin-6 (NF-IL-6), Pecam-1,Phospholipase A2, Prostanoid Receptors, Stat-4, Stat-6, VLA-4, and others.

The oligos of this invention may be obtained by first selecting fragments of a target nucleic acid having at least 4 contiguous nucleic acids selected from the group consisting of G and C, and then obtaining a first oligonucleotide 4 to 60 nucleotides long which comprises the selected fragment and has a C and G nucleic acid content of up to and including about 15%. The latter step may be conducted by obtaining a second oligonucleotide 4 to 60 nucleotides long comprising a sequence which is anti-sense to the selected fragment, the second oligonucleotide having an adenosine base content of up to and including about 15%. This method may also comprise, when the selected fragment comprises at least one thymidine base, substituting an adenosine base in the corresponding nucleotide of the anti-sense fragment with a universal base selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have antagonist activity and less than about 0.3 of the adenosine base agonist activity at the adenosine A_1, A_{2b} and A_3 receptors, and heteroaromatic bases which have no activity or have an agonist activity at the adenosine A_{2a} receptor. The analogue heteroaromatic bases may be selected from all pyrimidines and purines, which may be substituted by O, halo, NH_2, SH, SO, SO_2, SO_3, COOH and branched and fused primary and secondary amino, alkyl, alkenyl, alkynyl, cycloalkyl, heterocycloalkyl, aryl, heteroaryl, alkoxy, alkenoxy, acyl, cycloacyl, arylacyl, alkynoxy, cycloalkoxy, aroyl, arylthio, arylsulfoxyl, halocycloalkyl, alkylcycloalkyl, alkenylcycloalkyl, alkynylcycloalkyl, haloaryl, alkylaryl, alkenylaryl, alkynylaryl, arylalkyl, arylalkenyl, arylalkynyl, arylcycloalkyl, which may be further substituted by O, halo, NH_2, primary, secondary and tertiary amine, SH, SO, SO_2, SO_3, cycloalkyl, heterocycloalkyl and heteroaryl. The pyrimidines and purines may be substituted at all positions as is known in the art, but preferred are those which are substituted at positions 1, 2, 3, 4, 7 and/or 8. More preferred are pyrimidines and purines such as theophylline, caffeine, dyphylline, etophylline, acephylline piperazine, bamifylline, enprofylline and xantine having the chemical formula



wherein R^1 and R^2 are independently H, alkyl, alkenyl or alkynyl and R^3 is H, aryl, dicycloalkyl, dicycloalkenyl, dicycloalkynyl, cycloalkyl, cycloalkenyl, cycloalkynyl, O-cycloalkyl, O-cycloalkenyl, O-cycloalkynyl, NH_2-alkylamino-ketoxyalkyloxy-aryl, mono and dialkylaminoalkyl-N-alkylamino-SO_2 aryl, among others.

The inventor reduced the adenosine content of the anti-sense oligos corresponding to the thymidines (T) present in the target RNA to less than about 15%, or fully eliminated A from the oligonucleotide sequence as a means for preventing their breakdown products from freeing adenosine into the lung tissue environment and, thereby, aggravating the subject's ailment and/or countering the beneficial effect of the administered agent.

By means of example, the Nf6B transcription factor may be selected as a target, and its mRNA or DNA searched for low thymidine (T) or desthymidine (desT) fragments. Only desT segments of the mRNA or DNA are selected which, in turn, will produce desA anti-sense as their complementary strand. When a number of RNA desT segments are found, the sequence of the anti-sense segments may be deduced. Typically, about 10 to 30 and even larger numbers of desA anti-sense sequences may be obtained. These anti-sense sequences may include some or all desA anti-sense oligonucleotide sequences corresponding to desT segments of the mRNA of the target, such as anyone of those shown in Table 1 above or Table 2 below. When this occurs, the anti-sense oligonucleotides found are said to be 100% A-free. For each of the original desA anti-sense oligonucleotide sequences corresponding to the target gene, e.g. the NF6B transcription factor, typically about 10 to 30 sequences

may be found within the target gene or RNA which have a low content of thymidine (RNA). In accordance with this invention, the selected fragment sequences may also contain a small number of thymidine (RNA) nucleotides within the secondary or tertiary or quaternary sequences. In some cases, a large adenosine content may suffice to render the anti-sense oligonucleotide less active or even inactive against the target. In accordance with this invention, these so called A non-fully desA sequences may preferably have a content of adenosine of less than about 15%, more preferably less than about 10%, and still more preferably less than 5%, and some even less than 2% adenosine. In some instances a higher content of adenosine is acceptable and the oligonucleotides are still active, particularly where the adenosine nucleotide may be Afixed@ or replaced with a AUniversal@ base that may base-pair with similar or equal affinity to two or more of the four nucleotide present in natural DNA: A, G, C, and T. A universal base is defined in this patent as any compound, more commonly an adenosine analogue, having the capacity to hybridize to thymidine, preferably having substantially reduced, or substantially lacking, ability to bind adenosine receptors. Alternatively, adenosine analogs which do not activate adenosine receptors, such as the adenosine A_1, A_{2b} and/or A_3 receptors, most preferably A_1 receptors, may be used. One example of a universal base is α-deoxyribofuranosol-(5-nitroindole), and an artisan will know how to select others. This Afixing@ step generates a further novel sequence, different from the one found in nature, that permits the anti-sense oligonucleotide to bind, preferably equally well, with the target RNA. An example of a universal base is 2-deoxyribosyl-(5-nitroindole). Other examples of universal bases are 3-nitropyrrole-2'-deoxynucleoside, 5-nitro-indole, 2-deoxyribosyl-(5-nitroindole), 2-deoxyribofuranosyl-(5-nitroindole), 2'-deoxyinosine, 2'-deoxynebularine, 6H, 8H-3,4-dihydropyrimido [4,5-c] oxazine-7-one and 2-amino-6-methoxyaminopurine. In addition to the above, Universal bases which may be substituted for any other base although with somewhat reduced hybridization potential, include 3-nitropyrrole 2'-deoxynucleoside 2-deoxyribofuranosyl-(5-nitroindole), 2'-deoxyinosine and 2'-deoxynebularine (Glen Research, Sterling, VA). More specific mismatch repairs may be made using "P" nucleotide, 6H, 8H-3, 4-dihydropyrimido[4,5-c] [1,2] oxazin-7-one, which base pairs with either guanine (G) or adenine (A) and "K" nucleotide, 2-amino-6-methoxyaminopurine, which base pairs with either cytidine (C) or thymidine (T), among others. Others which are known in the art are also suitable. See, for example, Loakes, D. and Brown, D. M., Nucl .Acids Res. 22:4039-4043 (1994); Ohtsuka, E. et al., J. Biol. Chem.260(5):2605-2608 (1985); Lin, P.K.T. and Brown, D. M., Nucleic Acids Res. 20(19):5149-5152 (1992; Nichols, R. et al., Nature 369(6480): 492-493 (1994); Rahmon , M. S. and Humayun, N. Z., Mutation Research 377 (2): 263-8 (1997); Amosova, O., et al., Nucleic Acids Res. 25 (!0): 1930-1934 (1997); Loakes D. & Brown, D. M., Nucleic Acids Res. 22 (20): 4039-4043 (1994), the entire sections relating to universal bases and their preparation and use in nucleic acid binding is inceorporated herein by reference.

When non-fully desT sequences are found in the naturally occurring target, they typically are selected so that about 1 to 3 universal base substitutions will suffice to obtain a 100% AdesA@ anti-sense oligonucleotide. Thus, the present method provides either anti-sense oligonucleotides to different targets which are low in, or devoid of, A content, as well as anti-sense oligonucleotides where one or more adenosine nucleotides, e. g. about 1 to 3, or more, may be Afixed@ by replacement with a AUniversal@ base. Universal bases are known in the art and need not be listed herein. An artisan will know which bases may act as universal bases, and replace them for A.

The present approach to the design of anti-sense oligonucleotide approach is also applicable to a variety of other diseases or conditions, including other inflammatory diseases, such as cystic fibrosis, chronic obstructive pulmonary disease, chronic bronchitis, pulmonary hypertension, cancers, including those which metastasize to the lung, such as breast cancer, colon cancer, respiratory distress syndrome, prostate cancer, pancreatic cancer, kidney cancer, lymphomas, melanomas, hepatocellular carcinomas, etc.

As used herein, the term "treat" or "treating" asthma or other respiratory and inflammatory conditions or diseases refers to a treatment which decreases the likelihood that the subject administered such treatment will manifest symptoms of a respiratory or inflammatory lung disease or other lung conditions. The term "down-regulate" refers to inducing a decrease in production, secretion or availability (and thus a decrease in concentration) of the targeted intracellular protein.

The present invention is concerned primarily with the treatment of vertebrates, and within this group, of mammals, including human and non-human simians, wild and domesticated animals, marine and land animals, household pets, and zoo animals, for example, felines, canines, equines, pachiderms, cetaceans, and still more preferably to human subjects. One particularly suitable application of this technology is for veterinary purposes,

and includes all types of small and large animals in the care of a veterinarian, including wild animals, marine animals, household animals, zoo animals, and the like. Targeted genes and proteins are preferably mammalian, and the sequences targeted are preferably of the same species as the subject being treated. Although in many instances, targets of a different species are also suitable, particularly those segments of the target RNA or gene that display greater than about 45% homology, preferably greater than about 85% homology, still more preferably greater than about 95% homology, with the recipient's sequence. A preferable group of agents is composed of des-A anti-sense oligos. Another preferred group is composed of non-fully desA oligonucleotides, where one or more adenosine bases are replaced with universal bases.

The terms "anti-sense" oligonucleotides generally refers to small, synthetic oligonucleotides, resembling single-stranded DNA, which in this patent are applied to the inhibition of gene expression by inhibition of a target messenger RNA (mRNA). See, Milligan, J. F. et al., J. Med. Chem. 36(14), 1923-1937 (1993), the relevant portion of which is hereby incorporated in its entirety by reference. The present agents inhibit gene expression of target genes, such as those of the adenosine A_1 A_{2a}, A_{2b}, or A_3 receptors, CCR3 (chemical receptor 320, also known as the eotaxin receptor), VCAM (vascular cell adhesion molecule), eonophil receptor, bradykinin 2B receptor, and many others listed in Table 1 above. This is generally attained by hybridization of the anti-sense oligonucleotides to coding (sense) sequences of a targeted messenger RNA (mRNA), as is known in the art. The exogenously administered agents of the invention decrease the levels of mRNA and protein encoded by the target gene and/or cause changes in the growth characteristics or shapes of the thus treated cells. See, Milligan et al. (1993); Helene, C. and Toulme, J. Biochim. Biophys. Acta 1049, 99-125 (1990); Cohen, J. S. D., Ed., Oligodeoxynucleotides as Anti-sense Inhibitors of Gene Expression; CRC Press: Boca Raton, FL (1987), the relevant portion of which is hereby incorporated in its entirety by reference. As used herein, "anti-sense oligonucleotide" is generally a short sequence of synthetic nucleotide that (1) hybridizes to any segment of a mRNA encoding a targeted protein under appropriate hybridization conditions, and which (2) upon hybridization causes a decrease in gene expression of the targeted protein.

The terms Ades-adenosine@ (desA) and Ades-thymidine@ (desT) refer to oligonucleotides substantially lacking either adenosine (desA) or thymidine (desT). In some instances, the des T sequences are naturally occurring, and in others they may result from substitution of an undesirable nucleotide (A) by another one lacking its undesirable activity. In the present context, the substitution is generally accomplished by substitution of A with a Auniversal base@, as is known in the art.

The mRNA sequence of the targeted protein may be derived from the nucleotide sequence of the gene expressing the protein. For example, the sequence of the genomic human adenosine A_1 receptor and that of the rat and human adenosine A_3 receptors are known. See, US Pat. No. 5,320,962; Zhou, F., et al., Proc. Nat'l Acad. Sci. (USA) 89 :7432 (1992); Jacobson, M.A., et al., U.K. Pat. Appl. No. 9304582.1. The sequence of the adenosine A_{2b} receptor gene is also known. See, Salvatore, C. A., Luneau, C. J., Johnson, R. G. and Jacobson, M., Genomics (1995), the relevant portion of which is hereby incorporated in its entirety by reference. The sequences of many of the exemplary target genes are also known. See, GenBank, NIH. The sequences of those genes whose sequences are not yet available may be obtained by isolating the target segments applying technology known in the art. Once the sequence of the gene, its RNA and/or the protein are known, an anti-sense oligonucleotides may be produced according to this invention as described above to reduce the production of the targeted protein in accordance with standard techniques.

In one aspect of this invention, the anti-sense oligonucleotide has a sequence which specifically binds to a portion or segment of an mRNA molecule which encodes a protein associated with a disease or condition associated with impeded breathing, lung inflammation, airway obstruction, bronchitis, and the like. One effect of this binding is to reduce or even prevent the translation of the corresponding mRNA and, thereby, reduce the available amount of target protein in the subject's lung.

In one preferred embodiment of this invention, the phosphodiester residues of the anti-sense oligonucleotide are modified or substituted. Chemical analogs of oligonucleotides with modified or substituted phosphodiester residues, e.g., to the methylphosphonate, the phosphotriester, the phosphorothioate, the phosphorodithioate, or the phosphoramidate, which increase the in vivo stability of the oligonucleotide are particularly preferred. The naturally occurring phosphodiester linkages of oligonucleotides are susceptible to some degree of degradation by cellular nucleases. Many of the residues proposed herein, on the contrary, are highly resistant to nuclease degradation. See Milligan et al., and Cohen, J. S. D., supra. In another preferred

embodiment of the invention, the oligonucleotides may be protected from degradation by adding a "3'-end cap" by which nuclease-resistant linkages are substituted for phosphodiester linkages at the 3' end of the oligonucleotide. See, Tidd, D. M. and Warenius, H.M., Be. J. Cancer 60: 343-350 (1989); Shaw, J.P. et al., Nucleic Acids Res. 19: 747-750 (1991), the relevant section of which are incorporated in their entireties herein by reference. Phosphoramidates, phosphorothioates, and methylphosphonate linkages all function adequately in this manner for the purposes of this invention. The more extensive the modification of the phosphodiester backbone the more stable the resulting agent, and in many instances the higher their RNA affinity and cellular permeation. See Milligan, et al., supra. Thus, the number of residues which may be modified or substituted will vary depending on the need, target, and route of administration, and may be from 1 to all the residues, to any number in between. Many different methods for replacing the entire phosphodiester backbone with novel linkages are known. See, Millikan et al, supra. Preferred backbone analogue residues include phosphorothioate, methylphosphonate, phosphotriester, thioformacetal, phosphorodithioate, phosphoramidate, formacetal boranophosphate, 3'-thioformacetal, 5'-thioether, carbonate, 5'-N-carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite., 2'-O methyl, sulfoxide, sulfide, hydroxylamine, methylene(methylimino) (MMI), and methyleneoxy(methylimino) (MOMI) residues. Phosphorothioate and methylphosphonate-modified oligonucleotides are particularly preferred due to their availability through automated oligonucleotide synthesis. See, Millikan et al, supra. Where appropriate, the agent of this invention may be administered in the form of their pharmaceutically acceptable salts, or as a mixture of the anti-sense oligonucleotide and its salt. In another embodiment of this invention, a mixture of different anti-sense oligonucleotides or their pharmaceutically acceptable slats is administered.

The agents of this invention have the capacity to attenuate the expression of one target mRNA and/or to enhance or attenuate the activity of one pathway. By means of example, the present method may be practiced by identifying all possible deoxyribonucleotide segments which are low in thymidine (T) or deoxynucleotide segments low in adenosine (A) of about 7 or more mononucleotides, preferably up to about 60 mononucleotides, more preferably about 10 to about 36 mononucleotides, and still more preferably about 12 to about 21 mononucleotides, in a target mRNA or a gene, respectively. This may be attained by searching for mononucleotide segments within a target sequence which are low in, or lack thymidine (RNA), a nucleotide which is complementary to adenosine, or that are low in adenosine (gene), that are 7 or more nucleotides long. In most cases, this search typically results in about 10 to 30 such sequences, I. e. naturally lacking or having less than about 40% adenosine, anti-sense oligonucleotides of varying lengths for a typical target mRNA of average length, i. e., about 1800 nucleotides long. Those with high content of T or A, respectively, may be fixed by substitution of a universal base for one or more As.

The agent(s) of this invention may be of any suitable length, including but not limited to, about 7 to about 60 nucleotides long, preferably about 12 to about 45, more preferably up to about 30 nucleotides long, and still more preferably up to about 21, although they may be of other lengths as well, depending on the particular target and the mode of delivery. The agent(s) of the invention may be directed to any and all segments of a target RNA. One preferred group of agent(s) includes those directed to an mRNA region containing a junction between an intron and an exon. Where the agent is directed to an intron/exon junction, it may either entirely overlie the junction or it may be sufficiently close to the junction to inhibit the splicing-out of the intervening exon during processing of precursor mRNA to mature mRNA, e.g. with the 3' or 5' terminus of the anti-sense oligonucleotide being positioned within about, for example, within about 2 to 10, preferably about 3 to 5, nucleotide of the intron/exon junction. Also preferred are anti-sense oligonucleotides which overlap the initiation codon, and those near the 5' and 3' termini of the coding region.

Table 2 below provides a selected number of targets to which the agents of the invention are effectively applied. Others, however, may also be targeted.

Table 2: Cancer Targets

Transf rming Oncogenes	Therapy Targets
ras	thymidylate synthetase
src	thymidylate synthetase
myc	dihydrofolate reductase
bcl-2	thymidine kinase
	deoxycytidine kinase
	ribonucleotide reductase

A group of preferred targets for the treatment of cancer are genes associated with any of different types of cancers, or those generally known to be associated with malignancies, whether they are regulatory or involved in the production of RNA and/or proteins. Examples are transforming oncogenes, including, but not limited to, ras, src, myc, and bcl-2, among others. Other targets are those to which present cancer chemotherapeutic agents are directed to, such as various enzymes, primarily, although not exclusively, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, ribonucleotide reductase, and the like.

The present technology is particularly useful in the treatment of cancer ailments given that traditional cancer therapies are fraught with the unresolved problem of selectively killing cancer cells while preserving normal living cells from the devastating effects of treatments such as chemotherapy, radiotherapy, and the like. The present technology provides the ability of selectively attenuating or enhancing a desired pathway or target. This approach provides a significant advantage over standard treatments of cancer because it permits the selection of a pathway, including primary, secondary and possibly tertiary targets, which are not generally expressed simultaneously in normal cells. Thus, the present agent may be administered to a subject to cause a selective increase in toxicity within tumor cells that, for instance, express all three targets while normal cells that may expresses only one or two of the targets will be significantly less affected or even spared.

A group of preferred targets for the treatment of cancers are genes associated with different types of cancers, or those generally known to be associated with malignancies, whether they are regulatory or involved in the production of RNA and/or proteins. Examples are transforming oncogenes, including, but not limited to, ras, src, myc, and bcl-2, among others. Other targets are those to which present cancer chemotherapeutic agents are directed to, such as various enzymes, primarily, although not exclusively, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, ribonucleotide reductase, and the like.

In one embodiment, at least one of the mRNAs to which the MTA oligo of the invention is targeted encodes a protein such as transcription factors, stimulating and activating factors, intracellular and extracellular receptors and peptide transmitters in general, interleukins, interleukin receptors, chemokines, chemokine receptors, endogenously produced specific and non-specific enzymes, immunoglobulins, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules, defensines, growth factors, vasoactive peptides and receptors, and binding proteins, among others; or the mRNA is corresponding to an oncogene and other genes associated with various diseases or conditions.

Examples of target proteins are eotaxin, major basic protein, preproendothelin, eosinophil cationic protein, P-selectin, STAT 4, MIP-1α, MCP-2, MCP-3, MCP-4, STAT 6, c-mas, NF-IL-6, cyclophillins, PDG2, cyclosporin A-binding protein, FK5-binding protein, fibronectin, LFA-1 (CD11a/CD18), PECAM-1, C3bi, PSGL-1,CD-34, substance P, p150,95, Mac-1 (CD11b/CD18), VLA-4, CD-18/CD11a, CD11b/CD18, C5a, CCR1, CCR2, CCR4, CCR5, and LTB-4, among others. Others are, however, suitable, as well.

In another embodiment, at least one of the mRNAs to which the MTA oligo is targeted encodes intracellular and extracellular receptors and peptide transmitters such as sympathomimetic receptors, parasympathetic receptors, GABA receptors, adenosine receptors, bradykinin receptors, insulin receptors, glucagon receptors, prostaglandin receptors, thyroid receptors, androgen receptors, anabolic receptors, estrogen receptors, progesterone receptors, receptors associated with the coagulation cascade, adenohypophyseal receptors,

adenohypophyseal peptide transmitters, and histamine receptors (HisR), among others. However others are also contemplated.

The encoded sympathomimetic receptors and parasympathomimetic receptors include acetylcholinesterase receptors (AcChaseR) acetylcholine receptors (AcChR), atropine receptors, muscarinic receptors, epinephrine receptors (EpiR), dopamine receptors (DOPAR), and norepinephrine receptors (NEpiR), among others. Further examples of encoded receptors are adenosine A_1 receptor, adenosine A_2B receptor, adenosine A_3 receptor, endothelin receptor A, endothellin receptor B, IgE high affinity receptor, muscarinic acetylcholine receptors, substance P receptor, histamine receptor, CCR-1 CC chemokine receptor, CCR-2 CC chemokine receptor, CCR-3 CC chemokine receptor (Eotaxin Receptor), interleukin-1β receptor (IL-1βR), interleukin-1 receptor (IL-1R), interleukin-1β receptor (IL-1βR), interleukin-3 receptor (IL-3R), CCR-4 CC chemokine receptor, cysteinyl leukotriene receptors, prostanoid receptors, GATA-3 transcription factor receptor, interleukin-1 receptor (IL-1R), interleukin-4 receptor (IL-4R), interleukin-5 receptor (IL-5R), interleukin-8 receptor (IL-8R), interleukin-9 receptor (IL-9R), interleukin-11 receptor (IL-11R), bradykinin B2 receptor, sympathomimetic receptors, parasympathomimetic receptors, GABA receptors, adenosine receptors, bradykinin receptors, insulin receptors, glucagon receptors, prostaglandin receptors, thyroid receptors, androgen receptors, anabolic receptors, estrogen receptors, progesterone receptors, receptors associated with the coagulation cascade, adenohypophyseal receptors, and histamine receptors (HisR). Others are also contemplated even though not listed herein.

The encoded enzymes for development of the MTA oligos of the invention include synthetases, kinases, oxidases, phosphatases, reductases, polysaccharide, triglyceride, and protein hydrolases, esterases, elastases, and , polysaccharide, triglyceride, lipid, and protein synthases, among others. Examples of target enzymes are tryptase, inducible nitric oxide synthase, cyclooxygenase (Cox), MAP kinase, eosinophil peroxidase, β2-adrenergic receptor kinase, leukotriene c-4 synthase, 5-lipooxygenase, phosphodiesterase IV, metalloproteinase, tryptase, CSBP/p38 MAP kinase, neutrophil elastase, phospholipase A2, cyclooxygenase 2 (Cox-2), fucosyl transferase, chymase, protein kinase C, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, and ribonucleotide reductase, among others. Any enzyme associated with a disease or condition , however, is suitable as a target for this invention.

Suitable encoded factors for application of this invention are, among others, Nf6B transcription factor, granulocyte macrophage colony stimulating factor (GM-CSF), AP-1 transcription factor, GATA-3 transcription factor, monocyte activating factor, neutrophil chemotactic factor, granulocyte/macrophage colony-stimulating-factor (G-CSF), NFAT transcription factors, platelet activating factor, tumor necrosis factor α (TNF α), and basic fibroblast growth factor (BFGF). Additional factors are also within the invention even though not specifically mentioned.

Suitable adhesion molecules for use with this invention include intracellular adhesion molecules 1 (ICAM-1), 2 (ICAM-2) and 3 (ICAM-3), vascular cellular adhesion molecule (VCAM), endothelial leukocyte adhesion molecule-1 (ELAM-1), neutrophil adherence receptor, mad CAM-1, and the like. Other known and unknown factors (at this time) may also be targeted herein.

Among the cytokines, lymphokines and chemokines preferred are interleukin-1 (IL-1), interleukin-1β (IL-1)interleukin-3 (IL-3), interleukin-4 (IL-4), interleukin-5 (IL-5), interleukin-8 (IL-8), interleukin-9 (IL-9), interleukin-11 (IL-11),CCR-5 CC chemokine, and Rantes. Others, however, may also be targeted, as they are known to be involved in specific diseases or conditions to be treated, or for their generic activities, such as inflammation.

Examples of defensins for the practice of this invention are defensin 1, defensin 2, and defensin 3, and of selectins are α4β1 selectin, α4β7 selectin, LFA-1 selectin, E-selectin, P-selectin, and L-selectin. Examples of oncogenes, although not an all inclusive list, are ras, src, myc, and bcl-2. Others, however, are also suitable for use with this invention.

In another preferred embodiment, the composition and formulations further comprise one or more surfactants. Suitable surfactants or surfactant components for enhancing the uptake of the anti-sense oligonucleotides of the invention include synthetic and natural as well as full and truncated forms of surfactant protein A, surfactant protein B, surfactant protein C, surfactant protein D and surfactant Protein E, di-saturated phosphatidylcholine (other than dipalmitoyl), dipalmitoylphosphatidylcholine, phosphatidylcholine, phosphatidylglycerol, phosphatidylinositol, phosphatidylethanolamine, phosphatidylserine; phosphatidic acid,

ubiquinones, lysophosphatidylethanolamine, lysophosphatidylcholine, palmitoyl-lysophosphatidylcholine, dehydroepiandrosterone, dolichols, sulfatidic acid, glycerol-3-phosphate, dihydroxyacetone phosphate, glycerol, glycero-3-phosphocholine, dihydroxyacetone, palmitate, cytidine diphosphate (CDP) diacylglycerol, CDP choline, choline, choline phosphate; as well as natural and artificial lamelar bodies which are the natural carrier vehicles for the components of surfactant, omega-3 fatty acids, polyenic acid, polyenoic acid, lecithin, palmitinic acid, non-ionic block copolymers of ethylene or propylene oxides, polyoxypropylene, monomeric and polymeric, polyoxyethylene, monomeric and polymeric, poly (vinyl amine) with dextran and/or alkanoyl side chains, Brij 35, Triton X-100 and synthetic surfactants ALEC, Exosurf, Survan and Atovaquone, among others. However, others may also be employed. These surfactants may be useed either as single or part of a multiple component surfactant in a formulation, or as covalently bound additions to the 5' and/or 3' ends ofthe anti-sense oligonucleotides (oligos).

The agents administered in accordance with this invention are preferably designed to be anti-sense to target genes and/or mRNAs related in origin to the species to which it is to be administered. When treating humans, the agents are preferably designed to be anti-sense to a human gene or RNA. The agents of the invention encompass oligonucleotides which are anti-sense to naturally occurring DNA and/or RNA sequences, fragments thereof of up to a length of one (1) base less than the targeted sequence, preferably at least about 7 nucleotides long, oligos having only over about 0.02%, more preferably over about 0.1%, still more preferably over about 1%, and even more preferably over about 4% adenosine nucleotides, and up to about 30%, more preferably up to about 15%, still more preferably up to about 10% and even more preferably up to about 5%, adenosine nucleotide, or lacking adenosine altogether, and oligos in which one or more of the adenosine nucleotides have been replaced with so-called universal bases, which may pair up with thymidine nucleotides but fail to substantially trigger adenosine receptor activity. Examples of human sequences and fragments, which are not limiting, of anti-sense oligonucleotide of the invention are the following fragments as well as shorter segments of the fragments and of the full gene or mRNA coding sequences, exons and intron-exon junctions encompassing preferably 7, 10, 15, 18 to 21, 24, 27, 30, n-1 nucleotides for each sequence, where n is the sequence's total number of nucleotides. These fragments may be selected from any portion of the longer oligo, for example, from the middle, 5'- end, 3'- end or starting at any other site of the original sequence. Of particular importance are fragments of low adenosine nucleotide content, that is, those fragments containing less than or about 30%, preferably less than or about 15%, more preferably less than or about 10%, and even more preferably less than or about 5%, and most preferably those devoid of adenosine nucleotide, either by choice or by replacement with a universal base in accordance with this invention. The agent of the invention includes as a most preferred group sequences and their fragments where one or more adenosines present in the sequence have been replaced by a universal base (B), as exemplified here. Similarly, also encompassed are all shorter fragments of the B-containing fragments designed by substitution of B(s) for adenosine(s) (A(s)) contained in the sequences, fragments thereof or segments thereof, as described above. A limited list of sequences and fragments is provided below.

Some of the examples of anti-sense oligonucleotide sequence fragments target the initiation codon of the respective gene, and in some cases adenosine is substituted with a universal base adenosine analogue denoted as "B", which lacks ability to bind to the adenosine A_1 and/or A_3 receptors. In fact, such replacement nucleotide acts as a "spacer". In fact, in all examples provided, whether it is an A or a B written in, either one of these may be substituted. In fact, what this means is that if an A is present A denotes adenosine or any universal base which may substitute for it, and id B is written in it also signifies adenosine or any universal base. Many of the examples shown below provide one such sequence and many fragments overlapping the initiation codon, preferably wherein the number of nucleotides n is about 7, about 10, about 12, about 15, about 18, about 21 and up to about 28, about 35, about 40, about 50, about 60. It may also be generally said that for the exemplary sequences B is adenosine or a universal base as well as an adenosine A2a receptor agonist, or adenosine A1, A2b or A3 receptor antagonist.

Human Receptor-related Antisense Polvnucleotide

5'-GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGGG C TGCTTTTCT TTTCTGGGCC TCTGTGGTCT GTTTTTTTCT GGCCCTGCTG GGGCGCTCTC CGCCGCCCGC CTGGCTCCCG GBGCCCBTGB TGGGCBTGCC GTGGTTCTTG CCCTCCTTTG GCTGCCGTGC CCGCTCCCCG GCCTCCTGGC GGGTGGCCGT TGGGCCCGTG TTCCCCTGGG GCCTGGGGCT CCCTTCTCTC GCCCTTCTTG CTGGGCCTCT GCTGCTGCTG GTGCTGTGGC CCCCGTACA CCGAGGAGCC CATGATGGGC ATGCCACAGA CGACAGGCGT BCBCCGBGGB GCCCBTGBTG GGCBTGCCBC BGBCGBCBGG C GGC GCC GTG CCG CGT CTT GGT GGC GGC GG GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC GTT CGC GCC CGC GCG GGG CCC

CTC CGG TCC CGG GTC GGG GCC CCC CGC GGC C GCC TCG GGG CTG GGG CGC TGG TGG CCG GG CCG CGC CTC CGC
CTG CCG CTT CTG GCT GGG CCC CGG GCG CCC CCT CCC CTC TTG CTC GGG TCC CCG TG ACA GCG CGT CCT GTG TCT
CCA GCA GCA TGG CCG GGC CAG CTG GGC CCC BCB GCG CGT CCT GTG TCT CCB GCB GCB TGG CCG GGC CBG CTG
GGC CCC ACA GAG CAG TGC TGT TGT TGG GCA TCT TGC CTT CCC AGG G BCB GBG CB TGC TGT TGT TGG GCB TCT
TGC CTT CCC BGG GCC CTT TTC TGG TGG GGT GGT GCT GTT GTT GGG CTT TCT TCT GTT CCC BCB GBG CBG TGC TGT
TGT TGG GCB TCT TGC CTT CCC BGG GCC CTT TTC TGG TGG GGT GGT GCT GTT GTT GGG C TTT CTT CTG TTC CC TTT
CCC CTG GGT CTT CC CTC CTG CTC TTT TTT C ATT TGC TCT CCT ATT ACT TTC TGT GTC CAT TTT TTC ATT AAC CGA
GCT GT BTT TGC TCT CCT BTT BCT TTC TGT GTC CBT TTT TTC BTT BBC CGB GCT GT GCC TGT GTC TGT CCT CCT GCT
TCG TTC CTC TCG TTC CTG CTT GGT GCC CTT GCC G GTC CTG CTC CTC CGG GCT GTG G GTC GTG GCC CTG GCT CCG
GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG C GGG TCT TGC TCT GGG CCT GGC TGT GGC CGT
GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC TCT CTG AAT ATT GAC CTT CCT CCA TGG CGG TCC TGC TTG
GAT TCT CCC GA TCT CTG BBT BTT GBC CTT CCT CCB TGG CGG TCC TGC TTG GBT TCT CCC GB GCC TTT CCT GGT
TCT CTT GTT GTT TTT GGG GTT TGG CTT ACA GTA GAG TAG GGG ATT CCA TGG CAG GAG CCA TCT TCT TCA TGG
ACT CC TTC AAG GAG ACC TTA GGT TTC TGA GGG ACT GCT AAC ACG CCA TCT GGA GC BCB GTB GBG TBG GGG BTT
CCB TGG CBG GBG CCB TCT TCT TCB TGG BCT CC TTC BBG GBG BCC TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB
TCT GGB GC GTT GTT TTT GGG GTT TGG CTT GCC TTT CCT GGT TCT CTT BCB GTB GBG TBG GGG BTT CCB TGG CBG
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Human Enzyme-related Antisense Polynucleotide

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Human Factor Related Anti-sense Oligonucleotide

5'-CCT CCT TCC TGG TCT GTC TGC CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC CBG TCT CTG BGC TGT GGC GCC CTG CTG CTC TTT CTG CT TCC CTT GGT GGG TTG GGC C GCT GGT TGT TCT GGG GTT C TTG CTG CCC CTT CTG TCC C TGT TTG CTG GTG TCT GCG C CCC CBB CBG BBG BBG CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC TGT GCG CTC GGC CTG GTC CCG G GGG TCT CCT CTT GTT GTT GC TTG CGC CTC CTG CTG GGG GT CC CTC TGT TCT TGT TTT GGG GGC GGG CCC GGC CGT TGT CTT G GTT TGG GGG TTT CCG TTG GGG TTC TCC TGG CCC GGG CCT TGC CC GGC CGT GGT CCC GGC TTC GTTCCT GTC TCC GTC TCG GCT CTT CTG GGG CCT TGC GCT GTC TTT GGT G GCB CCG TCC BGT GBT GGT GCG GTB CTT GTC GCT GCB GCG CTC GGC CTG GTC CCG GBG BGC GCG CGG GCC GGG GGC TGC TGG G GGT TGG CCC GGG GTG CCC C GCC GCT GGG TGC CCT CGT CCT CTG CGG TC GTG TCT CCT GGC TCT GGT TCC CC GCT GCG CCC GTT GTC CTC TGG GGT GGC CTT C GCT CCC GGG TCT GGT TCT TGT GT TGG GGG TCC CTT TTT GGG CCT GTT GT GGC GTG GCT TGT GTG TTC GGT TTC TGC CCT GTC CTC CGG CGT CCC CGG BGC CTC CCC GGG GCB GGB TGB CTT TTG BGG GGG BCB CBG BTG TCT GGG CBT TGC CBG GTC CTG GGB BCB GBG CCC CGB GCB GGB CCB GGB GTG CGG GCB GCG CGG GCC GGG GGC TGC TGG GBG CCB TBG CGB GGC TGB G CCT CTT TTC TGT TTT TCC C CTC TGC CTT TGT TTG GGT TCG CTT CCT TTC TGC TTC TTC C CTG TGT CTC CTG TCT CCG CTT TTT TCT TC GTC TTT GTT GTT TTC TCT TCC TTG CTG BGC BBG BTB TCT BGB TTC TGG GGT GGT CTC GBT TTT BBBB GCT TGB GBB GCT GCB BBC BTT BTC CBB BGT BTB TTT GBG GCT CCB BGG BTC BCG BCC BTC TTC CCB GGC BTT TTB BGT TGC TGT CGT BBG TGB GBG CTG BGB GBB BCT GTG BBG CBB TCB TGB CTT CBB GBG TTC TTT TCB CCC GTT CTT GGC TTC TTC TGT C CGT TGG CTT CTC GTT GTC CC TGT GGG CTT CTC GTT GTC CC CCC TTC GGG GGC TGG TGG GGC CGT CCT TGC CTG CTG G GTT CTT GGC TTC TTC TGT CCG T TGG CTT CTC GTT GTC CC TGT GGG CTT CTC GTT GTC CC CCC TTC GGG GGC TGG TGG GGC CGT CCT TGC CTG CTG G TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT CTT TTC TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT CTT TTC CTC TGT CTT GTT CTG GTC CTT CGT GGG GCT CTG TGT CGC GTG G GTG CGG CCG TGG CC GGC GGB CCB GGB GTT GGB GCB GGB GCB GGB CGG GCB GGC GGC TCB TGT TTG GBT CGG CBG GBG GCB CTC CTC TGG TTG GCT TCC TTC GCC GGC BCB TGC TBG CBG GBB GBB CBG BGG GGG BBG CBG TTG GGB GGT GBG BCC CBT TBB TBG GTG TCG B TCCCTGTTTC CCCCCTTTCG TTCTGCGTTT GCCTTTGGCG TTTTTTGTTT GTTTTCTCTC TCCGTCTTTC TTCTCCCCT GTGGGBBTTT CTGTGGGGBT GGCBTBCBCG TBGGCBGCTC CBBGBGCTBG CBBBCTCBBB TGCBGBBGCB TCCTCBTGGC TCTGBBBCGG TGGGAATTTC TGTGGGGBTG GCATACACGT AGGCAGCTCC AAGAGCTAGC AAACTCAAAT GCAGAAGCATC CTCATGGCTC TGAAACG GGGGGTGGCT TCCTGCCGCG TCTCTGGGCC GTCCCGTCCC TCGGCCCCGC GCCGCGCTCG GCTCCTCTCC CTCTGGCCCG GCTCGGGGCG GGGCGGGGCG GTGGGCGGGC GGCGCTGCCC TGCGCGCGGC GCTGGCCCCT GCTGGCCGTC GGCTGCGCGC TGCTGGCTGC CCTGCTGGCC GCGCCGGGGC CTGTCCGCCT CTGCGGGCGC TGTCTCCTGG CTTGTCTTCC GGCTCTTCTG CTGGGGTGGG GCTGGGCGGC

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Human Adenosine A_1 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG TGCCCGGGAA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT CATCGTCTCG CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC CTCATGGTTG CCTGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC CCCCGGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG CCCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGGG AGCCCGTGAT CAAGTGCGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT GTGGGTGCTG CCCCCGCTTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTCGGC CTCCTCCGGC GACCCGCAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC CCTCATCCTC TTCCTCTTTG CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC CCTCTTCTGC CCGTCCTGCC ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC TCGGCCATGA ACCCCATTGT CTATGCCTTC CGCATCCAGA AGTTCCGCGT CACCTTCCTT AAGATTTGGA ATGACCATTT CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA GAAGAGAGGC CTGATGACTA G ATGAGTGTCA GAAGTGTGAA GGGTGCCTGT TCTGAATCCC AGAGCCTCCT CTCCCTCTGT GAGGCTGGCA GGTGAGGAAG GGTTTAACCT CACTGGAAGG AATCCCTGGA GCTAGCGGCT GCTGAAGGCG TCGAGGTGTG GGGGCACTTG GACAGAACAG TCAGGCAGCC GGGAGCTCTG CCAGCTTTGG TGACCTTGGG CCGGGCTGGG AGCGCTGCGG CGGGAGCCGG AGGACTATGA GCTGCCGCGC GTTGTCCAGA GCCCAGCCCA GCCCTACGCG CGCGGCCCGG AGCTCTGTTC CCTGGAACTT TGGGCACTGC CTCTGGGACC CCTGCCGGCC AGCAGGCAGG ATGGTGCTTG CCTCGTGCCC CTTGGTGCCC GTCTGCTGAT GTGCCCAGCC TGTGCCCGCC ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG TGCCCGGGAA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT CATCGTGTCG CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC CTCATGGTTG CCTGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC CCCCGGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG ACCCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGGG AGCCCGTGAT CAAGTGCGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT GTGGGTGCTG CCCCCGCTTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTCGGC CTCCTCCGGC GACCCGCAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC CCTCATCCTC TTCCTCTTTG CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC CCTCTTCTGC CCGTCCTGCC ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC TCGGCCATGA

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GAGAAGGTCA TCAGCATGGA GTACATGGTC TACTTCAACT TCTTTGTGTG GGTGCTGCCC CCGCTTCTCC TCATGGTCCT
CATCTACCTG GAGGTCTTCT ACCTAATCCG CAAGCAGCTC AACAAGAAGG TGTCGGCCTC CTCCGGCGAC CCGCAGAAGT
ACTATGGGAA GGAGCTGAAG ATCGCCAAGT CGCTGGCCCT CATCCTCTTC CTCTTTGCCC TCAGCTGGCT GCCTTTGCAC
ATCCTCAACT GCATCACCCT CTTCTGCCCG TCCTGCCACA AGCCCAGCAT CCTTACCTAC ATTGCCATCT TCCTCACGCA
CGGCAACTCG GCCATGAACC CCATTGTCTA TGCCTTCCGC ATCCAGAAGT TCCGCGTCAC CTTCCTTAAG ATTTGGAATG
ACCATTTCCG CTGCCAGCCT GCACCTCCCA TTGACGAGGA TCTCCCAGAA GAGAGGCCTG ATGACTAGAC CCCGCCTTCC

GCTCCCACCG CCCACATCCA GTGGGGTCTC AGTCCAGTCC TCACATGCCC GCTGTCCCAG GGGTCTCCCT GAGCCTGCCC CAGCTGGGCT GTTGGCTGGG GGCATGGGGG AGGCTCTGAA GAGATACCCA CAGAGTGTGG TCCCTCCACT AGGAGTTAAC TACCCTACAC CTCTGGGCCC TGCAGGAGGC CTGGGAGGGC AAGGGTCCTA CGGAGGGACC AGGTGTCTAG AGGCAACAGT GTTCTGAGCC CCCACCTGCC TGACCATCCC ATGAGCAGTC CAGAGCTTCA GGGCTGGGCA GGTCCTGGGG AGGCTGAGAC TGCAGAGGAG CCACCTGGGC TGGGAGAAGG TGCTTGGGCT TCTGCGGTGA GGCAGGGGAG TCTGCTTGTC TTAGATGTTG GTGGTGCAGC CCCAGGACCA AGCTTAAGGA GAGGAGAGCA TCTGCTCTGA GACGGATGGA AGGAGAGAGG TTGAGGATGC ACTGGCCTGT TCTGTAGGAG AGACTGGCCA GA -3' **(FRAG. NO:_)(SEQ. ID NO: 2434)**

5'- ATGAGTGTCA GAAGTGTGAA GGGTGCCTGT TCTGAATCCC AGAGCCTCCT CTCCCTCTGT GAGGCTGGCA GGTGAGGAAG GGTTTAACCT CACTGGAAGG AATCCCTGGA GCTAGCGGCT GCTGAAGGCG TCGAGGTGTG GGGGCACTTG GACAGAACAG TCAGGCAGCC GGGAGCTCTG CCAGCTTTGG TGACCTTGGG CCGGGCTGGG AGCGCTGCGG CGGGAGCCGG AGGACTATGA GCTGCCGCGC GTTGTCCAGA GCCCAGCCCA GCCCTACGCG CGCGGCCCGG AGCTCTGTTC CCTGGAACTT TGGGCACTGC CTCTGGGACC CCTGCCGGCC AGCAGGCAGG ATGGTGCTTG CCTCGTGCCC CTTGGTGCCC GTCTGCTGAT GTGCCCAGCC TGTGCCCGCC ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG TGCCCGGGAA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT CATCGTGTCG CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC CTCATGGTTG CCTGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC CCCCGGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG ACCCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGGG AGCCCGTGAT CAAGTGCGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT GTGGGTGCTG CCCCCGCTTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTCGGC CTCCTCCGGC GACCCGCAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC CCTCATCCTC TTCCTCTTTG CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC CCTCTTCTGC CCGTCCTGCC ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC TCGGCCATGA ACCCCATTGT CTATGCCTTC CGCATCCAGA AGTTCCGCGT CACCTTCCTT AAGATTTGGA ATGACCATTT CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA GAAGAGAGGC CTGATGACTA GACCCCGCCT TCCGCTCCCA CCAGCCCACA TCCAGTGGGG TCTCAGTCCA GTCCTCACAT GCCCGCTGTC CCAGGGGTCT CCCTGAGCCT GCCCCAGCTG GGCTGTTGGC TGGGGGCATG GGGGAGGCTC TGAAGAGATA CCCACAGAGT GTGGTCCCTC CACTAGGAGT TAACTACCCT ACACCTCTGG GCCCTGCAGG AGGCCTGGGA GGGCAAGGGT CCTACGGAGG GACCAGGTGT CTAGAGGCAA CAGTGTTCTG AGCCCCCACC TGCCTGACCA TCCCATGAGC AGTCCAGCGC TTCAGGGCTG GGCAGGTCCT GGGGAGGCTG AGACTGCAGA GGAGCCACCT GGGCTGGGAG AAGGTGCTTG GGCTTCTGCG GTGAGGCAGG GGAGTCTGCT TGTCTTAGAT GTTGGTGGTG CAGCCCCAGG ACCAAGCTTA AGGAGAGGAG AGCATCTGCT CTGAGACGGA TGGAAGGAGA GAGGTTGAGG ATGCACTGGC CTGTTCTGTA GGAGAGACTG GCCAGAGGCA GCTAAGGGGC AGGAATCAAG GAGCCTCCGT TCCCACCTCT GAGGACTCTG GACCCCAGGC CATACCAGGT GCTAGGGTGC CTGCTCTCCT TGCCCTGGGC CAGCCCAGGA TTGTACGTGG GAGAGGCAGA AAGGGTAGGT TCAGTAATCA TTTCTGATGA TTTGCTGGAG TGCTGGCTCC ACGCCCTGGG GAGTGAGCTT GGTGCGGTAG GTGCTGGCCT CAAACAGCCA CGAGGTGGTA GCTCTGAGCC CTCCTTCTTG CCCTGAGCTT TCCGGGGAGG AGCCTGGAGT GTAATTACCT GTCATCTGGG CCACCAGCTC CACTGGCCCC CGTTGCCGGG CCTGGACTGT CCTAGGTGAC CCCATCTCTG CTGCTTCTGG GCCTGATGGA GAGGAGAACA CTAGACATGC CAACTCGGGA GCATTCTGCC TGCCTGGGAA CGGGGTGGAC GAGGGAGTGT CTGTAAGGAC TCAGTGTTGA CTGTAGGCGC CCCTGGGGTG GGTTTAGCAG GCTGCAGCAG GCAGAGGAGG AGTACCCCCC TGAGAGCATG TGGGGGAAGG CCTTGCTGTC ATGTGAATCC CTCAATACCC CTAGTATCTG GCTGGGTTTT CAGGGGCTTT GGAAGCTCTG TTGCAGGTGT CCGGGGGTCT AGGACTTTAG GGATCTGGGA TCTGGGGAAG GACCAACCCA TGCCCTGCCA AGCCTGGAGC CCCTGTGTTG GGGGGCAAGG TGGGGGAGCC TGGAGCCCCT GTGTGGGAGG GCGAGGCGGG GGAGCCTGGA GCCCCTGTGT GGGAGGGCGA GGCGGGGGAT CCTGGAGCCC CTGTGTCGGG GGCGAGGGGA GGGGAGGTGG CCGTCGGTTG ACCTTCTGAA CATGAGTGTC AACTCCAGGA CTTGCTTCCA AGCCCTTCCC TCTGTTGGAA ATTGGGTGTG CCCTGGCTCC CAAGGGAGGC CCATGTGACT AATAAAAAAC TGTGAACCCT -3' **(FRAG. NO:_)(SEQ. ID NO: 2433)**

5'- ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG TGCCCGGGAA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT CATCGTCTCG CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC CTCATGGTTG CCTGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC CCCCGGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG ACCCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGGG AGCCCGTGAT CAAGTGCGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT GTGGGTGCTG CCCCCGCTTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTCGGC CTCCTCCGGC GACCCGCAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC CCTCATCCTC TTCCTCTTTG CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC CCTCTTCTGC CCGTCCTGCC ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC TCGGCCATGA ACCCCATTGT CTATGCCTTC CGCATCCAGA AGTTCCGCGT CACCTTCCTT AAGATTTGGA ATGACCATTT CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA GAAGAGAGGC CTGATGACTA G -3' **(FRAG. NO:_)(SEQ. ID NO: 2432)**

5'-CGCATTTGTG TTTTAATAAA AGAATCTGGA AGATAAATAG TCTTGAAGAG AGACAAAGGA AGGAAAATTT AAATCCTTAG ATTCAAGCAG AAGAATTCCA TGTGGAAGGT TTGGGTTGTT GTTGTTGTTG TTTGGTGTGT TTTTTGTTTT TTTGTTTTTT TGTTTTTTTT TGAGATGGAG TCTCGCTGTG TTACCGGGAG CGACAGAGCC GCACGGCCGA GTCGAGTCCC AGCCAGCTAC CATCCCTCTG GAGCTTACCG GCCGGCCTTG GCTTCCCCAG GAATCCCTGG AGCTAGCGGC TGCTGAAGGC GTCGAGGTGT GGGGGCACTT GGACAGAACA GTCAGGCAGC CGGGAGCTCT GCCAGCTTTG GTGACCTTGG GTGCTTGCCT CGTGCCCCTT GGTGCCCGTC TGCTGATGTG CCCAGCCTGT GCCCGCCATG CCGCCCTCCA TCTCAGCTTT CCAGGCCGCC TACATCGGCA TCGAGGTGCT CATCGCCCTG GTCTCTGTGC CCGGGAACGT GCTGGTGATC TGGGCGGTGA AGGTGAACCA GGCGCTGCGG GATGCCACCT TCTGCTTCAT CGTGTCGCTG GCGGTGGCTG ATGTGGCCGT GGGTGCCCTG GTCATCCCCC TCGCCATCCT CATCAACATT GGGCCACAGA CCTACTTCCA CACCTGCCTC ATGGTTGCCT GTCCGGTCCT CATCCTCACC CAGAGCTCCA TCCTGGCCCT GCTGGCAATT GCTGTGGACC GCTACCTCCG GGTCAAGATC CCTCTCCGGT ACAAGATGGT GGTGACCCCC CGGAGGGCGG CGGTGGCCAT AGCCGGCTGC TGGATCCTCT CCTTCGTGGT GGGACTGACC CCTATGTTTG GCTGGAACAA TCTGAGTGCG GTGGAGCGGG CCTGGGCAGC CAACGGCAGC ATGGGGGAGC CCGTGATCAA GTGCGAGTTC

GAGAAGGTCA TCAGCATGGA GTACATGGTC TACTTCAACT TCTTTGTGTG GGTGCTGCCC CCGCTTCTCC TCATGGTCCT CATCTACCTG GAGGTCTTCT ACCTAATCCG CAAGCAGCTC AACAAGAAGG TGTCGGCCTC CTCCGGCGAC CCGCAGAAGT ACTATGGGAA GGAGCTGAAG ATCGCCAAGT CGCTGGCCCT CATCCTCTTC CTCTTTGCCC TCAGCTGGCT GCCTTTGCAC ATCCTCAACT GCATCACCCT CTTCTGCCCG TCCTGCCACA AGCCCAGCAT CCTTACCTAC ATTGCCATCT TCCTCACGCA CGGCAACTCG GCCATGAACC CCATTGTCTA TGCCTTCCGC ATCCAGAAGT TCCGCGTCAC CTTCCTTAAG ATTTGGAATG ACCATTTCCG CTGCCAGCCT GCACCTCCCA TTGACGAGGA TCTCCCAGAA GAGAGGCCTG ATGACTAGAC CCCGCCTTCC GCTCCCACCG CCCACATCCA GTGGGGTCTC AGTCCAGTCC TCACATGCCC GCTGTCCCAG GGGTCTCCCT GAGCCTGCCC CAGCTGGGCT GTTGGCTGGG GGCATGGGGG AGGCTCTGAA GAGATACCCA CAGAGTGTGG TCCCTCCACT AGGAGTTAAC TACCCTACAC CTCTGGGCCC TGCAGGAGGC CTGGGAGGGC AAGGGTCCTA CGGAGGGACC AGGTGTCTAG AGGCAACAGT GTTCTGAGCC CCCACCTGCC TGACCATCCC ATGAGCAGTC CAGAGCTTCA GGGCTGGGCA GGTCCTGGGG AGGCTGAGAC TGCAGAGGAG CCACCTGGGC TGGGAGAAGG TGCTTGGGCT TCTGCGGTGA GGCAGGGGAG TCTGCTTGTC TTAGATGTTG GTGGTGCAGC CCCAGGACCA AGCTTAAGGA GAGGAGAGCA TCTGCTCTGA GACGGATGGA AGGAGAGAGG TTGAGGATGC ACTGGCCTGT TCTGTAGGAG AGACTGGCCA GA -3' **(FRAG. NO:__)(SEQ. ID NO: 2422)**

5'-ATGAGTGTCA GAAGTGTGAA GGGTGCCTGT TCTGAATCCC AGAGCCTCCT CTCCCTCTGT GAGGCTGGCA GGTGAGGAAG GGTTTAACCT CACTGGAAGG AATCCCTGGA GCTAGCGGCT GCTGAAGGCG TCGAGGTGTG GGGGCACTTG GACAGAACAG TCAGGCAGCC GGGAGCTCTG CCAGCTTTGG TGACCTTGGG CCGGGCTGGG AGCGCTGCGG CGGGAGCCGG AGGACTATGA GCTGCCGCGC GTTGTCCAGA GCCCAGCCCA GCCCTACGCG CGCGGCCCGG AGCTCTGTTC CCTGGAACTT TGGGCACTGC CTCTGGGACC CCTGCCGGCC AGCAGGCAGG ATGGTGCTTG CCTCGTGCCC CTTGGTGCCC GTCTGCTGAT GTGCCCAGCC TGTGCCCGCC ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG TGCCCGGGAA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT CATCGTGTCG CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC CTCATGGTTG CCTGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC CCCCGGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG ACCCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGGG AGCCCGTGAT CAAGTGCGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT GTGGGTGCTG CCCCCGCTTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTCGGC CTCCTCCGGC GACCCGCAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC CCTCATCCTC TTCCTCTTTG CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC CCTCTTCTGC CCGTCCTGCC ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC TCGGCCATGA ACCCCATTGT CTATGCCTTC CGCATCCAGA AGTTCCGCGT CACCTTCCTT AAGATTTGGA ATGACCATTT CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA GAAGAGAGGC CTGATGACTA GACCCCGCCT TCCGCTCCCA CCAGCCCACA TCCAGTGGGG TCTCAGTCCA GTCCTCACAT GCCCGCTGTC CCAGGGGTCT CCCTGAGCCT GCCCCAGCTG GGCTGTTGGC TGGGGGCATG GGGGAGGCTC TGAAGAGATA CCCACAGAGT GTGGTCCCTC CACTAGGAGT TAACTACCCT ACACCTCTGG GCCCTGCAGG AGGCCTGGGA GGGCAAGGGT CCTACGGAGG GACCAGGTGT CTAGAGGCAA CAGTGTTCTG AGCCCCCACC TGCCTGACCA TCCCATGAGC AGTCCAGCGC TTCAGGGCTG GGCAGGTCCT GGGGAGGCTG AGACTGCAGA GGAGCCACCT GGGCTGGGAG AAGGTGCTTG GGCTTCTGCG GTGAGGCAGG GGAGTCTGCT TGTCTTAGAT GTTGGTGGTG CAGCCCCAGG ACCAAGCTTA AGGAGAGGAG AGCATCTGCT CTGAGACGGA TGGAAGGAGA GAGGTTGAGG ATGCACTGGC CTGTTCTGTA GGAGAGACTG GCCAGAGGCA GCTAAGGGGC AGGAATCAAG GAGCCTCCGT TCCCACCTCT GAGGACTCTG GACCCCAGGC CATACCAGGT GCTAGGGTGC CTGCTCTCCT TGCCCTGGGC CAGCCCAGGA TTGTACGTGG GAGAGGCAGA AAGGGTAGGT TCAGTAATCA TTTCTGATGA TTTGCTGGAG TGCTGGCTCC ACGCCCTGGG GAGTGAGCTT GGTGCGGTAG GTGCTGGCCT CAAACAGCCA CGAGGTGGTA GCTCTGAGCC CTCCTTCTTG CCCTGAGCTT TCCGGGGAGG AGCCTGGAGT GTAATTACCT GTCATCTGGG CCACCAGCTC CACTGGCCCC CGTTGCCGGG CCTGGACTGT CCTAGGTGAC CCCATCTCTG CTGCTTCTGG GCCTGATGGA GAGGAGAACA CTAGACATGC CAACTCGGGA GCATTCTGCC TGCCTGGGAA CGGGGTGGAC GAGGGAGTGT CTGTAAGGAC TCAGTGTTGA CTGTAGGCGC CCCTGGGGTG GGTTTAGCAG GCTGCAGCAG GCAGAGGAGG AGTACCCCCC TGAGAGCATG TGGGGGAAGG CCTTGCTGTC ATGTGAATCC CTCAATACCC CTAGTATCTG GCTGGGTTTT CAGGGGCTTT GGAAGCTCTG TTGCAGGTGT CCGGGGGTCT AGGACTTTAG GGATCTGGGA TCTGGGGAAG GACCAACCCA TGCCCTGCCA AGCCTGGAGC CCCTGTGTTG GGGGGCAAGG TGGGGGAGCC TGGAGCCCCT GTGTGGGAGG GCGAGGCGGG GGAGCCTGGA GCCCCTGTGT GGGAGGGCGA GGCGGGGGAT CCTGGAGCCC CTGTGTCGGG GGGCGAGGGA GGGGAGGTGG CCGTCGGTTG ACCTTCTGAA CATGAGTGTC AACTCCAGGA CTTGCTTCCA AGCCCTTCCC TCTGTTGGAA ATTGGGTGTG CCCTGGCTCC CAAGGGAGGC CCATGTGACT AATAAAAAAC TGTGAACCCT -3' **(FRAG. NO:__) (SEQ. ID NO: 2421)**

5'-ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG TGCCCGGGAA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT CATCGTCTCG CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC CTCATGGTTG CCTGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC CCCCGGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG CCCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGGG AGCCCGTGAT CAAGTGCGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT GTGGGTGCTG CCCCCGCTTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTCGGC CTCCTCCGGC GACCCGCAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC CCTCATCCTC TTCCTCTTTG CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC CCTCTTCTGC CCGTCCTGCC ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC TCGGCCATGA ACCCCATTGT CTATGCCTTC CGCATCCAGA AGTTCCGCGT CACCTTCCTT AAGATTTGGA ATGACCATTT CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA GAAGAGAGGC CTGATGACTA G **(FRAG NO: __) (SEQ. ID NO: 2420)**

5'-GAT GGA GGG CGG CAT GGC GGG-3' **(FRAG. NO: 1657) (SEQ ID NO:1670)**

5'-G CGG GTC GCC GG-3' **(FRAG. NO: 1658) (SEQ ID NO:1671)**

5'-GGC GGG CBC BGG C-3' **(FRAG. NO: 1659) (SEQ ID NO:1672)**

5'-GGC GGG CBC-3' **(FRAG. NO: 1660) (SEQ ID NO:1673)**

5'-GC GGC CTG G-3' **(FRAG. NO: 1661) (SEQ ID NO:1674)**

5'-GGB GGG CGG C-3' **(FRAG. NO: 1662) (SEQ ID NO:1675)**

5'-GBT GGB GGG-3' (FRAG. NO: 1663) (SEQ ID NO:1676)
5'-GG CTG GGC-3' (FRAG. NO: 1664) (SEQ ID NO:1677)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG.1) (SEQ. ID NO: 11)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 2) (SEQ. ID NO: 12)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 3) (SEQ. ID NO: 13)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 4) (SEQ. ID NO: 14)
5'-C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 5) (SEQ. ID NO: 15)
5'-CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 6) (SEQ. ID NO: 16)
5'-TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 7) (SEQ. ID NO: 17)
5'-G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 8) (SEQ. ID NO: 18)
5'-GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 9) (SEQ. ID NO: 19)
5'-AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 10) (SEQ. ID NO: 20)
5'-A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 11) (SEQ. ID NO: 21)
5'-AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 12) (SEQ. ID NO: 22)
5'-GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 13) (SEQ. ID NO: 23)
5'-C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 14) (SEQ. ID NO: 24)
5'-TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 15) (SEQ. ID NO: 25)
5'-GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 16) (SEQ. ID NO: 26)
5'-A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 17) (SEQ. ID NO: 27)
5'-GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 18) (SEQ. ID NO: 28)
5'-AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 19) (SEQ. ID NO: 29)
5'-T GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 20) (SEQ. ID NO: 30)
5'-GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 21) (SEQ. ID NO: 31)
5'-GA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 22) (SEQ. ID NO: 32)
5'-A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 23) (SEQ. ID NO: 33)
5'-GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 24) (SEQ. ID NO: 34)
5'-GG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 25) (SEQ. ID NO: 35)
5'-G CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 26) (SEQ. ID NO: 36)
5'-CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 27) (SEQ. ID NO: 37)
5'-GG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 28) (SEQ. ID NO: 38)
5'-G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 29) (SEQ. ID NO: 39)
5'-CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 30) (SEQ. ID NO: 40)
5'-AT GGC GGG CAC AGG CTG GGC-3' (FRAG 31) (SEQ. ID NO: 41)
5'-T GGC GGG CAC AGG CTG GGC-3' (FRAG 32) (SEQ. ID NO: 42)
5'-GGC GGG CAC AGG CTG GGC-3' (FRAG 33) (SEQ. ID NO: 43)
5'-GC GGG CAC AGG CTG GGC-3' (FRAG 34) (SEQ. ID NO: 44)
5'-C GGG CAC AGG CTG GGC-3' (FRAG 35) (SEQ. ID NO: 45)
5'-GGG CAC AGG CTG GGC-3' (FRAG 36) (SEQ. ID NO: 46)
5'-GG CAC AGG CTG GGC-3' (FRAG 37) (SEQ. ID NO: 47)
5'-G CAC AGG CTG GGC-3' (FRAG 38) (SEQ. ID NO: 48)
5'-CAC AGG CTG GGC-3' (FRAG 39) (SEQ. ID NO: 49)
5'-AC AGG CTG GGC-3' (FRAG 40) (SEQ. ID NO: 50)
5'-C AGG CTG GGC-3' (FRAG 41) (SEQ. ID NO: 51)
5'-AGG CTG GGC-3' (FRAG 42) (SEQ. ID NO: 52)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 43) (SEQ. ID NO: 53)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 44) (SEQ. ID NO: 54)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 45) (SEQ. ID NO: 55)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 46) (SEQ. ID NO: 56)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 47) (SEQ. ID NO: 57)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 48) (SEQ. ID NO: 58)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 49) (SEQ. ID NO: 59)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 50) (SEQ. ID NO: 60)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 51) (SEQ. ID NO: 61)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 52) (SEQ. ID NO: 62)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 53) (SEQ. ID NO: 63)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 54) (SEQ. ID NO: 64)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 55) (SEQ. ID NO: 65)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 56) (SEQ. ID NO: 66)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3'(FRAG 57) (SEQ. ID NO: 67)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 58) (SEQ. ID NO: 68)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 59) (SEQ. ID NO: 69)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 60) (SEQ. ID NO: 70)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 61) (SEQ. ID NO: 71)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 62) (SEQ. ID NO: 72)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 63) (SEQ. ID NO: 73)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 64) (SEQ. ID NO: 74)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 65) (SEQ. ID NO: 75)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 66) (SEQ. ID NO: 76)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 67) (SEQ. ID NO: 77)

5'-GGC GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 68) (SEQ. ID NO: 78)
5'-GGC GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 69) (SEQ. ID NO: 79)
5'-GGC GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 70) (SEQ. ID NO: 80)
5'-GGC GGC CTG GAA AGC TGA GAT GG -3' (FRAG 71) (SEQ. ID NO: 81)
5'-GGC GGC CTG GAA AGC TGA GAT G -3' (FRAG 72) (SEQ. ID NO: 82)
5'-GGC GGC CTG GAA AGC TGA GAT -3' (FRAG 73) (SEQ. ID NO: 83)
5'-GGC GGC CTG GAA AGC TGA GA-3' (FRAG 74) (SEQ. ID NO: 84)
5'-GGC GGC CTG GAA AGC TGA G-3' (FRAG 75) (SEQ. ID NO: 85)
5'-GGC GGC CTG GAA AGC TGA-3' (FRAG 76) (SEQ. ID NO: 86)
5'-GGC GGC CTG GAA AGC TG-3' (FRAG 77) (SEQ. ID NO: 87)
5'-GGC GGC CTG GAA AGC T-3' (FRAG 78) (SEQ. ID NO: 88)
5'-GGC GGC CTG GAA AGC-3' (FRAG 79) (SEQ. ID NO: 89)
5'-GGC GGC CTG GAA AG-3' (FRAG 80) (SEQ. ID NO: 90)
5'-GGC GGC CTG GAA A-3' (FRAG 81) (SEQ. ID NO: 91)
5'-GGC GGC CTG GAA-3' (FRAG 82) (SEQ. ID NO: 92)
5'-GGC GGC CTG GA-3' (FRAG 83) (SEQ. ID NO: 93)
5'-GGC GGC CTG G-3' (FRAG 84) (SEQ. ID NO: 94)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 85) (SEQ. ID NO: 95)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 86) (SEQ. ID NO: 96)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 87) (SEQ. ID NO: 97)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 88) (SEQ. ID NO: 98)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 89) (SEQ. ID NO: 99)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 90) (SEQ. ID NO: 100)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 91) (SEQ. ID NO: 101)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 92) (SEQ. ID NO: 102)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 93) (SEQ. ID NO: 103)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 94) (SEQ. ID NO: 104)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 95) (SEQ. ID NO: 105)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 96) (SEQ. ID NO: 106)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 97) (SEQ. ID NO: 107)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 98) (SEQ. ID NO: 108)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 99) (SEQ. ID NO: 109)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 100) (SEQ. ID NO: 110)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 101) (SEQ. ID NO: 111)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 102) (SEQ. ID NO: 112)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 103) (SEQ. ID NO: 113)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 104) (SEQ. ID NO: 114)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 105) (SEQ. ID NO: 115)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 106) (SEQ. ID NO: 116)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 107) (SEQ. ID NO: 117)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 108) (SEQ. ID NO: 118)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 109) (SEQ. ID NO: 119)
5'-GC GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 110) (SEQ. ID NO: 120)
5'-GC GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 111) (SEQ. ID NO: 121)
5'-GC GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 112) (SEQ. ID NO: 122)
5'-GC GGC CTG GAA AGC TGA GAT GG -3' (FRAG 113) (SEQ. ID NO: 123)
5'-GC GGC CTG GAA AGC TGA GAT G -3' (FRAG 114) (SEQ. ID NO: 124)
5'-GC GGC CTG GAA AGC TGA GAT -3' (FRAG 115) (SEQ. ID NO: 125)
5'-GC GGC CTG GAA AGC TGA GA-3' (FRAG 116) (SEQ. ID NO: 126)
5'-GC GGC CTG GAA AGC TGA G-3' (FRAG 117) (SEQ. ID NO: 127)
5'-GC GGC CTG GAA AGC TGA-3' (FRAG 118) (SEQ. ID NO: 128)
5'-GC GGC CTG GAA AGC TG-3' (FRAG 119) (SEQ. ID NO: 129)
5'-GC GGC CTG GAA AGC T-3' (FRAG 120) (SEQ. ID NO: 130)
5'-GC GGC CTG GAA AGC-3' (FRAG 121) (SEQ. ID NO: 131)
5'-GC GGC CTG GAA AG-3' (FRAG 122) (SEQ. ID NO: 132)
5'-GC GGC CTG GAA A-3' (FRAG 123) (SEQ. ID NO: 133)
5'-GC GGC CTG GAA-3' (FRAG 124) (SEQ. ID NO: 134)
5'-GC GGC CTG GA-3' (FRAG 125) (SEQ. ID NO: 135)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 126) (SEQ. ID NO: 136)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 127) (SEQ. ID NO: 137)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 128) (SEQ. ID NO: 138)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 129) (SEQ. ID NO: 139)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 130) (SEQ. ID NO: 140)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 131) (SEQ. ID NO: 141)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 132) (SEQ. ID NO: 142)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 133) (SEQ. ID NO: 143)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 134) (SEQ. ID NO: 144)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 135) (SEQ. ID NO: 145)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 136) (SEQ. ID NO: 146)

5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 137) (SEQ. ID NO: 147)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 138) (SEQ. ID NO: 148)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 139) (SEQ. ID NO: 149)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 140) (SEQ. ID NO: 150)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 141) (SEQ. ID NO: 151)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 142) (SEQ. ID NO: 152)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRA 143) (SEQ. ID NO: 153)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 144) (SEQ. ID NO: 154)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 145) (SEQ. ID NO: 155)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 146) (SEQ. ID NO: 156)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 147) (SEQ. ID NO: 157)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 148) (SEQ. ID NO: 158)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 148) (SEQ. ID NO: 159)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 150) (SEQ. ID NO: 160)
5'-C GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 151) (SEQ. ID NO: 161)
5'-C GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 152) (SEQ. ID NO: 162)
5'-C GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 153) (SEQ. ID NO: 163)
5'-C GGC CTG GAA AGC TGA GAT GG -3' (FRAG 154) (SEQ. ID NO: 164)
5'-C GGC CTG GAA AGC TGA GAT G -3' (FRAG 155) (SEQ. ID NO: 165)
5'-C GGC CTG GAA AGC TGA GAT -3' (FRAG 156) (SEQ. ID NO: 166)
5'-C GGC CTG GAA AGC TGA GA-3' (FRAG 157) (SEQ. ID NO: 167)
5'-C GGC CTG GAA AGC TGA G-3' (FRAG 158) (SEQ. ID NO: 168)
5'-C GGC CTG GAA AGC TGA-3' (FRAG 159) (SEQ. ID NO: 169)
5'-C GGC CTG GAA AGC TG-3' (FRAG 160) (SEQ. ID NO: 170)
5'-C GGC CTG GAA AGC T-3' (FRAG 161) (SEQ. ID NO: 171)
5'-C GGC CTG GAA AGC-3' (FRAG 162) (SEQ. ID NO: 172)
5'-C GGC CTG GAA AG-3' (FRAG 163) (SEQ. ID NO: 173)
5'-C GGC CTG GAA A-3' (FRAG 164) (SEQ. ID NO: 174)
5'-C GGC CTG GAA-3' (FRAG 165) (SEQ. ID NO: 175)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 166) (SEQ. ID NO: 176)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 167) (SEQ. ID NO: 177)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 168) (SEQ. ID NO: 178)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 169) (SEQ. ID NO: 179)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 170) (SEQ. ID NO: 180)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 171) (SEQ. ID NO: 181)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 172) (SEQ. ID NO: 182)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 173) (SEQ. ID NO: 183)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 174) (SEQ. ID NO: 184)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 175) (SEQ. ID NO: 185)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 176) (SEQ. ID NO: 186)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 177) (SEQ. ID NO: 187)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 178) (SEQ. ID NO: 188)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 179) (SEQ. ID NO: 189)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 180) (SEQ. ID NO: 190)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 181) (SEQ. ID NO: 191)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 182) (SEQ. ID NO: 192)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 183) (SEQ. ID NO: 193)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 184) (SEQ. ID NO: 194)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 185) (SEQ. ID NO: 195)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 186) (SEQ. ID NO: 196)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 187) (SEQ. ID NO: 197)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 188) (SEQ. ID NO: 198)
5'- GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 189) (SEQ. ID NO: 199)
5'- GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 190) (SEQ. ID NO: 200)
5'- GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 191) (SEQ. ID NO: 201)
5'- GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 192) (SEQ. ID NO: 202)
5'- GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 193) (SEQ. ID NO: 203)
5'- GGC CTG GAA AGC TGA GAT GG -3' (FRAG 194) (SEQ. ID NO: 204)
5'- GGC CTG GAA AGC TGA GAT G -3' (FRAG 195) (SEQ. ID NO: 205)
5'- GGC CTG GAA AGC TGA GAT -3' (FRAG 196) (SEQ. ID NO: 206)
5'- GGC CTG GAA AGC TGA GA-3' (FRAG 197) (SEQ. ID NO: 207)
5'- GGC CTG GAA AGC TGA G-3' (FRAG 198) (SEQ. ID NO: 208)
5'- GGC CTG GAA AGC TGA-3' (FRAG 199) (SEQ. ID NO: 209)
5'- GGC CTG GAA AGC TG-3' (FRAG 200 (SEQ. ID NO: 210)
5'- GGC CTG GAA AGC T-3' (FRAG 201) (SEQ. ID NO: 211)
5'- GGC CTG GAA AGC-3' (FRAG 202) (SEQ. ID NO: 212)
5'- GGC CTG GAA AG-3' (FRAG 203) (SEQ. ID NO: 213)
5'- GGC CTG GAA A-3' (FRAG 204) (SEQ. ID NO: 214)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 205) (SEQ. ID NO: 215)

5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 206) (SEQ. ID NO: 216)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 207) (SEQ. ID NO: 217)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 208) (SEQ. ID NO: 218)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 209) (SEQ. ID NO: 219)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 210) (SEQ. ID NO: 220)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 211) (SEQ. ID NO: 221)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 212) (SEQ. ID NO: 222)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 213) (SEQ. ID NO: 223)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 214) (SEQ. ID NO: 224)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 215) (SEQ. ID NO: 225)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 216) (SEQ. ID NO: 226)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 217) (SEQ. ID NO: 227)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 218) (SEQ. ID NO: 228)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 219) (SEQ. ID NO: 229)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 220) (SEQ. ID NO: 230)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 221) (SEQ. ID NO: 231)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 222) (SEQ. ID NO: 232)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 223) (SEQ. ID NO: 233)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 224) (SEQ. ID NO: 234)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 225) (SEQ. ID NO: 235)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 226) (SEQ. ID NO: 236)
5'- GC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 227) (SEQ. ID NO: 237)
5'- GC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 228) (SEQ. ID NO: 238)
5'- GC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 229) (SEQ. ID NO: 239)
5'- GC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 230) (SEQ. ID NO: 240)
5'- GC CTG GAA AGC TGA GAT GGA G -3' (FRAG 231) (SEQ. ID NO: 241)
5'- GC CTG GAA AGC TGA GAT GGA -3' (FRAG 232) (SEQ. ID NO: 242)
5'- GC CTG GAA AGC TGA GAT GG -3' (FRAG 233) (SEQ. ID NO: 243)
5'- GC CTG GAA AGC TGA GAT G -3' (FRAG 234) (SEQ. ID NO: 244)
5'- GC CTG GAA AGC TGA GAT -3' (FRAG 235) (SEQ. ID NO: 245)
5'- GC CTG GAA AGC TGA GA-3' (FRAG 236) (SEQ. ID NO: 246)
5'- GC CTG GAA AGC TGA G-3' (FRAG 237) (SEQ. ID NO: 247)
5'- GC CTG GAA AGC TGA-3' (FRAG 238) (SEQ. ID NO: 248)
5'- GC CTG GAA AGC TG-3' (FRAG 239) (SEQ. ID NO: 249)
5'- GC CTG GAA AGC T-3' (FRAG 240) (SEQ. ID NO: 250)
5'- GC CTG GAA AGC-3' (FRAG 241) (SEQ. ID NO: 251)
5'- GC CTG GAA AG-3' (FRAG 242) (SEQ. ID NO: 252)
5'- C CTG GAA AGC TGA GAT GG A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 243) (SEQ. ID NO: 253)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 244) (SEQ. ID NO: 254)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 245) (SEQ. ID NO: 255)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 246) (SEQ. ID NO: 256)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 247) (SEQ. ID NO: 257)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 248) (SEQ. ID NO: 258)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 249) (SEQ. ID NO: 259)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 250) (SEQ. ID NO: 260)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 251) (SEQ. ID NO: 261)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 252) (SEQ. ID NO: 262)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 253) (SEQ. ID NO: 263)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 254) (SEQ. ID NO: 264)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 255) (SEQ. ID NO: 265)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 256) (SEQ. ID NO: 266)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 257) (SEQ. ID NO: 267)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 258) (SEQ. ID NO: 268)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 259) (SEQ. ID NO: 269)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 260) (SEQ. ID NO: 270)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 261) (SEQ. ID NO: 271)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 262) (SEQ. ID NO: 272)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 263) (SEQ. ID NO: 273)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 264) (SEQ. ID NO: 274)
5'- C CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 265) (SEQ. ID NO: 275)
5'- C CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 266) (SEQ. ID NO: 276)
5'- C CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 267) (SEQ. ID NO: 277)
5'- C CTG GAA AGC TGA GAT GGA GG -3' (FRAG 268) (SEQ. ID NO: 278)
5'- C CTG GAA AGC TGA GAT GGA G -3' (FRAG 269) (SEQ. ID NO: 279)
5'- C CTG GAA AGC TGA GAT GGA -3' (FRAG 270) (SEQ. ID NO: 280)
5'- C CTG GAA AGC TGA GAT GG -3' (FRAG 271) (SEQ. ID NO: 281)
5'- C CTG GAA AGC TGA GAT G -3' (FRAG 272) (SEQ. ID NO: 282)
5'- C CTG GAA AGC TGA GAT -3' (FRAG 273) (SEQ. ID NO: 283)
5'- C CTG GAA AGC TGA GA-3' (FRAG 274) (SEQ. ID NO: 284)

5'- C CTG GAA AGC TGA G-3' (FRAG 275) (SEQ. ID NO: 285)
5'- C CTG GAA AGC TGA-3' (FRAG 276) (SEQ. ID NO: 286)
5'- C CTG GAA AGC TG-3' (FRAG 277) (SEQ. ID NO: 287)
5'- C CTG GAA AGC T-3' (FRAG 278) (SEQ. ID NO: 288)
5'- C CTG GAA AGC-3' (FRAG 279) (SEQ. ID NO: 289)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 280) (SEQ. ID NO: 290)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 281) (SEQ. ID NO: 291)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 282) (SEQ. ID NO: 292)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 283) (SEQ. ID NO: 293)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 284) (SEQ. ID NO: 294)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 285) (SEQ. ID NO: 295)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 286) (SEQ. ID NO: 296)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 287) (SEQ. ID NO: 297)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 288) (SEQ. ID NO: 298)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 289) (SEQ. ID NO: 299)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 290) (SEQ. ID NO: 300)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 291) (SEQ. ID NO: 301)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 292) (SEQ. ID NO: 302)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 293) (SEQ. ID NO: 303)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 294) (SEQ. ID NO: 304)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 295) (SEQ. ID NO: 305)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 296) (SEQ. ID NO: 306)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 297) (SEQ. ID NO: 307)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 298) (SEQ. ID NO: 308)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 299) (SEQ. ID NO: 309)
5'- CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 300) (SEQ. ID NO: 310)
5'- CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 301) (SEQ. ID NO: 311)
5'- CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 302) (SEQ. ID NO: 312)
5'- CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 303) (SEQ. ID NO: 313)
5'- CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 304) (SEQ. ID NO: 314)
5'- CTG GAA AGC TGA GAT GGA GG -3' (FRAG 305) (SEQ. ID NO: 315)
5'- CTG GAA AGC TGA GAT GGA G -3' (FRAG 306) (SEQ. ID NO: 316)
5'- CTG GAA AGC TGA GAT GGA -3' (FRAG 307) (SEQ. ID NO: 317)
5'- CTG GAA AGC TGA GAT GG -3' (FRAG 308) (SEQ. ID NO: 318)
5'- CTG GAA AGC TGA GAT G -3' (FRAG 309) (SEQ. ID NO: 319)
5'- CTG GAA AGC TGA GAT -3' (FRAG 310) (SEQ. ID NO: 320)
5'- CTG GAA AGC TGA GA-3' (FRAG 311) (SEQ. ID NO: 321)
5'- CTG GAA AGC TGA G-3' (FRAG 312) (SEQ. ID NO: 322)
5'- CTG GAA AGC TGA-3' (FRAG 313) (SEQ. ID NO: 323)
5'- CTG GAA AGC TG-3' (FRAG 314) (SEQ. ID NO: 324)
5'- CTG GAA AGC T-3' (FRAG 315) (SEQ. ID NO: 325)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 316) (SEQ. ID NO: 326)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 317) (SEQ. ID NO: 327)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 318) (SEQ. ID NO: 328)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 319) (SEQ. ID NO: 329)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 320) (SEQ. ID NO: 330)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 321) (SEQ. ID NO: 331)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 322) (SEQ. ID NO: 332)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 323) (SEQ. ID NO: 333)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 324) (SEQ. ID NO: 334)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 325) (SEQ. ID NO: 335)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 326) (SEQ. ID NO: 336)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 327) (SEQ. ID NO: 337)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 328) (SEQ. ID NO: 338)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 329) (SEQ. ID NO: 339)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 330) (SEQ. ID NO: 340)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 331) (SEQ. ID NO: 341)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 332) (SEQ. ID NO: 342)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 333) (SEQ. ID NO: 343)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 334) (SEQ. ID NO: 344)
5'- TG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 335) (SEQ. ID NO: 345)
5'- TG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 336) (SEQ. ID NO: 346)
5'- TG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 337) (SEQ. ID NO: 347)
5'- TG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 338) (SEQ. ID NO: 348)
5'- TG GAA AGC TGA GAT GGA GGG C -3' (FRAG 339) (SEQ. ID NO: 349)
5'- TG GAA AGC TGA GAT GGA GGG -3' (FRAG 340) (SEQ. ID NO: 350)
5'- TG GAA AGC TGA GAT GGA GG -3' (FRAG 341) (SEQ. ID NO: 351)
5'- TG GAA AGC TGA GAT GGA G -3' (FRAG 342) (SEQ. ID NO: 352)
5'- TG GAA AGC TGA GAT GGA -3' (FRAG 343) (SEQ. ID NO: 353)

5'- TG GAA AGC TGA GAT GG -3' (FRAG 344) (SEQ. ID NO: 354)
5'- TG GAA AGC TGA GAT G -3' (FRAG 345) (SEQ. ID NO: 355)
5'- TG GAA AGC TGA GAT -3' (FRAG 346) (SEQ. ID NO: 356)
5'- TG GAA AGC TGA GA-3' (FRAG 347) (SEQ. ID NO: 357)
5'- TG GAA AGC TGA G-3' (FRAG 348) (SEQ. ID NO: 358)
5'- TG GAA AGC TGA-3' (FRAG 349) (SEQ. ID NO: 359)
5'- TG GAA AGC TG-3' (FRAG 350) (SEQ. ID NO: 360)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 351) (SEQ. ID NO: 361)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 352) (SEQ. ID NO: 362)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 353) (SEQ. ID NO: 363)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 354) (SEQ. ID NO: 364)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 355) (SEQ. ID NO: 365)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 356) (SEQ. ID NO: 366)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 357) (SEQ. ID NO: 367)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 358) (SEQ. ID NO: 368)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 359) (SEQ. ID NO: 369)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 360) (SEQ. ID NO: 370)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 361) (SEQ. ID NO: 371)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 362) (SEQ. ID NO: 372)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 363) (SEQ. ID NO: 373)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 364) (SEQ. ID NO: 374)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 365) (SEQ. ID NO: 375)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 366) (SEQ. ID NO: 376)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 367) (SEQ. ID NO: 377)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 368) (SEQ. ID NO: 378)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 369) (SEQ. ID NO: 379)
5'- G GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 370) (SEQ. ID NO: 380)
5'- G GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 371) (SEQ. ID NO: 381)
5'- G GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 372) (SEQ. ID NO: 382)
5'- G GAA AGC TGA GAT GGA GGG CG -3' (FRAG 373) (SEQ. ID NO: 383)
5'- G GAA AGC TGA GAT GGA GGG C -3' (FRAG 374) (SEQ. ID NO: 384)
5'- G GAA AGC TGA GAT GGA GGG -3' (FRAG 375) (SEQ. ID NO: 385)
5'- G GAA AGC TGA GAT GGA GG -3' (FRAG 376) (SEQ. ID NO: 386)
5'- G GAA AGC TGA GAT GGA G -3' (FRAG 377) (SEQ. ID NO: 387)
5'- G GAA AGC TGA GAT GGA -3' (FRAG 378) (SEQ. ID NO: 388)
5'- G GAA AGC TGA GAT GG -3' (FRAG 379) (SEQ. ID NO: 389)
5'- G GAA AGC TGA GAT G -3' (FRAG 380) (SEQ. ID NO: 390)
5'- G GAA AGC TGA GAT -3' (FRAG 381) (SEQ. ID NO: 391)
5'- G GAA AGC TGA GA-3' (FRAG 382) (SEQ. ID NO: 392)
5'- G GAA AGC TGA G-3' (FRAG 383) (SEQ. ID NO: 393)
5'- G GAA AGC TGA-3' (FRAG 384) (SEQ. ID NO: 394)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 385) (SEQ. ID NO: 395)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 386) (SEQ. ID NO: 396)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 387) (SEQ. ID NO: 397)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 388) (SEQ. ID NO: 398)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 389) (SEQ. ID NO: 399)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 390) (SEQ. ID NO: 400)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 391) (SEQ. ID NO: 401)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 392) (SEQ. ID NO: 402)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 393) (SEQ. ID NO: 403)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 394) (SEQ. ID NO: 404)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 395) (SEQ. ID NO: 405)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 396) (SEQ. ID NO: 406)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 397) (SEQ. ID NO: 407)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 398) (SEQ. ID NO: 408)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 399) (SEQ. ID NO: 409)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 400) (SEQ. ID NO: 410)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 401) (SEQ. ID NO: 411)
5'- GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 402) (SEQ. ID NO: 412)
5'- GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 403) (SEQ. ID NO: 413)
5'- GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 404) (SEQ. ID NO: 414)
5'- GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 405) (SEQ. ID NO: 415)
5'- GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 406) (SEQ. ID NO: 416)
5'- GAA AGC TGA GAT GGA GGG CG -3' (FRAG 407) (SEQ. ID NO: 417)
5'- GAA AGC TGA GAT GGA GGG C -3' (FRAG 408) (SEQ. ID NO: 418)
5'- GAA AGC TGA GAT GGA GGG -3' (FRAG 409) (SEQ. ID NO: 419)
5'- GAA AGC TGA GAT GGA GG -3' (FRAG 410) (SEQ. ID NO: 420)
5'- GAA AGC TGA GAT GGA G -3' (FRAG 411) (SEQ. ID NO: 421)
5'- GAA AGC TGA GAT GGA -3' (FRAG 412) (SEQ. ID NO: 422)

5'- GAA AGC TGA GAT GG -3' (FRAG 413) (SEQ. ID NO: 423)
5'- GAA AGC TGA GAT G -3' (FRAG 414) (SEQ. ID NO: 424)
5'- GAA AGC TGA GAT -3' (FRAG 415) (SEQ. ID NO: 425)
5'- GAA AGC TGA GA-3' (FRAG 416) (SEQ. ID NO: 426)
5'- GAA AGC TGA G-3' (FRAG 417) (SEQ. ID NO: 427)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 418) (SEQ. ID NO: 428)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 419) (SEQ. ID NO: 429)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 420) (SEQ. ID NO: 430)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 421) (SEQ. ID NO: 431)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 422) (SEQ. ID NO: 432)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 423) (SEQ. ID NO: 433)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3'(FRAG 424) (SEQ. ID NO: 434)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 425) (SEQ. ID NO: 435)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 426) (SEQ. ID NO: 436)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 427) (SEQ. ID NO: 437)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 428) (SEQ. ID NO: 438)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 429) (SEQ. ID NO: 439)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 430) (SEQ. ID NO: 440)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 431) (SEQ. ID NO: 441)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 432) (SEQ. ID NO: 442)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 433) (SEQ. ID NO: 443)
5'- AA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 434) (SEQ. ID NO: 444)
5'- AA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 435) (SEQ. ID NO: 445)
5'- AA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 436) (SEQ. ID NO: 446)
5'- AA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 437) (SEQ. ID NO: 447)
5'- AA AGC TGA GAT GGA GGG CGG C-3' (FRAG 438) (SEQ. ID NO: 448)
5'- AA AGC TGA GAT GGA GGG CGG -3' (FRAG 439) (SEQ. ID NO: 449)
5'- AA AGC TGA GAT GGA GGG CG -3' (FRAG 440) (SEQ. ID NO: 450)
5'- AA AGC TGA GAT GGA GGG C -3' (FRAG 441) (SEQ. ID NO: 451)
5'- AA AGC TGA GAT GGA GGG -3' (FRAG 442) (SEQ. ID NO: 452)
5'- AA AGC TGA GAT GGA GG -3' (FRAG 443) (SEQ. ID NO: 453)
5'- AA AGC TGA GAT GGA G -3' (FRAG 444) (SEQ. ID NO: 454)
5'- AA AGC TGA GAT GGA -3' (FRAG 445) (SEQ. ID NO: 455)
5'- AA AGC TGA GAT GG -3' (FRAG 446) (SEQ. ID NO: 456)
5'- AA AGC TGA GAT G -3' (FRAG 447) (SEQ. ID NO: 457)
5'- AA AGC TGA GAT -3' (FRAG 448) (SEQ. ID NO: 458)
5'- AA AGC TGA GA-3' (FRAG 449) (SEQ. ID NO: 459)
5'- A AGC TGA GAT GGA GGG CG G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 450) (SEQ. ID NO: 460)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 451) (SEQ. ID NO: 461)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 452) (SEQ. ID NO: 462)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 453) (SEQ. ID NO: 463)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 454) (SEQ. ID NO: 464)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 455) (SEQ. ID NO: 465)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 456) (SEQ. ID NO: 466)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 457) (SEQ. ID NO: 467)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 458) (SEQ. ID NO: 468)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 459) (SEQ. ID NO: 469)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 460) (SEQ. ID NO: 470)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 461) (SEQ. ID NO: 471)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 462) (SEQ. ID NO: 472)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 463) (SEQ. ID NO: 473)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 464) (SEQ. ID NO: 474)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 465) (SEQ. ID NO: 475)
5'- A AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 466) (SEQ. ID NO: 476)
5'- A AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 467) (SEQ. ID NO: 477)
5'- A AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 468) (SEQ. ID NO: 478)
5'- A AGC TGA GAT GGA GGG CGG CA-3' (FRAG 469) (SEQ. ID NO: 479)
5'- A AGC TGA GAT GGA GGG CGG C-3' (FRAG 470) (SEQ. ID NO: 480)
5'- A AGC TGA GAT GGA GGG CGG -3' (FRAG 471) (SEQ. ID NO: 481)
5'- A AGC TGA GAT GGA GGG CG -3' (FRAG 472) (SEQ. ID NO: 482)
5'- A AGC TGA GAT GGA GGG C -3' (FRAG 473) (SEQ. ID NO: 483)
5'- A AGC TGA GAT GGA GGG -3' (FRAG 474) (SEQ. ID NO: 484)
5'- A AGC TGA GAT GGA GG -3' (FRAG 475) (SEQ. ID NO: 485)
5'- A AGC TGA GAT GGA G -3' (FRAG 476) (SEQ. ID NO: 486)
5'- A AGC TGA GAT GGA -3' (FRAG 477) (SEQ. ID NO: 487)
5'- A AGC TGA GAT GG -3' (FRAG 478) (SEQ. ID NO: 488)
5'- A AGC TGA GAT G -3' (FRAG 479) (SEQ. ID NO: 489)
5'- A AGC TGA GAT -3' (FRAG 480) (SEQ. ID NO: 490)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 481) (SEQ. ID NO: 491)

5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 482) (SEQ. ID NO: 492)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 483) (SEQ. ID NO: 493)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 484) (SEQ. ID NO: 494)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 485) (SEQ. ID NO: 495)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 486) (SEQ. ID NO: 496)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 487) (SEQ. ID NO: 497)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 488) (SEQ. ID NO: 498)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 489) (SEQ. ID NO: 499)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 490) (SEQ. ID NO: 500)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 491) (SEQ. ID NO: 501)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 492) (SEQ. ID NO: 502)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 493) (SEQ. ID NO: 503)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 494) (SEQ. ID NO: 504)
5'- AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 495) (SEQ. ID NO: 505)
5'- AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 496) (SEQ. ID NO: 506)
5'- AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 497) (SEQ. ID NO: 507)
5'- AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 498) (SEQ. ID NO: 508)
5'- AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 499) (SEQ. ID NO: 509)
5'- AGC TGA GAT GGA GGG CGG CA-3' (FRAG 500) (SEQ. ID NO: 510)
5'- AGC TGA GAT GGA GGG CGG C-3' (FRAG 501) (SEQ. ID NO: 511)
5'- AGC TGA GAT GGA GGG CGG -3' (FRAG 502) (SEQ. ID NO: 512)
5'- AGC TGA GAT GGA GGG CG -3' (FRAG 503) (SEQ. ID NO: 513)
5'- AGC TGA GAT GGA GGG C -3' (FRAG 504) (SEQ. ID NO: 514)
5'- AGC TGA GAT GGA GGG -3' (FRAG 505) (SEQ. ID NO: 515)
5'- AGC TGA GAT GGA GG -3' (FRAG 506) (SEQ. ID NO: 516)
5'- AGC TGA GAT GGA G -3' (FRAG 507) (SEQ. ID NO: 517)
5'- AGC TGA GAT GGA -3' (FRAG 508) (SEQ. ID NO: 518)
5'- AGC TGA GAT GG -3' (FRAG 509) (SEQ. ID NO: 519)
5'- AGC TGA GAT G -3' (FRAG 510) (SEQ. ID NO: 520)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 511) (SEQ. ID NO: 521)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 512) (SEQ. ID NO: 522)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 513) (SEQ. ID NO: 523)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 514) (SEQ. ID NO: 524)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 515) (SEQ. ID NO: 525)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 516) (SEQ. ID NO: 526)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 517) (SEQ. ID NO: 527)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 518) (SEQ. ID NO: 528)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 519) (SEQ. ID NO: 529)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 520) (SEQ. ID NO: 530)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 521) (SEQ. ID NO: 531)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 522) (SEQ. ID NO: 532)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 523) (SEQ. ID NO: 533)
5'- GC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 524) (SEQ. ID NO: 534)
5'- GC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 525) (SEQ. ID NO: 535)
5'- GC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 526) (SEQ. ID NO: 536)
5'- GC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 527) (SEQ. ID NO: 537)
5'- GC TGA GAT GGA GGG CGG CAT G -3' (FRAG 528) (SEQ. ID NO: 538)
5'- GC TGA GAT GGA GGG CGG CAT -3' (FRAG 529) (SEQ. ID NO: 539)
5'- GC TGA GAT GGA GGG CGG CA-3' (FRAG 530) (SEQ. ID NO: 540)
5'- GC TGA GAT GGA GGG CGG C-3' (FRAG 531) (SEQ. ID NO: 541)
5'- GC TGA GAT GGA GGG CGG -3' (FRAG 532) (SEQ. ID NO: 542)
5'- GC TGA GAT GGA GGG CG -3' (FRAG 533) (SEQ. ID NO: 543)
5'- GC TGA GAT GGA GGG C -3' (FRAG 534) (SEQ. ID NO: 544)
5'- GC TGA GAT GGA GGG -3' (FRAG 535) (SEQ. ID NO: 545)
5'- GC TGA GAT GGA GG -3' (FRAG 536) (SEQ. ID NO: 546)
5'- GC TGA GAT GGA G -3' (FRAG 537) (SEQ. ID NO: 547)
5'- GC TGA GAT GGA -3' (FRAG 538) (SEQ. ID NO: 548)
5'- GC TGA GAT GG -3' (FRAG 539) (SEQ. ID NO: 549)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 540) (SEQ. ID NO: 550)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 541) (SEQ. ID NO: 551)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 542) (SEQ. ID NO: 552)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 543) (SEQ. ID NO: 553)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 544) (SEQ. ID NO: 554)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 545) (SEQ. ID NO: 555)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 546) (SEQ. ID NO: 556)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 547) (SEQ. ID NO: 557)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 548) (SEQ. ID NO: 558)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 549) (SEQ. ID NO: 559)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 550) (SEQ. ID NO: 560)

5'- C TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 551) (SEQ. ID NO: 561)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 552) (SEQ. ID NO: 562)
5'- C TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 553) (SEQ. ID NO: 563)
5'- C TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 554) (SEQ. ID NO: 564)
5'- C TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 555) (SEQ. ID NO: 565)
5'- C TGA GAT GGA GGG CGG CAT GG -3' (FRAG 556) (SEQ. ID NO: 566)
5'- C TGA GAT GGA GGG CGG CAT G -3' (FRAG 557) (SEQ. ID NO: 567)
5'- C TGA GAT GGA GGG CGG CAT -3' (FRAG 558) (SEQ. ID NO: 568)
5'- C TGA GAT GGA GGG CGG CA-3' (FRAG 559) (SEQ. ID NO: 569)
5'- C TGA GAT GGA GGG CGG C-3' (FRAG 560) (SEQ. ID NO: 570)
5'- C TGA GAT GGA GGG CGG -3' (FRAG 561) (SEQ. ID NO: 571)
5'- C TGA GAT GGA GGG CG -3' (FRAG 562) (SEQ. ID NO: 572)
5'- C TGA GAT GGA GGG C -3' (FRAG 563) (SEQ. ID NO: 573)
5'- C TGA GAT GGA GGG -3' (FRAG 564) (SEQ. ID NO: 574)
5'- C TGA GAT GGA GG -3' (FRAG 565) (SEQ. ID NO: 575)
5'- C TGA GAT GGA G -3' (FRAG 566) (SEQ. ID NO: 576)
5'- C TGA GAT GGA -3' (FRAG 567) (SEQ. ID NO: 577)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 568) (SEQ. ID NO: 578)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 569) (SEQ. ID NO: 579)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 570) (SEQ. ID NO: 580)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 571) (SEQ. ID NO: 581)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 572) (SEQ. ID NO: 582)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 573) (SEQ. ID NO: 583)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 574) (SEQ. ID NO: 584)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 575) (SEQ. ID NO: 585)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 576) (SEQ. ID NO: 586)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 577) (SEQ. ID NO: 587)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 578) (SEQ. ID NO: 588)
5'- TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 579) (SEQ. ID NO: 589)
5'- TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 580) (SEQ. ID NO: 590)
5'- TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 581) (SEQ. ID NO: 591)
5'- TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 582) (SEQ. ID NO: 592)
5'- TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 583) (SEQ. ID NO: 593)
5'- TGA GAT GGA GGG CGG CAT GG -3' (FRAG 584) (SEQ. ID NO: 594)
5'- TGA GAT GGA GGG CGG CAT G -3' (FRAG 585) (SEQ. ID NO: 595)
5'- TGA GAT GGA GGG CGG CAT -3' (FRAG 586) (SEQ. ID NO: 596)
5'- TGA GAT GGA GGG CGG CA-3' (FRAG 587) (SEQ. ID NO: 597)
5'- TGA GAT GGA GGG CGG C-3' (FRAG 588) (SEQ. ID NO: 598)
5'- TGA GAT GGA GGG CGG -3' (FRAG 589) (SEQ. ID NO: 599)
5'- TGA GAT GGA GGG CG -3' (FRAG 590) (SEQ. ID NO: 600)
5'- TGA GAT GGA GGG C -3' (FRAG 591) (SEQ. ID NO: 601)
5'- TGA GAT GGA GGG -3' (FRAG 592) (SEQ. ID NO: 602)
5'- TGA GAT GGA GG -3' (FRAG 593) (SEQ. ID NO: 603)
5'- TGA GAT GGA G -3' (FRAG 594) (SEQ. ID NO: 604)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 595) (SEQ. ID NO: 605)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 596) (SEQ. ID NO: 606)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 597) (SEQ. ID NO: 607)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 598) (SEQ. ID NO: 608)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 599) (SEQ. ID NO: 609)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 600) (SEQ. ID NO: 610)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 601) (SEQ. ID NO: 611)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 602) (SEQ. ID NO: 612)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 603) (SEQ. ID NO: 613)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 604) (SEQ. ID NO: 614)
5'- GA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 605) (SEQ. ID NO: 615)
5'- GA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 606) (SEQ. ID NO: 616)
5'- GA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 607) (SEQ. ID NO: 617)
5'- GA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 608) (SEQ. ID NO: 618)
5'- GA GAT GGA GGG CGG CAT GGC G-3' (FRAG 609) (SEQ. ID NO: 619)
5'- GA GAT GGA GGG CGG CAT GGC -3' (FRAG 610) (SEQ. ID NO: 620)
5'- GA GAT GGA GGG CGG CAT GG -3' (FRAG 611) (SEQ. ID NO: 621)
5'- GA GAT GGA GGG CGG CAT G -3' (FRAG 612) (SEQ. ID NO: 622)
5'- GA GAT GGA GGG CGG CAT -3' (FRAG 613) (SEQ. ID NO: 623)
5'- GA GAT GGA GGG CGG CA-3' (FRAG 614) (SEQ. ID NO: 624)
5'- GA GAT GGA GGG CGG C-3' (FRAG 615) (SEQ. ID NO: 625)
5'- GA GAT GGA GGG CGG -3' (FRAG 616) (SEQ. ID NO: 626)
5'- GA GAT GGA GGG CG -3' (FRAG 617) (SEQ. ID NO: 627)
5'- GA GAT GGA GGG C -3' (FRAG 618) (SEQ. ID NO: 628)
5'- GA GAT GGA GGG -3' (FRAG 619) (SEQ. ID NO: 629)

5'- GA GAT GGA GG -3' (FRAG 620) (SEQ. ID NO: 630)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 621) (SEQ. ID NO: 631)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 622) (SEQ. ID NO: 632)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 623) (SEQ. ID NO: 633)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 624) (SEQ. ID NO: 634)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 625) (SEQ. ID NO: 635)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 626) (SEQ. ID NO: 636)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 627) (SEQ. ID NO: 637)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 628) (SEQ. ID NO: 638)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 629) (SEQ. ID NO: 639)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 630) (SEQ. ID NO: 640)
5'- A GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 631) (SEQ. ID NO: 641)
5'- A GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 632) (SEQ. ID NO: 642)
5'- A GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 633) (SEQ. ID NO: 643)
5'- A GAT GGA GGG CGG CAT GGC GG-3' (FRAG 634) (SEQ. ID NO: 644)
5'- A GAT GGA GGG CGG CAT GGC G-3' (FRAG 635) (SEQ. ID NO: 645)
5'- A GAT GGA GGG CGG CAT GGC -3' (FRAG 636) (SEQ. ID NO: 646)
5'- A GAT GGA GGG CGG CAT GG -3' (FRAG 637) (SEQ. ID NO: 647)
5'- A GAT GGA GGG CGG CAT G -3' (FRAG 638) (SEQ. ID NO: 648)
5'- A GAT GGA GGG CGG CAT -3' (FRAG 639) (SEQ. ID NO: 649)
5'- A GAT GGA GGG CGG CA-3' (FRAG 640) (SEQ. ID NO: 650)
5'- A GAT GGA GGG CGG C-3' (FRAG 641) (SEQ. ID NO: 651)
5'- A GAT GGA GGG CGG -3' (FRAG 642) (SEQ. ID NO: 652)
5'- A GAT GGA GGG CG -3' (FRAG 643) (SEQ. ID NO: 653)
5'- A GAT GGA GGG C -3' (FRAG 644) (SEQ. ID NO: 654)
5'- A GAT GGA GGG -3' (FRAG 645) (SEQ. ID NO: 655)
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 646) (SEQ. ID NO: 656)
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 647) (SEQ. ID NO: 657)
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 648) (SEQ. ID NO: 658)
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 6) (SEQ. ID NO: 659)
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 650) (SEQ. ID NO: 660)
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 651) (SEQ. ID NO: 661)
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 652) (SEQ. ID NO: 662)
5'- GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 653) (SEQ. ID NO: 663)
5'- GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 654) (SEQ. ID NO: 664)
5'- GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 655) (SEQ. ID NO: 665)
5'- GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 656) (SEQ. ID NO: 666)
5'- GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 657) (SEQ. ID NO: 667)
5'- GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 658) (SEQ. ID NO: 668)
5'- GAT GGA GGG CGG CAT GGC GG-3' (FRAG 659) (SEQ. ID NO: 669)
5'- GAT GGA GGG CGG CAT GGC G-3' (FRAG 660) (SEQ. ID NO: 670)
5'- GAT GGA GGG CGG CAT GGC -3' (FRAG 661) (SEQ. ID NO: 671)
5'- GAT GGA GGG CGG CAT GG -3' (FRAG 662) (SEQ. ID NO: 672)
5'- GAT GGA GGG CGG CAT G -3' (FRAG 663) (SEQ. ID NO: 673)
5'- GAT GGA GGG CGG CAT -3' (FRAG 664) (SEQ. ID NO: 674)
5'- GAT GGA GGG CGG CA-3' (FRAG 665) (SEQ. ID NO: 675)
5'- GAT GGA GGG CGG C-3' (FRAG 666) (SEQ. ID NO: 676)
5'- GAT GGA GGG CGG -3' (FRAG 667) (SEQ. ID NO: 677)
5'- GAT GGA GGG CG -3' (FRAG 668) (SEQ. ID NO: 678)
5'- GAT GGA GGG C -3' (FRAG 669) (SEQ. ID NO: 679)
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 670) (SEQ. ID NO: 680)
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 671) (SEQ. ID NO: 681)
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 672) (SEQ. ID NO: 682)
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 673) (SEQ. ID NO: 683)
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 674) (SEQ. ID NO: 684)
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 675) (SEQ. ID NO: 685)
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 676) (SEQ. ID NO: 686)
5'- AT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 677) (SEQ. ID NO: 687)
5'- AT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 678) (SEQ. ID NO: 688)
5'- AT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 679) (SEQ. ID NO: 689)
5'- AT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 680) (SEQ. ID NO: 690)
5'- AT GGA GGG CGG CAT GGC GGG C-3' (FRAG 681) (SEQ. ID NO: 691)
5'- AT GGA GGG CGG CAT GGC GGG -3' (FRAG 682) (SEQ. ID NO: 692)
5'- AT GGA GGG CGG CAT GGC GG-3' (FRAG 683) (SEQ. ID NO: 693)
5'- AT GGA GGG CGG CAT GGC G-3' (FRAG 684) (SEQ. ID NO: 694)
5'- AT GGA GGG CGG CAT GGC -3' (FRAG 685) (SEQ. ID NO: 695)
5'- AT GGA GGG CGG CAT GG -3' (FRAG 686) (SEQ. ID NO: 696)
5'- AT GGA GGG CGG CAT G -3' (FRAG 687) (SEQ. ID NO: 697)
5'- AT GGA GGG CGG CAT -3' (FRAG 688) (SEQ. ID NO: 698)

5'- AT GGA GGG CGG CA-3' (FRAG 689) (SEQ. ID NO: 699)
5'- AT GGA GGG CGG C-3' (FRAG 690) (SEQ. ID NO: 700)
5'- AT GGA GGG CGG -3' (FRAG 691) (SEQ. ID NO: 701)
5'- AT GGA GGG CG -3' (FRAG 692) (SEQ. ID NO: 702)
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 693) (SEQ. ID NO: 703)
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 694) (SEQ. ID NO: 704)
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 695) (SEQ. ID NO: 705)
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 696) (SEQ. ID NO: 706)
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 697) (SEQ. ID NO: 707)
5'- T GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 698) (SEQ. ID NO: 708)
5'- T GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 699) (SEQ. ID NO: 709)
5'- T GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 700) (SEQ. ID NO: 710)
5'- T GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 701) (SEQ. ID NO: 711)
5'- T GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 702) (SEQ. ID NO: 712)
5'- T GGA GGG CGG CAT GGC GGG CA-3' (FRAG 703) (SEQ. ID NO: 713)
5'- T GGA GGG CGG CAT GGC GGG C-3' (FRAG 704) (SEQ. ID NO: 714)
5'- T GGA GGG CGG CAT GGC GGG -3' (FRAG 705) (SEQ. ID NO: 715)
5'- T GGA GGG CGG CAT GGC GG-3' (FRAG 706) (SEQ. ID NO: 716)
5'- T GGA GGG CGG CAT GGC G-3' (FRAG 707) (SEQ. ID NO: 717)
5'- T GGA GGG CGG CAT GGC -3' (FRAG 708) (SEQ. ID NO: 718)
5'- T GGA GGG CGG CAT GG -3' (FRAG 709) (SEQ. ID NO: 719)
5'- T GGA GGG CGG CAT G -3' (FRAG 710) (SEQ. ID NO: 720)
5'- T GGA GGG CGG CAT -3' (FRAG 711) (SEQ. ID NO: 721)
5'- T GGA GGG CGG CA-3' (FRAG 712) (SEQ. ID NO: 722)
5'- T GGA GGG CGG C-3' (FRAG 713) (SEQ. ID NO: 723)
5'- T GGA GGG CGG -3' (FRAG 714) (SEQ. ID NO: 724)
5'- GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 715) (SEQ. ID NO: 725)
5'- GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 716) (SEQ. ID NO: 726)
5'- GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 717) (SEQ. ID NO: 727)
5'- GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 718) (SEQ. ID NO: 728)
5'- GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 719) (SEQ. ID NO: 729)
5'- GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 720) (SEQ. ID NO: 730)
5'- GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 721) (SEQ. ID NO: 731)
5'- GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 722) (SEQ. ID NO: 732)
5'- GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 723) (SEQ. ID NO: 733)
5'- GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 724) (SEQ. ID NO: 734)
5'- GGA GGG CGG CAT GGC GGG CA-3' (FRAG 725) (SEQ. ID NO: 735)
5'- GGA GGG CGG CAT GGC GGG C-3' (FRAG 726) (SEQ. ID NO: 736)
5'- GGA GGG CGG CAT GGC GGG -3' (FRAG 727) (SEQ. ID NO: 737)
5'- GGA GGG CGG CAT GGC GG-3' (FRAG 728) (SEQ. ID NO: 738)
5'- GGA GGG CGG CAT GGC G-3' (FRAG 729) (SEQ. ID NO: 739)
5'- GGA GGG CGG CAT GGC -3' (FRAG 730) (SEQ. ID NO: 740)
5'- GGA GGG CGG CAT GG -3' (FRAG 731) (SEQ. ID NO: 741)
5'- GGA GGG CGG CAT G -3' (FRAG 732) (SEQ. ID NO: 742)
5'- GGA GGG CGG CAT -3' (FRAG 733) (SEQ. ID NO: 743)
5'- GGA GGG CGG CA-3' (FRAG 734) (SEQ. ID NO: 744)
5'- GGA GGG CGG C-3' (FRAG 735) (SEQ. ID NO: 745)
5'- GA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 736) (SEQ. ID NO: 746)
5'- GA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 737) (SEQ. ID NO: 747)
5'- GA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 738) (SEQ. ID NO: 748)
5'- GA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 739) (SEQ. ID NO: 749)
5'- GA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 740) (SEQ. ID NO: 750)
5'- GA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 741) (SEQ. ID NO: 751)
5'- GA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 742) (SEQ. ID NO: 752)
5'- GA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 743) (SEQ. ID NO: 753)
5'- GA GGG CGG CAT GGC GGG CAC A-3' (FRAG 744) (SEQ. ID NO: 754)
5'- GA GGG CGG CAT GGC GGG CAC-3' (FRAG 745) (SEQ. ID NO: 755)
5'- GA GGG CGG CAT GGC GGG CA-3' (FRAG 746) (SEQ. ID NO: 756)
5'- GA GGG CGG CAT GGC GGG C-3' (FRAG 747) (SEQ. ID NO: 757)
5'- GA GGG CGG CAT GGC GGG -3' (FRAG 748) (SEQ. ID NO: 758)
5'- GA GGG CGG CAT GGC GG-3' (FRAG 749) (SEQ. ID NO: 759)
5'- GA GGG CGG CAT GGC G-3' (FRAG 750) (SEQ. ID NO: 760)
5'- GA GGG CGG CAT GGC -3' (FRAG 751) (SEQ. ID NO: 761)
5'- GA GGG CGG CAT GG -3' (FRAG 752) (SEQ. ID NO: 762)
5'- GA GGG CGG CAT G -3' (FRAG 753) (SEQ. ID NO: 763)
5'- GA GGG CGG CAT -3' (FRAG 754) (SEQ. ID NO: 764)
5'- GA GGG CGG CA-3' (FRAG 755) (SEQ. ID NO: 765)
5'- A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 756) (SEQ. ID NO: 766)
5'- A GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 757) (SEQ. ID NO: 767)

5'- A GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 758) (SEQ. ID NO: 768)
5'- A GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 759) (SEQ. ID NO: 769)
5'- A GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 760) (SEQ. ID NO: 770)
5'- A GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 761) (SEQ. ID NO: 771)
5'- A GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 762) (SEQ. ID NO: 772)
5'- A GGG CGG CAT GGC GGG CAC AG-3' (FRAG 763) (SEQ. ID NO: 773)
5'- A GGG CGG CAT GGC GGG CAC A-3' (FRAG 764) (SEQ. ID NO: 774)
5'- A GGG CGG CAT GGC GGG CAC-3' (FRAG 765) (SEQ. ID NO: 775)
5'- A GGG CGG CAT GGC GGG CA-3' (FRAG 766) (SEQ. ID NO: 776)
5'- A GGG CGG CAT GGC GGG C-3' (FRAG 767) (SEQ. ID NO: 777)
5'- A GGG CGG CAT GGC GGG -3' (FRAG 768) (SEQ. ID NO: 778)
5'- A GGG CGG CAT GGC GG-3' (FRAG 769) (SEQ. ID NO: 779)
5'- A GGG CGG CAT GGC G-3' (FRAG 770) (SEQ. ID NO: 780)
5'- A GGG CGG CAT GGC -3' (FRAG 771) (SEQ. ID NO: 781)
5'- A GGG CGG CAT GG -3' (FRAG 772) (SEQ. ID NO: 782)
5'- A GGG CGG CAT G -3' (FRAG 773) (SEQ. ID NO: 783)
5'- A GGG CGG CAT -3' (FRAG 774) (SEQ. ID NO: 784)
5'- GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 775) (SEQ. ID NO: 785)
5'- GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 776) (SEQ. ID NO: 786)
5'- GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 777) (SEQ. ID NO: 787)
5'- GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 778) (SEQ. ID NO: 788)
5'- GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 779) (SEQ. ID NO: 789)
5'- GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 780) (SEQ. ID NO: 790)
5'- GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 781) (SEQ. ID NO: 791)
5'- GGG CGG CAT GGC GGG CAC AG-3' (FRAG 782) (SEQ. ID NO: 792)
5'- GGG CGG CAT GGC GGG CAC A-3' (FRAG 783) (SEQ. ID NO: 793)
5'- GGG CGG CAT GGC GGG CAC-3' (FRAG 784) (SEQ. ID NO: 794)
5'- GGG CGG CAT GGC GGG CA-3' (FRAG 785) (SEQ. ID NO: 795)
5'- GGG CGG CAT GGC GGG C-3' (FRAG 786) (SEQ. ID NO: 796)
5'- GGG CGG CAT GGC GGG -3' (FRAG 787) (SEQ. ID NO: 797)
5'- GGG CGG CAT GGC GG-3' (FRAG 788) (SEQ. ID NO: 798)
5'- GGG CGG CAT GGC G-3' (FRAG 789) (SEQ. ID NO: 799)
5'- GGG CGG CAT GGC -3' (FRAG 790) (SEQ. ID NO: 800)
5'- GGG CGG CAT GG -3' (FRAG 791) (SEQ. ID NO: 801)
5'- GGG CGG CAT G -3' (FRAG 792) (SEQ. ID NO: 802)
5'- GG CGG CAT GGC GGG CAC AG G CTG GGC-3' (FRAG 793) (SEQ. ID NO: 803)
5'- GG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 794) (SEQ. ID NO: 804)
5'- GG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 795) (SEQ. ID NO: 805)
5'- GG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 796) (SEQ. ID NO: 806)
5'- GG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 797) (SEQ. ID NO: 807)
5'- GG CGG CAT GGC GGG CAC AGG C-3' (FRAG 798) (SEQ. ID NO: 808)
5'- GG CGG CAT GGC GGG CAC AGG -3' (FRAG 799) (SEQ. ID NO: 809)
5'- GG CGG CAT GGC GGG CAC AG-3' (FRAG 800) (SEQ. ID NO: 810)
5'- GG CGG CAT GGC GGG CAC A-3' (FRAG 801) (SEQ. ID NO: 811)
5'- GG CGG CAT GGC GGG CAC-3' (FRAG 802) (SEQ. ID NO: 812)
5'- GG CGG CAT GGC GGG CA-3' (FRAG 803) (SEQ. ID NO: 813)
5'- GG CGG CAT GGC GGG C-3' (FRAG 804) (SEQ. ID NO: 814)
5'- GG CGG CAT GGC GGG -3' (FRAG 805) (SEQ. ID NO: 815)
5'- GG CGG CAT GGC GG-3' (FRAG 806) (SEQ. ID NO: 816)
5'- GG CGG CAT GGC G-3' (FRAG 807) (SEQ. ID NO: 817)
5'- GG CGG CAT GGC -3' (FRAG 808) (SEQ. ID NO: 818)
5'- GG CGG CAT GG -3' (FRAG 809) (SEQ. ID NO: 819)
5'- G CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 810) (SEQ. ID NO: 820)
5'- G CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 811) (SEQ. ID NO: 821)
5'- G CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 812) (SEQ. ID NO: 822)
5'- G CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 813) (SEQ. ID NO: 823)
5'- G CGG CAT GGC GGG CAC AGG CT-3' (FRAG 814) (SEQ. ID NO: 824)
5'- G CGG CAT GGC GGG CAC AGG C-3' (FRAG 815) (SEQ. ID NO: 825)
5'- G CGG CAT GGC GGG CAC AGG -3' (FRAG 816) (SEQ. ID NO: 826)
5'- G CGG CAT GGC GGG CAC AG-3' (FRAG 817) (SEQ. ID NO: 827)
5'- G CGG CAT GGC GGG CAC A-3' (FRAG 818) (SEQ. ID NO: 828)
5'- G CGG CAT GGC GGG CAC-3' (FRAG 819) (SEQ. ID NO: 829)
5'- G CGG CAT GGC GGG CA-3' (FRAG 820) (SEQ. ID NO: 830)
5'- G CGG CAT GGC GGG C-3' (FRAG 821) (SEQ. ID NO: 831)
5'- G CGG CAT GGC GGG -3' (FRAG 822) (SEQ. ID NO: 832)
5'- G CGG CAT GGC GG-3' (FRAG 823) (SEQ. ID NO: 833)
5'- G CGG CAT GGC G-3' (FRAG 824) (SEQ. ID NO: 834)
5'- G CGG CAT GGC -3' (FRAG 825) (SEQ. ID NO: 835)
5'- CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 826) (SEQ. ID NO: 836)

5'- CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 827) (SEQ. ID NO: 837)
5'- CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 828) (SEQ. ID NO: 838)
5'- CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 829) (SEQ. ID NO: 839)
5'- CGG CAT GGC GGG CAC AGG CT-3' (FRAG 830) (SEQ. ID NO: 840)
5'- CGG CAT GGC GGG CAC AGG C-3' (FRAG 831) (SEQ. ID NO: 841)
5'- CGG CAT GGC GGG CAC AGG -3' (FRAG 832) (SEQ. ID NO: 842)
5'- CGG CAT GGC GGG CAC AG-3' (FRAG 833) (SEQ. ID NO: 843)
5'- CGG CAT GGC GGG CAC A-3' (FRAG 834) (SEQ. ID NO: 844)
5'- CGG CAT GGC GGG CAC-3' (FRAG 835) (SEQ. ID NO: 845)
5'- CGG CAT GGC GGG CA-3' (FRAG 836) (SEQ. ID NO: 846)
5'- CGG CAT GGC GGG C-3' (FRAG 837) (SEQ. ID NO: 847)
5'- CGG CAT GGC GGG -3' (FRAG 838) (SEQ. ID NO: 848)
5'- CGG CAT GGC GG-3' (FRAG 839) (SEQ. ID NO: 849)
5'- CGG CAT GGC G-3' (FRAG 840) (SEQ. ID NO: 850)
5'- GG CAT GGC GGG CAC AGG C TG GGC-3' (FRAG 841) (SEQ. ID NO: 851)
5'- GG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 842) (SEQ. ID NO: 852)
5'- GG CAT GGC GGG CAC AGG CTG G-3' (FRAG 843) (SEQ. ID NO: 853)
5'- GG CAT GGC GGG CAC AGG CTG -3' (FRAG 844) (SEQ. ID NO: 854)
5'- GG CAT GGC GGG CAC AGG CT-3' (FRAG 845) (SEQ. ID NO: 855)
5'- GG CAT GGC GGG CAC AGG C-3' (FRAG 846) (SEQ. ID NO: 856)
5'- GG CAT GGC GGG CAC AGG -3' (FRAG 847) (SEQ. ID NO: 857)
5'- GG CAT GGC GGG CAC AG-3' (FRAG 848) (SEQ. ID NO: 858)
5'- GG CAT GGC GGG CAC A-3' (FRAG 849) (SEQ. ID NO: 859)
5'- GG CAT GGC GGG CAC-3' (FRAG 850) (SEQ. ID NO: 860)
5'- GG CAT GGC GGG CA-3' (FRAG 851) (SEQ. ID NO: 861)
5'- GG CAT GGC GGG C-3' (FRAG 852) (SEQ. ID NO: 862)
5'- GG CAT GGC GGG -3' (FRAG 853) (SEQ. ID NO: 863)
5'- GG CAT GGC GG-3' (FRAG 854) (SEQ. ID NO: 864)
5'- G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 855) (SEQ. ID NO: 865)
5'- G CAT GGC GGG CAC AGG CTG GG-3' (FRAG 856) (SEQ. ID NO: 866)
5'- G CAT GGC GGG CAC AGG CTG G-3' (FRAG 857) (SEQ. ID NO: 867)
5'- G CAT GGC GGG CAC AGG CTG -3' (FRAG 858) (SEQ. ID NO: 868)
5'- G CAT GGC GGG CAC AGG CT-3' (FRAG 859) (SEQ. ID NO: 869)
5'- G CAT GGC GGG CAC AGG C-3' (FRAG 860) (SEQ. ID NO: 870)
5'- G CAT GGC GGG CAC AGG -3' (FRAG 861) (SEQ. ID NO: 871)
5'- G CAT GGC GGG CAC AG-3' (FRAG 862) (SEQ. ID NO: 872)
5'- G CAT GGC GGG CAC A-3' (FRAG 863) (SEQ. ID NO: 873)
5'- G CAT GGC GGG CAC-3' (FRAG 864) (SEQ. ID NO: 874)
5'- G CAT GGC GGG CA-3' (FRAG 865) (SEQ. ID NO: 875)
5'- G CAT GGC GGG C-3' (FRAG 866) (SEQ. ID NO: 876)
5'- G CAT GGC GGG -3' (FRAG 867) (SEQ. ID NO: 877)
5'- CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 868) (SEQ. ID NO: 878)
5'- CAT GGC GGG CAC AGG CTG GG-3' (FRAG 869) (SEQ. ID NO: 879)
5'- CAT GGC GGG CAC AGG CTG G-3' (FRAG 870) (SEQ. ID NO: 880)
5'- CAT GGC GGG CAC AGG CTG -3' (FRAG 871) (SEQ. ID NO: 881)
5'- CAT GGC GGG CAC AGG CT-3' (FRAG 872) (SEQ. ID NO: 882)
5'- CAT GGC GGG CAC AGG C-3' (FRAG 873) (SEQ. ID NO: 883)
5'- CAT GGC GGG CAC AGG -3' (FRAG 874) (SEQ. ID NO: 884)
5'- CAT GGC GGG CAC AG-3' (FRAG 875) (SEQ. ID NO: 885)
5'- CAT GGC GGG CAC A-3' (FRAG 876) (SEQ. ID NO: 886)
5'- CAT GGC GGG CAC-3' (FRAG 877) (SEQ. ID NO: 887)
5'- CAT GGC GGG CA-3' (FRAG 878) (SEQ. ID NO: 888)
5'- CAT GGC GGG C-3' (FRAG 879) (SEQ. ID NO: 889)
5'- AT GGC GGG CAC AGG CTG GGC-3' (FRAG 880) (SEQ. ID NO: 890)
5'- AT GGC GGG CAC AGG CTG GG-3' (FRAG 881) (SEQ. ID NO: 891)
5'- AT GGC GGG CAC AGG CTG G-3' (FRAG 882) (SEQ. ID NO: 892)
5'- AT GGC GGG CAC AGG CTG -3' (FRAG 883) (SEQ. ID NO: 893)
5'- AT GGC GGG CAC AGG CT-3' (FRAG 884) (SEQ. ID NO: 894)
5'- AT GGC GGG CAC AGG C-3' (FRAG 885) (SEQ. ID NO: 895)
5'- AT GGC GGG CAC AGG -3' (FRAG 886) (SEQ. ID NO: 896)
5'- AT GGC GGG CAC AG-3' (FRAG 887) (SEQ. ID NO: 897)
5'- AT GGC GGG CAC A-3' (FRAG 888) (SEQ. ID NO: 898)
5'- AT GGC GGG CAC-3' (FRAG 889) (SEQ. ID NO: 899)
5'- AT GGC GGG CA-3' (FRAG 890) (SEQ. ID NO: 900)
5'- T GGC GGG CAC AGG CTG GGC-3' (FRAG 891) (SEQ. ID NO: 901)
5'- T GGC GGG CAC AGG CTG GG-3' (FRAG 892) (SEQ. ID NO: 902)
5'- T GGC GGG CAC AGG CTG G-3' (FRAG 893) (SEQ. ID NO: 903)
5'- T GGC GGG CAC AGG CTG -3' (FRAG 894) (SEQ. ID NO: 904)
5'- T GGC GGG CAC AGG CT-3' (FRAG 895) (SEQ. ID NO: 905)

5'- T GGC GGG CAC AGG C-3' (FRAG 896) (SEQ. ID NO: 906)
5'- T GGC GGG CAC AGG -3' (FRAG 897) (SEQ. ID NO: 907)
5'- T GGC GGG CAC AG-3' (FRAG 898) (SEQ. ID NO: 908)
5'- T GGC GGG CAC A-3' (FRAG 899) (SEQ. ID NO: 909)
5'- T GGC GGG CAC-3' (FRAG 900) (SEQ. ID NO: 910)
5'- GGC GGG CAC AGG CTG GGC-3' (FRAG 901) (SEQ. ID NO: 911)
5'- GGC GGG CAC AGG CTG GG-3' (FRAG 902) (SEQ. ID NO: 912)
5'- GGC GGG CAC AGG CTG G-3' (FRAG 903) (SEQ. ID NO: 913)
5'- GGC GGG CAC AGG CTG -3' (FRAG 904) (SEQ. ID NO: 914)
5'- GGC GGG CAC AGG CT-3' (FRAG 905) (SEQ. ID NO: 915)
5'- GGC GGG CAC AGG C-3' (FRAG 906) (SEQ. ID NO: 916)
5'- GGC GGG CAC AGG -3' (FRAG 907) (SEQ. ID NO: 917)
5'- GGC GGG CAC AG-3' (FRAG 908) (SEQ. ID NO: 918)
5'- GGC GGG CAC A-3' (FRAG 909) (SEQ. ID NO: 919)
5'- GC GGG CAC AGG CTG GGC-3' (FRAG 910) (SEQ. ID NO: 920)
5'- GC GGG CAC AGG CTG GG-3' (FRAG 911) (SEQ. ID NO: 921)
5'- GC GGG CAC AGG CTG G-3' (FRAG 912) (SEQ. ID NO: 922)
5'- GC GGG CAC AGG CTG -3' (FRAG 913) (SEQ. ID NO: 923)
5'- GC GGG CAC AGG CT-3' (FRAG 914) (SEQ. ID NO: 924)
5'- GC GGG CAC AGG C-3' (FRAG 915) (SEQ. ID NO: 925)
5'- GC GGG CAC AGG -3' (FRAG 916) (SEQ. ID NO: 926)
5'- GC GGG CAC AG-3' (FRAG 917) (SEQ. ID NO: 927)
5'- C GGG CAC AGG CTG GGC-3' (FRAG 918) (SEQ. ID NO: 928)
5'- GGG CAC AGG CTG GG-3' (FRAG 919) (SEQ. ID NO: 929)
5'- C GGG CAC AGG CTG G-3' (FRAG 920) (SEQ. ID NO: 930)
5'- C GGG CAC AGG CTG -3' (FRAG 921) (SEQ. ID NO: 931)
5'- C GGG CAC AGG CT-3' (FRAG 922) (SEQ. ID NO: 932)
5'- C GGG CAC AGG C-3' (FRAG 923) (SEQ. ID NO: 933)
5'- C GGG CAC AGG -3' (FRAG 924) (SEQ. ID NO: 934)
5'- GGG CAC AGG CTG GGC-3' (FRAG 925) (SEQ. ID NO: 935)
5'- GGG CAC AGG CTG GG-3' (FRAG 926) (SEQ. ID NO: 936)
5'- GGG CAC AGG CTG G-3' (FRAG 927) (SEQ. ID NO: 937)
5'- GGG CAC AGG CTG -3' (FRAG 928) (SEQ. ID NO: 938)
5'- GGG CAC AGG CT-3' (FRAG 929) (SEQ. ID NO: 939)
5'- GGG CAC AGG C-3' (FRAG 930) (SEQ. ID NO: 940)
5'- GG CAC AGG CTG GGC-3' (FRAG 931) (SEQ. ID NO: 941)
5'- GG CAC AGG CTG GG-3' (FRAG 932) (SEQ. ID NO: 942)
5'- GG CAC AGG CTG G-3' (FRAG 933) (SEQ. ID NO: 943)
5'-GG CAC AGG CTG -3' (FRAG 934) (SEQ. ID NO: 944)
5'- GG CAC AGG CT-3' (FRAG 935) (SEQ. ID NO: 945)
5'-G CAC AGG CTG GGC-3' (FRAG 936) (SEQ. ID NO: 946)
5'-G CAC AGG CTG GG-3' (FRAG 937) (SEQ. ID NO: 947)
5'-G CAC AGG CTG G-3' (FRAG 938) (SEQ. ID NO: 948)
5'-G CAC AGG CTG -3' (FRAG 939) (SEQ. ID NO: 949)
5'-CAC AGG CTG GGC-3' (FRAG 940) (SEQ. ID NO: 950)
5'-CAC AGG CTG GG-3' (FRAG 941) (SEQ. ID NO: 951)
5'-CAC AGG CTG G-3' (FRAG 942) (SEQ. ID NO: 952)
5'-AC AGG CTG GGC-3' (FRAG 943) (SEQ. ID NO: 953)
5'-AC AGG CTG GG-3' (FRAG 944) (SEQ. ID NO: 954)
5'-C AGG CTG GGC-3' (FRAG 945) (SEQ. ID NO: 955)
5'-TTT TCC TTC CTT TGT CTC TCT TC (FRAG 946) (SEQ. ID NO: 956)
5'-GCT CCC GGC TGC CTG (FRAG 947) (SEQ. ID NO: 957)
5'-CTC GGC CGT GCG GCT CTG TCG CTC CCG GT (FRAG 948) (SEQ. ID NO: 958)
5'-CCG CCG CCC TCC GGG GGG TC (FRAG 949) (SEQ. ID NO: 959)
5'-TGC TGC CGT TGG CTG CCC (FRAG 950) (SEQ. ID NO: 960)
5'-CTT CTG CGG GTC GCC GG (FRAG 951) (SEQ. ID NO: 961)
5'-TGC TGG GCT TGT GGC (FRAG 952) (SEQ. ID NO: 962)
5'-GGC CTC TCT TCT GGG (FRAG 953) (SEQ. ID NO: 963)
5'-CCT GGT CCC TCC GT (FRAG 954) (SEQ. ID NO: 964)
5'-GGT GGC TCC TCT GC (FRAG 955) (SEQ. ID NO: 965)
5'-GCT TGG TCC TGG GGC TGC (FRAG 956) (SEQ. ID NO: 966)
5'-TGC TCT CCT CTC CTT (FRAG 957) (SEQ. ID NO: 967)

Human Adenosine A2a Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TGC TTT TCT TTT CTG GGC CTC TGT GGT CTG TTT TTT TCT G GCC CTG CTG GGG CGC TCT CC GCC GCC CGC CTG GCT CCC GGB GCC CBT GBT GGG CBT GCC GTG GTT CTT GCC CTC CTT TGG CTG CCG TGC CCG CTC CCC GGC CTC CTG GCG GGT GGC CGT TG GGC CCG TGT TCC CCT GGG -GCC TGG GGC TCC CTT CTC TC GCC CTT CTT GCT GGG CCT C TGC TGC TGC TGG TGC TGT GGC CCC C GTA CAC CGA GGA GCC CAT GAT GGG CAT GCC ACA GAC GAC AGG C GTB CBC CGB GGB GCC CBT GBT GGG CBT GCC BCB GBC GBC BGG C-3' (FRAG. NO. 1665) (SEQ. ID NO:1678)
5'-CTG GGC CTC-3' (FRAG 1666) (SEQ. ID NO: 1679)

5'-GCC GCC CGC CTG-3' (FRAG 1667) (SEQ. ID NO: 1680)
5'-GC CCG CTC CCC GGC-3' (FRAG 1668) (SEQ. ID NO: 1681)
5'-CBCCGBGGBGCCC-3' (FRAG 1669) (SEQ. ID NO: 1682)
5'-TGC TTT TCT TTT CTG GGC CTC-3' (FRAG 958) (SEQ. ID NO: 968)
5'-TGT GGT CTG TTT TTT TCT G-3' (FRAG 959) (SEQ. ID NO: 969)
5'-GCC CTG CTG GGG CGC TCT CC-3' (FRAG 960) (SEQ. ID NO: 970)
5'-GCC GCC CGC CTG GCT CCC-3' (FRAG 961) (SEQ. ID NO: 971)
5'-GGB GCC CBT GBT GGG CBT GCC-3' (FRAG 962) (SEQ. ID NO: 972)
5'-GTG GTT CTT GCC CTC CTT TGG CTG-3' (FRAG 963) (SEQ. ID NO: 973)
5'-CCG TGC CCG CTC CCC GGC-3' (FRAG 964) (SEQ. ID NO: 974)
5'-CTC CTG GCG GGT GGC CGT TG-3' (FRAG 965) (SEQ. ID NO: 975)
5'-GGC CCG TGT TCC CCT GGG-3' (FRAG 966) (SEQ. ID NO: 976)
5'-GCC TGG GGC TCC CTT CTC TC-3' (FRAG 967) (SEQ. ID NO: 977)
5'-GCC CTT CTT GCT GGG CCT C-3' (FRAG 968) (SEQ. ID NO: 978)
5'-TGC TGC TGC TGG TGC TGT GGC CCC C-3' (FRAG 969) (SEQ. ID NO: 979)
5'-GTACACCGAGGAGCCCATGATGGGCATGCCACAGACGACAGGC-3' (FRAG 970) (SEQ. ID NO: 980)
5'-GTBCBCCGBGGBGCCCBTGBTGGGCBTGCCBCBGBCGBCBGGC-3' (FRAG 971) (SEQ. ID NO: 981)

Human Adenosine A2b Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGC GCC GTG CCG CGT CTT GGT GGC GGC GG GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC GTT CGC GCC CGC
GCG GGG CCC CTC CGG TCC CGG GTC GGG GCC CCC CGC GGC C GCC TCG GGG CTG GGG CGC TGG TGG CCG GG CCG
CGC CTC CGC CTG CCG CTT CTG GCT GGG CCC CGG GCG CCC CCT CCC CTC TTG CTC GGG TCC CCG TG ACA GCG CGT
CCT GTG TCT CCA GCA GCA TGG CCG GGC CAG CTG GGC CCC BCB GCG CGT CCT GTG TCT CCB GCB GCB TGG CCG
GGC CBG CTG GGC CCC CCCAGCCCCG AGGCTCAGAA GCGGCAGGCG GAGGCGCGGT CCGGGCGCTA TGGCCATGCC
CGGCGGGTCT CACGCGGCTG CCCCTCGCCC GGCGCGCCTT CGGTAGGGGG CGCCCGGGGC CCAGCTGGCC CGGCCATGCT
GCTGGAGACA CAGGACGCGC TGTACGTGGC GCTGGAGCTG GTCATCGCCG CGCTTTCGGT GGCGGGCAAC GTGCTGGTGT
GCGCCGCGGT GGGCACGGCG AACACTCTGC AGACGCCCAC CAACTACTTC CTGGTGTCCC TGGCTGCGGC CGACGTGGCC
GTGGGGCTCT TCGCCATCCC CTTTGCCATC ACCATCAGCC TGGGCTTCTG CACTGACTTC TACGGCTGCC TCTTCCTCGC
CTGCTTCGTG CTGGTGCTCA CGCAGAGCTC CATCTTCAGC CTTCTGGCCG TGGCAGTCGA CAGATACCTG GCCATCTGTG
TCCCGCTCAG GTATAAAAGT TTGGTCACGG GGACCCGAGC AAGAGGGGTC ATTGCTGTCC TCTGGGTCCT TGCCTTTGGC
ATCGGATTGA CTCCATTCCT GGGGTGGAAC AGTAAAGACA GTGCCACCAA CAACTGCACA GAACCCTGGG ATGGAACCAC
GAATGAAAGC TGCTGCCTTG TGAAGTGTCT CTTTGAGAAT GTGGTCCCCA TGAGCTACAT GGTATATTTC AATTTCTTTG
GGTGTGTTCT GCCCCCACTG CTTATAATGC TGGTGATCTA CATTAAGATC TTCCTGGTGG CCTGCAGGCA GCTTCAGCGC
ACTGAGCTGA TGGACCACTC GAGGACCACC CTCCAGCGGG AGATCCATGC AGCCAAGTCA CTGGCCATGA TTGTGGGGAT
TTTTGCCCTG TGCTGGTTAC CTGTGCATGC TGTTAACTGT GTCACTCTTT TCCAGCCAGC TCAGGGTAAA AATAAGCCCA
AGTGGGCAAT GAATATGGCC ATTCTTCTGT CACATGCCAA TTCAGTTGTC AATCCCATTG TCTATGCTTA CCGGAACCGA
GACTTCCGCT ACACTTTTCA CAAAATTATC TCCAGGTATC TTCTCTGCCA AGCAGATGTC AAGAGTGGGA ATGGTCAGGC
TGGGGTACAG CCTGCTCTCG GTGTGGGCCT ATGATCTAGG CTCTCGCCTC TTCCAGGAGA AGATACAAAT CCACAAGAAA
CAAAGAGGAC ACGGCTGGTT TTCATTGTGA AAGATAGCTA CACCTCACAA GGAAATGGAC TGCCTCTCTT GAGCACTTCC
CTGGAGCTAC CACGTATCTA GCTAATATGT ATGTGTCAGT AGTAGCACCA AGGATTGACA AATATATTTA TGATCTATTC
AGCTGCTTTT ACTGTGTGGA TTATGCCAAC AGCTTGAATG GATTCTAACA GACTCTTTTG TTTTTAAAAG TCTGCCTTGT
TTATGGTGGA AAATTACTGA AACTATTTTA CTGTGAAACA GTGTGAACTA TTATAATGCA AATACTTTTT AACTTAGAGG
CAATGGAAAA ATAAAAGTTG ACTGTACTAA AAATGTATAC TTGTTGCCAG GAAGGTGACC TCAAAAATTA AAAGTATAAT
TATTCGGCCG GGCATGGTGG CTCACACCTG TAATTCCAGC ACTTTGGGAG GCCAAGGCAG GCGGATCACG AGGTCAGGAG
TTCAAAACCA GCCTGTCCAA TATAGTG GGGCAATTTG TTAGTTATCC GCCGCCACCA AGACGCGGCA CGGCGCCTGG
ACCGGAGGGG CCCCGCGCGG GCGCGAACTT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA CGGGCGGGCG
CGCGGGCCAA TGGGTGCCGC CTCTTGGCCG CGGGGGGCCC CGACCCGTGG GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG
CTCAGAAGCG GCAGGCGGAG GCGCGGTCCG GGCGCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCCC CTCGCCCGGC
GCGCCTTCGG TAGGGGGCGC CCGGGGCCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG GACGCGCTGT ACGTGGCGCT
GGAGCTGGTC ATCGCCGCGC TTTCGGTGGC GGGCAACGTG CTGGTGTGCG CCGCGGTGGG CACGGCGAAC ACTCTGCAGA
CGCCCACCAA CTACTTCCTG GTGTCCCTGG CTGCGGCCGA CGTGGCCGTG GGGCTCTTCG CCATCCCCTT TGCCATCACC
ATCAGCCTGG GCTTCTGCAC TGACTTCTAC GGCTGCCTCT TCCTCGCCTG CTTCGTGCTG GTGCTCACGC AGAGCTCCAT
CTTCAGCCTT CTGGCCGTGG CAGTCGACAG ATACCTGGCC ATCTGTGTCC CGCTCAGGTA TAAAAGTTTG GTCACGGGGA
CCCGAGCAAG AGGGGTCATT GCTGTCCTCT GGGTCCTTGC CTTTGGCATC GGATTGACTC CATTCCTGGG GTGGAACAGT
AAAGACAGTG CCACCAACAA CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCTTGTGA AGTGTCTCTT
TGAGAATGTG GTCCCCATGA GCTACATGGT ATATTTCAAT TTCTTTGGGT GTGTTCTGCC CCCACTGCTT ATAATGCTGG
TGATCTACAT TAAGATCTTC CTGGTGGCCT GCAGGCAGCT TCAGCGCACT GAGCTGATGG ACCACTCGAG GACCACCCTC
CAGCGGGAGA TCCATGCAGC CAAGTCACTG GCCATGATTG TGGGGATTTT TGCCCTGTGC TGGTTACCTG TGCATGCTGT
TAACTGTGTC ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT GGGCAATGAA TATGGCCATT CTTCTGTCAC
ATGCCAATTC AGTTGTCAAT CCCATTGTCT ATGCTTACCG GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC
AGGTATCTTC TCTGCCAAGC AGATGTCAAG AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTCGGTG TGGGCCTATG
ATCTAGGCTC TCGCCTCTTC CAGGAGAAGA TACAAATCCA CAAGAAACAA AGAGGACACG GCTGGTTTTC ATTGTGAAAG
ATAGCTACAC CTCACAAGGA AATGGACTGC CTCTCTTGAG CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG
TGTCAGTAGT AGGCTCCAAG GATTGACAAA TATATTTATG ATCTATTCAG CTGCTTTTAC TGTGTGGATT ATGCCAACAG
CTTGAATGGA TTCTAACAGA CTCTTTTGTT TTTAAAAGTC TGCCTTGTTT ATGGTGGAAA ATTACTGAAA CTATTTTACT
GTGAAACAGT GTGAACTATT ATAATGCAAA TACTTTTTAA CTTAGAGGCA ATGGAAAAAT AAAAGTTGAC TGTACTAAAA

ATG CCCAGCCCCG AGGCTCAGAA GCGGCAGGCG GAGGCGCGGT CCGGGCGCTA TGGCCATGCC CGGCGGGTCT CACGCGGCTG CCCCTCGCCC GGCGCGCCTT CGGTAGGGGG CGCCCGGGGC CCAGCTGGCC CGGCCATGCT GCTGGAGACA CAGGACGCGC TGTACGTGGC GCTGGAGCTG GTCATCGCCG CGCTTTCGGT GGCGGGCAAC GTGCTGGTGT GCGCCGCGGT GGGCACGGCG AACACTCTGC AGACGCCCAC CAACTACTTC CTGGTGTCCC TGGCTGCGGC CGACGTGGCC GTGGGGCTCT TCGCCATCCC CTTTGCCATC ACCATCAGCC TGGGCTTCTG CACTGACTTC TACGGCTGCC TCTTCCTCGC CTGCTTCGTG CTGGTGCTCA CGCAGAGCTC CATCTTCAGC CTTCTGGCCG TGGCAGTCGA CAGATACCTG GCCATCTGTG TCCCGCTCAG GTATAAAAGT TTGGTCACGG GGACCCGAGC AAGAGGGGTC ATTGCTGTCC TCTGGGTCCT TGCCTTTGGC ATCGGATTGA CTCCATTCCT GGGGTGGAAC AGTAAAGACA GTGCCACCAA CAACTGCACA GAACCCTGGG ATGGAACCAC GAATGAAAGC TGCTGCCTTG TGAAGTGTCT CTTTGAGAAT GTGGTCCCCA TGAGCTACAT GGTATATTTC AATTTCTTTG GGTGTGTTCT GCCCCCACTG CTTATAATGC TGGTGATCTA CATTAAGATC TTCCTGGTGG CCTGCAGGCA GCTTCAGCGC ACTGAGCTGA TGGACCACTC GAGGACCACC CTCCAGCGGG AGATCCATGC AGCCAAGTCA CTGGCCATGA TTGTGGGGAT TTTTGCCCTG TGCTGGTTAC CTGTGCATGC TGTTAACTGT GTCACTCTTT TCCAGCCAGC TCAGGGTAAA AATAAGCCCA AGTGGGCAAT GAATATGGCC ATTCTTCTGT CACATGCCAA TTCAGTTGTC AATCCCATTG TCTATGCTTA CCGGAACCGA GACTTCCGCT ACACTTTTCA CAAAATTATC TCCAGGTATC TTCTCTGCCA AGCAGATGTC AAGAGTGGGA ATGGTCAGGC TGGGGTACAG CCTGCTCTCG GTGTGGGCCT ATGATCTAGG CTCTCGCCTC TTCCAGGAGA AGATACAAAT CCACAAGAAA CAAAGAGGAC ACGGCTGGTT TTCATTGTGA AAGATAGCTA CACCTCACAA GGAAATGGAC TGCCTCTCTT GAGCACTTCC CTGGAGCTAC CACGTATCTA GCTAATATGT ATGTGTCAGT AGTAGCACCA AGGATTGACA AATATATTTA TGATCTATTC AGCTGCTTTT ACTGTGTGGA TTATGCCAAC AGCTTGAATG GATTCTAACA GACTCTTTTG TTTTTAAAAG TCTGCCTTGT TTATGGTGGA AAATTACTGA AACTATTTTA CTGTGAAACA GTGTGAACTA TTATAATGCA AATACTTTTT AACTTAGAGG CAATGGAAAA ATAAAAGTTG ACTGTACTAA AAATGTATAC TTGTTGCCAG GAAGGTGACC TCAAAAATTA AAAGTATAAT TATTCGGCCG GGCATGGTGG CTCACACCTG TAATTCCAGC ACTTTGGGAG GCCAAGGCAG GCGGATCACG AGGTCAGGAG TTCAAAACCA GCCTGTCCAA TATAGTG GGGCAATTTG TTAGTTATCC GCCGCCACCA AGACGCGGCA CGGCGCCTGG ACCGGAGGGG CCCCGCGCGG GCGCGAACTT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA CGGGCGGGCG CGCGGGCCAA TGGGTGCCGC CTCTTGGCCG CGGGGGGCCC CGACCCGTGG GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG GCAGGCGGAG GCGCGGTCCG GGCGCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCCC CTCGCCCGGC GCGCCTTCGG TAGGGGGCGC CCGGGGCCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG GACGCGCTGT ACGTGGCGCT GGAGCTGGTC ATCGCCGCGC TTTCGGTGGC GGGCAACGTG CTGGTGTGCG CCGCGGTGGG CACGGCGAAC ACTCTGCAGA CGCCCACCAA CTACTTCCTG GTGTCCCTGG CTGCGGCCGA CGTGGCCGTG GGGCTCTTCG CCATCCCCTT TGCCATCACC ATCAGCCTGG GCTTCTGCAC TGACTTCTAC GGCTGCCTCT TCCTCGCCTG CTTCGTGCTG GTGCTCACGC AGAGCTCCAT CTTCAGCCTT CTGGCCGTGG CAGTCGACAG ATACCTGGCC ATCTGTGTCC CGCTCAGGTA TAAAAGTTTG GTCACGGGGA CCCGAGCAAG AGGGGTCATT GCTGTCCTCT GGGTCCTTGC CTTTGGCATC GGATTGACTC CATTCCTGGG GTGGAACAGT AAAGACAGTG CCACCAACAA CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCTTGTGA AGTGTCTCTT TGAGAATGTG GTCCCCATGA GCTACATGGT ATATTTCAAT TTCTTTGGGT GTGTTCTGCC CCCACTGCTT ATAATGCTGG TGATCTACAT TAAGATCTTC CTGGTGGCCT GCAGGCAGCT TCAGCGCACT GAGCTGATGG ACCACTCGAG GACCACCCTC CAGCGGGAGA TCCATGCAGC CAAGTCACTG GCCATGATTG TGGGGATTTT TGCCCTGTGC TGGTTACCTG TGCATGCTGT TAACTGTGTC ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT GGGCAATGAA TATGGCCATT CTTCTGTCAC ATGCCAATTC AGTTGTCAAT CCCATTGTCT ATGCTTACCG GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC AGGTATCTTC TCTGCCAAGC AGATGTCAAG AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTCGGTG TGGGCCTATG ATCTAGGCTC TCGCCTCTTC CAGGAGAAGA TACAAATCCA CAAGAAACAA AGAGGACACG GCTGGTTTTC ATTGTGAAAG ATAGCTACAC CTCACAAGGA AATGGACTGC CTCTCTTGAG CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG TGTCAGTAGT AGGCTCCAAG GATTGACAAA TATATTTATG ATCTATTCAG CTGCTTTTAC TGTGTGGATT ATGCCAACAG CTTGAATGGA TTCTAACAGA CTCTTTTGTT TTTAAAAGTC TGCCTTGTTT ATGGTGGAAA ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACTATT ATAATGCAAA TACTTTTTAA CTTAGAGGCA ATGGAAAAAT AAAAGTTGAC TGTACTAAAA ATG -3' **(FRAG. NO: 1670) (SEQ. ID NO:1683)**

5'- GGGCAATTTG TTAGTTATCC GCCGCCACCA AGACGCGGCA CGGCGCCTGG ACCGGAGGGG CCCCGCGCGG GCGCGAACTT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA CGGGCGGGCG CGCGGGCCAA TGGGTGCCGC CTCTTGGCCG CGGGGGGCCC CGACCCGTGG GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG GCAGGCGGAG GCGCGGTCCG GGCGCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCCC CTCGCCCGGC GCGCCTTCGG TAGGGGGCGC CCGGGGCCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG GACGCGCTGT ACGTGGCGCT GGAGCTGGTC ATCGCCGCGC TTTCGGTGGC GGGCAACGTG CTGGTGTGCG CCGCGGTGGG CACGGCGAAC ACTCTGCAGA CGCCCACCAA CTACTTCCTG GTGTCCCTGG CTGCGGCCGA CGTGGCCGTG GGGCTCTTCG CCATCCCCTT TGCCATCACC ATCAGCCTGG GCTTCTGCAC TGACTTCTAC GGCTGCCTCT TCCTCGCCTG CTTCGTGCTG GTGCTCACGC AGAGCTCCAT CTTCAGCCTT CTGGCCGTGG CAGTCGACAG ATACCTGGCC ATCTGTGTCC CGCTCAGGTA TAAAAGTTTG GTCACGGGGA CCCGAGCAAG AGGGGTCATT GCTGTCCTCT GGGTCCTTGC CTTTGGCATC GGATTGACTC CATTCCTGGG GTGGAACAGT AAAGACAGTG CCACCAACAA CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCTTGTGA AGTGTCTCTT TGAGAATGTG GTCCCCATGA GCTACATGGT ATATTTCAAT TTCTTTGGGT GTGTTCTGCC CCCACTGCTT ATAATGCTGG TGATCTACAT TAAGATCTTC CTGGTGGCCT GCAGGCAGCT TCAGCGCACT GAGCTGATGG ACCACTCGAG GACCACCCTC CAGCGGGAGA TCCATGCAGC CAAGTCACTG GCCATGATTG TGGGGATTTT TGCCCTGTGC TGGTTACCTG TGCATGCTGT TAACTGTGTC ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT GGGCAATGAA TATGGCCATT CTTCTGTCAC ATGCCAATTC AGTTGTCAAT CCCATTGTCT ATGCTTACCG GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC AGGTATCTTC TCTGCCAAGC AGATGTCAAG AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTCGGTG TGGGCCTATG ATCTAGGCTC TCGCCTCTTC CAGGAGAAGA TACAAATCCA CAAGAAACAA AGAGGACACG GCTGGTTTTC ATTGTGAAAG ATAGCTACAC CTCACAAGGA AATGGACTGC CTCTCTTGAG CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG TGTCAGTAGT AGGCTCCAAG GATTGACAAA TATATTTATG ATCTATTCAG CTGCTTTTAC TGTGTGGATT ATGCCAACAG CTTGAATGGA TTCTAACAGA CTCTTTTGTT TTTAAAAGTC TGCCTTGTTT ATGGTGGAAA ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACTATT ATAATGCAAA TACTTTTTAA CTTAGAGGCA ATGGAAAAAT AAAAGTTGAC TGTACTAAAA ATG -3' **(FRAG. NO:_) (SEQ. ID**

NO:2436)
5'- CCCAGCCCCG AGGCTCAGAA GCGGCAGGCG GAGGCGCGGT CCGGGCGCTA TGGCCATGCC CGGCGGGTCT CACGCGGCTG CCCCTCGCCC GGCGCGCCTT CGGTAGGGGG CGCCCGGGGC CCAGCTGGCC CGGCCATGCT GCTGGAGACA CAGGACGCGC TGTACGTGGC GCTGGAGCTG GTCATCGCCG CGCTTTCGGT GGCGGGCAAC GTGCTGGTGT GCGCCGCGGT GGGCACGGCG AACACTCTGC AGACGCCCAC CAACTACTTC CTGGTGTCCC TGGCTGCGGC CGACGTGGCC GTGGGGCTCT TCGCCATCCC CTTTGCCATC ACCATCAGCC TGGGCTTCTG CACTGACTTC TACGGCTGCC TCTTCCTCGC CTGCTTCGTG CTGGTGCTCA CGCAGAGCTC CATCTTCAGC CTTCTGGCCG TGGCAGTCGA CAGATACCTG GCCATCTGTG TCCCGCTCAG GTATAAAAGT TTGGTCACGG GGACCCGAGC AAGAGGGGTC ATTGCTGTCC TCTGGGTCCT TGCCTTTGGC ATCGGATTGA CTCCATTCCT GGGGTGGAAC AGTAAAGACA GTGCCACCAA CAACTGCACA GAACCCTGGG ATGGAACCAC GAATGAAAGC TGCTGCCTTG TGAAGTGTCT CTTTGAGAAT GTGGTCCCCA TGAGCTACAT GGTATATTTC AATTTCTTTG GGTGTGTTCT GCCCCCACTG CTTATAATGC TGGTGATCTA CATTAAGATC TTCCTGGTGG CCTGCAGGCA GCTTCAGCGC ACTGAGCTGA TGGACCACTC GAGGACCACC CTCCAGCGGG AGATCCATGC AGCCAAGTCA CTGGCCATGA TTGTGGGGAT TTTTGCCCTG TGCTGGTTAC CTGTGCATGC TGTTAACTGT GTCACTCTTT TCCAGCCAGC TCAGGGTAAA AATAAGCCCA AGTGGGCAAT GAATATGGCC ATTCTTCTGT CACATGCCAA TTCAGTTGTC AATCCCATTG TCTATGCTTA CCGGAACCGA GACTTCCGCT ACACTTTTCA CAAAATTATC TCCAGGTATC TTCTCTGCCA AGCAGATGTC AAGAGTGGGA ATGGTCAGGC TGGGGTACAG CCTGCTCTCG GTGTGGGCCT ATGATCTAGG CTCTCGCCTC TTCCAGGAGA AGATACAAAT CCACAAGAAA CAAAGAGGAC ACGGCTGGTT TTCATTGTGA AAGATAGCTA CACCTCACAA GGAAATGGAC TGCCTCTCTT GAGCACTTCC CTGGAGCTAC CACGTATCTA GCTAATATGT ATGTGTCAGT AGTAGCACCA AGGATTGACA AATATATTTA TGATCTATTC AGCTGCTTTT ACTGTGTGGA TTATGCCAAC AGCTTGAATG GATTCTAACA GACTCTTTTG TTTTTAAAAG TCTGCCTTGT TTATGGTGGA AAATTACTGA AACTATTTTA CTGTGAAACA GTGTGAACTA TTATAATGCA AATACTTTTT AACTTAGAGG CAATGGAAAA ATAAAAGTTG ACTGTACTAA AAATGTATAC TTGTTGCCAG GAAGGTGACC TCAAAAATTA AAAGTATAAT TATTCGGCCG GGCATGGTGG CTCACACCTG TAATTCCAGC ACTTTGGGAG GCCAAGGCAG GCGGATCACG AGGTCAGGAG TTCAAAACCA GCCTGTCCAA TATAGTG -3' **(FRAG. NO:_) (SEQ. ID NO:2435)**

5'- GGGCAATTTG TTAGTTATCC GCCGCCACCA AGACGCGGCA CGGCGCCTGG ACCGGAGGGG CCCCGCGCGG GCGCGAACTT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA CGGGCGGGCG CGCGGGCCAA TGGGTGCCGC CTCTTGGCCG CGGGGGGCCC CGACCCGTGG GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG GCAGGCGGAG GCGCGGTCCG GGCGCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCCC CTCGCCCGGC GCGCCTTCGG TAGGGGGCGC CCGGGGCCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG GACGCGCTGT ACGTGGCGCT GGAGCTGGTC ATCGCCGCGC TTTCGGTGGC GGGCAACGTG CTGGTGTGCG CCGCGGTGGG CACGGCGAAC ACTCTGCAGA CGCCCACCAA CTACTTCCTG GTGTCCCTGG CTGCGGCCGA CGTGGCCGTG GGGCTCTTCG CCATCCCCTT TGCCATCACC ATCAGCCTGG GCTTCTGCAC TGACTTCTAC GGCTGCCTCT TCCTCGCCTG CTTCGTGCTG GTGCTCACGC AGAGCTCCAT CTTCAGCCTT CTGGCCGTGG CAGTCGACAG ATACCTGGCC ATCTGTGTCC CGCTCAGGTA TAAAAGTTTG GTCACGGGGA CCCGAGCAAG AGGGGTCATT GCTGTCCTCT GGGTCCTTGC CTTTGGCATC GGATTGACTC CATTCCTGGG GTGGAACAGT AAAGACAGTG CCACCAACAA CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCTTGTGA AGTGTCTCTT TGAGAATGTG GTCCCCATGA GCTACATGGT ATATTTCAAT TTCTTTGGGT GTGTTCTGCC CCCACTGCTT ATAATGCTGG TGATCTACAT TAAGATCTTC CTGGTGGCCT GCAGGCAGCT TCAGCGCACT GAGCTGATGG ACCACTCGAG GACCACCCTC CAGCGGGAGA TCCATGCAGC CAAGTCACTG GCCATGATTG TGGGGATTTT TGCCCTGTGC TGGTTACCTG TGCATGCTGT TAACTGTGTC ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT GGGCAATGAA TATGGCCATT CTTCTGTCAC ATGCCAATTC AGTTGTCAAT CCCATTGTCT ATGCTTACCG GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC AGGTATCTTC TCTGCCAAGC AGATGTCAAG AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTCGGTG TGGGCCTATG ATCTAGGCTC TCGCCTCTTC CAGGAGAAGA TACAAATCCA CAAGAAACAA AGAGGACACG GCTGGTTTTC ATTGTGAAAG ATAGCTACAC CTCACAAGGA AATGGACTGC CTCTCTTGAG CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG TGTCAGTAGT AGGCTCCAAG GATTGACAAA TATATTTATG ATCTATTCAG CTGCTTTTAC TGTGTGGATT ATGCCAACAG CTTGAATGGA TTCTAACAGA CTCTTTTGTT TTTAAAAGTC TGCCTTGTTT ATGGTGGAAA ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACTATT ATAATGCAAA TACTTTTTAA CTTAGAGGCA ATGGAAAAAT AAAAGTTGAC TGTACTAAAA ATG -3' **(FRAG. NO:_) (SEQ. ID NO:2425)**

5'-CCCAGCCCCG AGGCTCAGAA GCGGCAGGCG GAGGCGCGGT CCGGGCGCTA TGGCCATGCC CGGCGGGTCT CACGCGGCTG CCCCTCGCCC GGCGCGCCTT CGGTAGGGGG CGCCCGGGGC CCAGCTGGCC CGGCCATGCT GCTGGAGACA CAGGACGCGC TGTACGTGGC GCTGGAGCTG GTCATCGCCG CGCTTTCGGT GGCGGGCAAC GTGCTGGTGT GCGCCGCGGT GGGCACGGCG AACACTCTGC AGACGCCCAC CAACTACTTC CTGGTGTCCC TGGCTGCGGC CGACGTGGCC GTGGGGCTCT TCGCCATCCC CTTTGCCATC ACCATCAGCC TGGGCTTCTG CACTGACTTC TACGGCTGCC TCTTCCTCGC CTGCTTCGTG CTGGTGCTCA CGCAGAGCTC CATCTTCAGC CTTCTGGCCG TGGCAGTCGA CAGATACCTG GCCATCTGTG TCCCGCTCAG GTATAAAAGT TTGGTCACGG GGACCCGAGC AAGAGGGGTC ATTGCTGTCC TCTGGGTCCT TGCCTTTGGC ATCGGATTGA CTCCATTCCT GGGGTGGAAC AGTAAAGACA GTGCCACCAA CAACTGCACA GAACCCTGGG ATGGAACCAC GAATGAAAGC TGCTGCCTTG TGAAGTGTCT CTTTGAGAAT GTGGTCCCCA TGAGCTACAT GGTATATTTC AATTTCTTTG GGTGTGTTCT GCCCCCACTG CTTATAATGC TGGTGATCTA CATTAAGATC TTCCTGGTGG CCTGCAGGCA GCTTCAGCGC ACTGAGCTGA TGGACCACTC GAGGACCACC CTCCAGCGGG AGATCCATGC AGCCAAGTCA CTGGCCATGA TTGTGGGGAT TTTTGCCCTG TGCTGGTTAC CTGTGCATGC TGTTAACTGT GTCACTCTTT TCCAGCCAGC TCAGGGTAAA AATAAGCCCA AGTGGGCAAT GAATATGGCC ATTCTTCTGT CACATGCCAA TTCAGTTGTC AATCCCATTG TCTATGCTTA CCGGAACCGA GACTTCCGCT ACACTTTTCA CAAAATTATC TCCAGGTATC TTCTCTGCCA AGCAGATGTC AAGAGTGGGA ATGGTCAGGC TGGGGTACAG CCTGCTCTCG GTGTGGGCCT ATGATCTAGG CTCTCGCCTC TTCCAGGAGA AGATACAAAT CCACAAGAAA CAAAGAGGAC ACGGCTGGTT TTCATTGTGA AAGATAGCTA CACCTCACAA GGAAATGGAC TGCCTCTCTT GAGCACTTCC CTGGAGCTAC CACGTATCTA GCTAATATGT ATGTGTCAGT AGTAGCACCA AGGATTGACA AATATATTTA TGATCTATTC AGCTGCTTTT ACTGTGTGGA TTATGCCAAC AGCTTGAATG GATTCTAACA GACTCTTTTG TTTTTAAAAG TCTGCCTTGT TTATGGTGGA AAATTACTGA AACTATTTTA CTGTGAAACA GTGTGAACTA TTATAATGCA AATACTTTTT AACTTAGAGG CAATGGAAAA ATAAAAGTTG ACTGTACTAA AAATGTATAC TTGTTGCCAG GAAGGTGACC TCAAAAATTA AAAGTATAAT TATTCGGCCG

GGCATGGTGG CTCACACCTG TAATTCCAGC ACTTTGGGAG GCCAAGGCAG GCGGATCACG AGGTCAGGAG TTCAAAACCA GCCTGTCCAA TATAGTG (FRAG. NO: __) (SEQ. ID NO: 2424)
5'-GCGCGTCCTG-3' (FRAG. NO: 1671) (SEQ. ID NO:1684)
5'-GCT GGG CCC CGG-3' (FRAG. NO: 1672) (SEQ. ID NO:1685)
5'-CGG GTC GGG GCC CCC C-3' (FRAG. NO: 1673) (SEQ. ID NO:1686)
5'- CGC GCC CGC G-3' (FRAG. NO: 1674) (SEQ. ID NO:1687)
5'-GGC GCC GTG CCG CGT CTT GGT GGC GGC GG-3' (FRAG 972) (SEQ. ID NO: 982)
5'-GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC-3' (FRAG 973) (SEQ. ID NO: 983)
5'-GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC-3' (FRAG 974) (SEQ. ID NO: 984)
5'-CGG GTC GGG GCC CCC CGC GGC C-3' (FRAG 975) (SEQ. ID NO: 985)
5'-GCC TCG GGG CTG GGG CGC TGG TGG CCG GG-3' (FRAG 976) (SEQ. ID NO: 986)
5'-CCG CGC CTC CGC CTG CCG CTT CTG-3' (FRAG 977) (SEQ. ID NO: 987)
5'-GCT GGG CCC CGG GCG CCC CCT-3' (FRAG 978) (SEQ. ID NO: 988)
5'-CCC CTC TTG CTC GGG TCC CCG TG-3' (FRAG 979) (SEQ. ID NO: 989)
5'-ACAGCGCGTCCTGTGTCTCCAGCAGCATGGCCGGGCCAGCTGGGCCCC-3' (FRAG 980) (SEQ. ID NO: 990)
5'-BCBGCGCGTCCTGTGTCTCCBGCBGCBTGGCCGGGCCBGCTGGGCCCC-3' (FRAG 981) (SEQ. ID NO: 991)

Human Adenosine A3 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-ACA GAG CAG TGC TGT TGT TGG GCA TCT TGC CTT CCC AGG G BCB GBG CB TGC TGT TGT TGG GCB TCT TGC CTT CCC BGG GCC CTT TTC TGG TGG GGT GGT GCT GTT GTT GGG CTT TCT TCT GTT CCC BCB GBG CBG TGC TGT TGT TGG GCB TCT TGC CTT CCC BGG GCC CTT TTC TGG TGG GGT GGT GCT GTT GTT GGG C TTT CTT CTG TTC CC

GAATTCCCAG ATGGGCAGAG GTGGCTGGGC TGGTGACCCT AAGTGTGTCT CCTGCCTTTA TTCTCTCTAG TGGGTTATTC TTTCATGTGG TATCTTGCCT ACAGCATGCT GTGTTTGGAC ACAAACCCCT TTCCTTGGTT TCTCTGACCC AGCTGAGATG GACTGATTCC AAAAGAACTC ACCTATGTAC TGGGGTAGGG GAGGGAGGGT TTTTTGCAGT ATTTAACTAA GGTTCAAAGA GTGCTATATA GTGAGAAAGG CTTCTTTTTT TTTTTTTTTT TTTTTTGGCA GAGTGCTGCC TCCTAGAAAT TTCTCTTGGT AACTTCCTTC TCTGAAGCAC AGATAAAGAA AACAATTACA GTAGAAACAT TTATGAGGGA CACATTGGAG GCCGATGAAG CTTTTCAAGT TCCAGCAGTG CAGGGATGTG GGCAGAACTG ACATTGGAAA ATACTAGAAT GATGGAAATT CAGTTGGAGA GGACTGCCCT TTTTAATGTC TGGGGAGTCT GCTCAGGGAG AAATGACAAG TCTGGCGGGG ACAAGTATGG GATTTGGTAA GACTTGGATC AACTTGGGAT ACAGGGTGGG GGTCGGGAGT GGAATCAATG AATGATGCCA GAGCAGATCA ACTAACAAGA GGACCCTGAT GAGCCCCAGG CAGAGGCGTC TCCCTTATGC CCCACTCTGA AGTGTTTGTT AGTAAACACC AGAACGCCAT TGTTGTTACT GCTGAATTTT ATTTTGGGCT GTACATATTT AGATGCTTAA GGTAAAAATG ATAAAGCCCT CAAGCCACTG TGTGGGTTTG GGTCCAAGTG TTCCTTCTTG CTGCCTCTCT AACACGCCTG GTTAAAATAA TCCCTTTGGA TGGTGCTGAG AAGCACCTGA ACCAAGTGGG TCCCCAAATA ACAATGGCGT GCAAGTGTCT GGTTCCCAGA AGTTGGTGAC TAGGTAAGCA GCTTCAGGGA GAGGGGGCTG ATTCCCAGAC AGTCGCCTGT TCCTGCGGGG ATGGGGCTGA GGCTTGGGGA ATGTGGGCAG GAGGATATGC CATTTGATTC TGTTGCACAC GTTCTTTTCC CTTCTTTCTG TATGTCTGGT CATTCTGCTA TTCTGTCGTT CCTCACATAG GTTGGACATT GGCCGGCTGC CAGCATAAGT GCCAGTGTGA TTTTGCTAGG TGTGAGCTGA GAAAGAGAGG TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTTGCCCT TCTGAGCAGG GAATCTTTGC TTATCCCTTT GACCAAGGAT CTTTGCTGCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT AAGGTTAGGA GGCTGCCACC AAAGTCTCTT TTTTGTTCCT CTGCTTCTCC CGTTTGCCTC CTTATCATGA GATCTTTTTG CTAAGCTGGC AGAAAGATTG CATAGTCAGT GCTTCCAGCT CTGCTCCCAC CTGATCCTGC ACTGTCCTCT GGTCCCTGAA TGAATGAACT CTGATACCCA ATCTTGTCTC GAGCCTTCTC TATGCCACTC ATGGCTCCTC TTCTGCTCTT TCCATCTTTT TGCTGAGAGT TCTGAGCTCT GTACTTCCTC TTGGCCCATC TCACTTCCTG AAACACCCCT GAAGAGGGTT GCTTATCTTG ATGGAACTCA AAAAGCCAAA AAGCTGCAGG CAGAGGCGTT GAGGACATCT GTTTGGGGAA CTAAGAGCAG CAGCACTTTC AGATTCAGTC CATATAGAGC TGTCCTACAG CATTCTGGAA ACTTGAGGAT GTGCGGTGCA TAAAGGGGCT GGAAGTGACC CACCTGTGAT GAGCCCTTTC TAAGGAGAAG GGTTTCCAAG AGATCACCCC ACCAGAAAAG GGTAGGAATG AGCAAGTTGG GAATTTTAGA CTGTCACTGC ACATGGACCT CTGGGAAGAC GTCTGGCGAG AGCTAGGCCC ACTGGCCCTA CAGACGGATC TTGCTGGCTC ACCTGTCCCT GTGGAGGTTC CCCTGGGAAG GCAAGATGCC CAACAACAGC ACTGCTCTGT CATTGGCCAA TGTTACCTAC ATCACCATGG AAATTTTCAT TGGACTCTGC GCCATAGTGG GCAACGTGCT GGTCATCTGC GTGGTCAAGC TGAACCCCAG CCTGCAGACC ACCACCTTCT ATTTCATTGT CTCTCTAGCC CTGGCTGACA TTGCTGTTGG GGTGCTGGTC ATGCCTTTGG CCATTGTTGT CAGCCTGGGC ATCACAATCC ACTTCTACAG CTGCCTTTTT ATGACTTGCC TACTGCTTAT CTTTACCCAC GCCTCCATCA TGTCCTTGCT GGCCATCGCT GTGGACCGAT ACTTGCGGGT CAAGCTTACC GTCAGGTAGC CTGCGGCGTG GGGTGGGCAG CAATTGAGGC AGCTGGGAAA TGAGGCTACA AAGCCAGAGC CTGCTGAATT TTATTTTGGA CTGTACATAT TTAGATGCTT AAGGTAAAAA TGATAAAGCC CTCAAGCCAC TGTGTGGGTT GGGTCCAAGT GTTCCTTGCT GCTGCCTCTC TAACACGCCT GGTTAAAATA ATCCCTTTGG ATGGTGCTGA GAAGCACCTG AACCAAGTGG GTCCCCAAAT AACTATGGCG TGCAAGTGTC TGGTTCCCAG AAGTTGGTGA CTAGGTAAGC GACTCAGGGA GAGGGGCTGA TTCCCAGACA GTCGCCTGTT CCTGCTGGGA TGGGGCTGAG GCTTGGGGAA TGTGGGCAGG AGGATATGCC ATTTGATTCT GTTGCACACG TTCTTTTCCC TTCTTTCTGT ATGTCTGGTC ATTCTGCTAT TCTGTCGTTC CTCACATAGG TTGGACATTG GCCGGCTGCC AGCATAAGTG CCAGTGTGAT TTTGCTAGGG TGTGAGCTGA GAAAGAGAGG TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTTGCCCT TCTGAGCAGG GAATCTTTGC TTATCCCTTT GACCAAGGAT CTTTGCTCCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT AAGGTTAGGA GGCTGCCACC AAAGTCTCTT TTTTGTTCCT CTGCTTCTCC CGTTTGCCTC CTTATCATGA GATCTTTTTG CTAAGCTGGC AGAAAGATTG CATAATCAGT GCTTCCAGCT CCGCTCCCAC CTGATCCTGC ACTGTCCTCT GGTCCCTGAA TGAATGAACT CTGATACCCA ATCTTGTCTC GAGCCTTCTC TATGCCACTC ATGGCTCCTC TTCTGCTCTT TCCATCTTTT TGCTGAGAGT TACTGAGCTC TGTACTTCCT CTTGGCCCAT CTCACTTCCT GAAACACCCC TGAAGAGGGT TGCTTATCTT GATGGAACTC AAAAAGCCAA AAAGCTGCAG GCAGAGGCGT TGAGGACATC TGTTTGGGGA ACTAAGAGCA GCAGCACTTT CAGATTCAGT CCATATAGAG CTGTCCTACA GCATTCTGGA AACTTGAGGA TGTGCGGTGC ATAAAGGGGC TGGAAGTGAC CCACCTGTGA TGAGCCCTTT CTAAGGAGAA GGGTTTCCAA GAGATCACCC CACCAGAAAA GGGTAGGAAT GAGCAAGTTG GGAATTTTAG

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5'- CGAATTCGGG GGACATCTGT TTGGGGAACT AAGAGCAGCA GCACTTTCAG ATTCAGTCCA TATAGAGCTG TCCTACAGCA TTCTGGAAAC TTGAGGATGT GCGGTGCATA AACGGGCTGG AAGTGACCCA CCTGTGATGA GCCCTTTCTA AGGAGAAGGG TTTCCAAGAG ATCACCCCAC CAGAAAAGGG TAGGAATGAG CAAGTTGGGA ATTTTAGACT GTCACTGCAC ATGGACCTCT GGGAAGACGT CTGGCGAGAG CTAGGCCCAC TGGCCCTACA GACGGATCTT GCTGGCTCAC CTGTCCCTGT GGAGGTTCCC CTGGGAAGGC AAGATGCCCA ACAACAGCAC TGCTCTGTCA TTGGCCAATG TTACCTACAT CACCATGGAA ATTTTCATTG GACTCTGCGC CATAGTGGGC AACGTGCTGG TCATCTGCGT GGTCAAGCTG AACCCCAGCC TGCAGACCAC CACCTTCTAT TTCATTGTCT CTCTAGCCCT GGCTGACATT GCTGTTGGGG TGCTGGTCAT GCCTTTGGCC ATTGTTGTCA GCCTGGGCAT CACAATCCAC TTCTACAGCT GCCTTTTTAT GACTTGCCTA CTGCTTATCT TTACCCACGC CTCCATCATG TCCTTGCTGG CCATCGCTGT GGACCGATAC TTGCGGGTCA AGCTTACCGT CAGATACAAG AGGGTCACCA CTCACAGAAG AATATGGCTG GCCCTGGGCC TTTGCTGGCT GGTGTCATTC CTGGTGGGAT TGACCCCCAT GTTTGGCTGG AACATGAAAC TGACCTCAGA GTACCACAGA AATGTCACCT TCCTTTCATG CCAATTTGTT TCCGTCATGA GGATGGACTA CATGGTATAC TTCAGCTTCC TCACCTGGAT TTTCATCCCC CTGGTTGTCA TGTGCGCCAT CTATCTTGAC ATCTTTTACA TCATTCGGAA CAAACTCAGT CTGAACTTAT CTAACTCCAA AGAGACAGGT GCATTTTATG GACGGGAGTT CAAGACGGCT AAGTCCTTGT TTCTGGTTCT TTTCTTGTTT GCTCTGTCAT GGCTGCCTTT ATCTCTCATC AACTGCATCA TCTACTTTAA TGGTGAGGTA CCACAGCTTG TGCTGTACAT GGGCATCCTG CTGTCCCATG CCAACTCCAT GATGAACCCT ATCGTCTATG CCTATAAAAT AAAGAAGTTC AAGGAAACCT ACCTTTTGAT CCTCAAAGCC TGTGTGGTCT GCCATCCCTC TGATTCTTTG GACACAAGCA TTGAGAAGAA TTCTGAGTAG TTATCCATCA GAGATGACTC TGTCTCATTG ACCTTCAGAT TCCCCATCAA CAAACACTTG AGGGCCTGTA TGCCTGGGCC AAGGGATTTT TACATCCTTG ATTACTTCCA CTGAGGTGGG AGCATCTCCA GTGCTCCCCA ATTATATCTC CCCCACTCCA CTACTCTCTT CCTCCACTTC ATTTTTCCTT TGTCCTTTCT CTCTAATTCA GTGTTTTGGA GGCCTGACTT GGGGACAACG TATTATTGAT ATTATTGTCT GTTTTCCTTC TTCCCAATAG AAGAATAAGT CATGGAGCCT GAAGGGTGCC TAGTTGACTT ACTGACAAAA GGCTCTAGTT GGGCTGAACA TGTGTGTGGT GGTGACTCAT TTCCATGCCA TTGTGGAATT GAGCAGAGAA CCTGCTCTCG GAGGATGCCT AGGAGATGTT GGGAACAGAA GAAATAAACT GAGTTTAAGG GGGACTTAAA CTGCTGAATT C -3' **(FRAG. NO:_) (SEQ. ID NO:2439)**

5'- CTGCTGAATT TTATTTTGGA CTGTACATAT TTAGATGCTT AAGGTAAAAA TGATAAAGCC CTCAAGCCAC TGTGTGGGTT GGGTCCAAGT GTTCCTTGCT GCTGCCTCTC TAACACGCCT GGTTAAAATA ATCCCTTTGG ATGGTGCTGA GAAGCACCTG AACCAAGTGG GTCCCCAAAT AACTATGGCG TGCAAGTGTC TGGTTCCCAG AAGTTGGTGA CTAGGTAAGC GACTCAGGGA GAGGGGCTGA TTCCCAGACA GTCGCCTGTT CCTGCTGGGA TGGGGCTGAG GCTTGGGGAA TGTGGGCAGG AGGATATGCC ATTTGATTCT GTTGCACACG TTCTTTTCCC TTCTTTCTGT ATGTCTGGTC ATTCTGCTAT TCTGTCGTTC CTCACATAGG TTGGACATTG GCCGGCTGCC AGCATAAGTG CCAGTGTGAT TTTGCTAGGG TGTGAGCTGA GAAAGAGAGG TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTTGCCCT TCTGAGCAGG GAATCTTTGC TTATCCCTTT GACCAAGGAT CTTTGCTCCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT AAGGTTAGGA GGCTGCCACC AAAGTCTCTT TTTTGTTCCT CTGCTTCTCC CGTTTGCCTC CTTATCATGA GATCTTTTTG CTAAGCTGGC AGAAAGATTG CATAATCAGT GCTTCCAGCT CCGCTCCCAC CTGATCCTGC ACTGTCCTCT GGTCCCTGAA TGAATGAACT CTGATACCCA ATCTTGTCTC GAGCCTTCTC TATGCCACTC ATGGCTCCTC TTCTGCTCTT TCCATCTTTT TGCTGAGAGT TACTGAGCTC TGTACTTCCT CTTGGCCCAT CTCACTTCCT GAAACACCCC TGAAGAGGGT TGCTTATCTT GATGGAACTC AAAAAGCCAA AAAGCTGCAG GCAGAGGCGT TGAGGACATC TGTTTGGGGA ACTAAGAGCA GCAGCACTTT

CAGATTCAGT CCATATAGAG CTGTCCTACA GCATTCTGGA AACTTGAGGA TGTGCGGTGC ATAAAGGGGC TGGAAGTGAC CCACCTGTGA TGAGCCCTTT CTAAGGAGAA GGGTTTCCAA GAGATCACCC CACCAGAAAA GGGTAGGAAT GAGCAAGTTG GGAATTTTAG ACTGTCACTG CACATGGACC TCTGGGAAGA CGTCTGGCGA GAGCTAGGCC CACTGGCCCT ACAGACGGAT CTTGCTGGCT CACCTGTCCC TGTGGAGGTT CCCCTGGGAA GGCAAGATGC CCAACAACAG CACTGCTCTG -3' **(FRAG. NO:_) (SEQ. ID NO:2438)**

5'- GAATTCCCAG ATGGGCAGAG GTGGCTGGGC TGGTGACCCT AAGTGTGTCT CCTGCCTTTA TTCTCTCTAG TGGGTTATTC TTTCATGTGG TATCTTGCCT ACAGCATGCT GTGTTTGGAC ACAAACCCCT TTCCTTGGTT TCTCTGACCC AGCTGAGATG GACTGATTCC AAAAGAACTC ACCTATGTAC TGGGGTAGGG GAGGGAGGGT TTTTTGCAGT ATTTAACTAA GGTTCAAAGA GTGCTATATA GTGAGAAAGG CTTCTTTTTT TTTTTTTTTT TTTTTTGGCA GAGTGCTGCC TCCTAGAAAT TTCTCTTGGT AACTTCCTTC TCTGAAGCAC AGATAAAGAA AACAATTACA GTAGAAACAT TTATGAGGGA CACATTGGAG GCCGATGAAG CTTTTCAAGT TCCAGCAGTG CAGGGATGTG GGCAGAACTG ACATTGGAAA ATACTAGAAT GATGGAAATT CAGTTGGAGA GGACTGCCCT TTTTAATGTC TGGGGAGTCT GCTCAGGGAG AAATGACAAG TCTGGCGGGG ACAAGTATGG GATTTGGTAA GACTTGGATC AACTTGGGAT ACAGGGTGGG GGTCGGGAGT GGAATCAATG AATGATGCCA GAGCAGATCA ACTAACAAGA GGACCCTGAT GAGCCCCAGG CAGAGGCGTC TCCCTTATGC CCCACTCTGA AGTGTTTGTT AGTAAACACC AGAACGCCAT TGTTGTTACT GCTGAATTTT ATTTTGGGCT GTACATATTT AGATGCTTAA GGTAAAAATG ATAAAGCCCT CAAGCCACTG TGTGGGTTTG GGTCCAAGTG TTCCTTCTTG CTGCCTCTCT AACACGCCTG GTTAAAATAA TCCCTTTGGA TGGTGCTGAG AAGCACCTGA ACCAAGTGGG TCCCCAAATA ACAATGGCGT GCAAGTGTCT GGTTCCCAGA AGTTGGTGAC TAGGTAAGCA GCTTCAGGGA GAGGGGGCTG ATTCCCAGAC AGTCGCCTGT TCCTGCGGGG ATGGGGCTGA GGCTTGGGGA ATGTGGGCAG GAGGATATGC CATTTGATTC TGTTGCACAC GTTCTTTTCC CTTCTTTCTG TATGTCTGGT CATTCTGCTA TTCTGTCGTT CCTCACATAG GTTGGACATT GGCCGGCTGC CAGCATAAGT GCCAGTGTGA TTTTGCTAGG TGTGAGCTGA GAAAGAGAGG TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTTGCCCT TCTGAGCAGG GAATCTTTGC TTATCCCTTT GACCAAGGAT CTTTGCTGCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT AAGGTTAGGA GGCTGCCACC AAAGTCTCTT TTTTGTTCCT CTGCTTCTCC CGTTTGCCTC CTTATCATGA GATCTTTTTG CTAAGCTGGC AGAAAGATTG CATAGTCAGT GCTTCCAGCT CTGCTCCCAC CTGATCCTGC ACTGTCCTCT GGTCCCTGAA TGAATGAACT CTGATACCCA ATCTTGTCTC GAGCCTTCTC TATGCCACTC ATGGCTCCTC TTCTGCTCTT TCCATCTTTT TGCTGAGAGT TCTGAGCTCT GTACTTCCTC TTGGCCCATC TCACTTCCTG AAACACCCCT GAAGAGGGTT GCTTATCTTG ATGGAACTCA AAAAGCCAAA AAGCTGCAGG CAGAGGCGTT GAGGACATCT GTTTGGGGAA CTAAGAGCAG CAGCACTTTC AGATTCAGTC CATATAGAGC TGTCCTACAG CATTCTGGAA ACTTGAGGAT GTGCGGTGCA TAAAGGGGCT GGAAGTGACC CACCTGTGAT GAGCCCTTTC TAAGGAGAAG GGTTTCCAAG AGATCACCCC ACCAGAAAAG GGTAGGAATG AGCAAGTTGG GAATTTTAGA CTGTCACTGC ACATGGACCT CTGGGAAGAC GTCTGGCGAG AGCTAGGCCC ACTGGCCCTA CAGACGGATC TTGCTGGCTC ACCTGTCCCT GTGGAGGTTC CCCTGGGAAG GCAAGATGCC CAACAACAGC ACTGCTCTGT CATTGGCCAA TGTTACCTAC ATCACCATGG AAATTTTCAT TGGACTCTGC GCCATAGTGG GCAACGTGCT GGTCATCTGC GTGGTCAAGC TGAACCCCAG CCTGCAGACC ACCACCTTCT ATTTCATTGT CTCTCTAGCC CTGGCTGACA TTGCTGTTGG GGTGCTGGTC ATGCCTTTGG CCATTGTTGT CAGCCTGGGC ATCACAATCC ACTTCTACAG CTGCCTTTTT ATGACTTGCC TACTGCTTAT CTTTACCCAC GCCTCCATCA TGTCCTTGCT GGCCATCGCT GTGGACCGAT ACTTGCGGGT CAAGCTTACC GTCAGGTAGC CTGCGGCGTG GGGTGGGCAG CAATTGAGGC AGCTGGGAAA TGAGGCTACA AAGCCAGAGC -3' **(FRAG. NO:_) (SEQ. ID NO:2437)**

5'-CGAATTCGGG GGACATCTGT TTGGGGAACT AAGAGCAGCA GCACTTTCAG ATTCAGTCCA TATAGAGCTG TCCTACAGCA TTCTGGAAAC TTGAGGATGT GCGGTGCATA AACGGGCTGG AAGTGACCCA CCTGTGATGA GCCCTTTCTA AGGAGAAGGG TTTCCAAGAG ATCACCCCAC CAGAAAAGGG TAGGAATGAG CAAGTTGGGA ATTTTAGACT GTCACTGCAC ATGGACCTCT GGGAAGACGT CTGGCGAGAG CTAGGCCCAC TGGCCCTACA GACGGATCTT GCTGGCTCAC CTGTCCCTGT GGAGGTTCCC CTGGGAAGGC AAGATGCCCA ACAACAGCAC TGCTCTGTCA TTGGCCAATG TTACCTACAT CACCATGGAA ATTTTCATTG GACTCTGCGC CATAGTGGGC AACGTGCTGG TCATCTGCGT GGTCAAGCTG AACCCCAGCC TGCAGACCAC CACCTTCTAT TTCATTGTCT CTCTAGCCCT GGCTGACATT GCTGTTGGGG TGCTGGTCAT GCCTTTGGCC ATTGTTGTCA GCCTGGGCAT CACAATCCAC TTCTACAGCT GCCTTTTTAT GACTTGCCTA CTGCTTATCT TTACCCACGC CTCCATCATG TCCTTGCTGG CCATCGCTGT GGACCGATAC TTGCGGGTCA AGCTTACCGT CAGATACAAG AGGGTCACCA CTCACAGAAG AATATGGCTG GCCCTGGGCC TTTGCTGGCT GGTGTCATTC CTGGTGGGAT TGACCCCCAT GTTTGGCTGG AACATGAAAC TGACCTCAGA GTACCACAGA AATGTCACCT TCCTTTCATG CCAATTTGTT TCCGTCATGA GGATGGACTA CATGGTATAC TTCAGCTTCC TCACCTGGAT TTTCATCCCC CTGGTTGTCA TGTGCGCCAT CTATCTTGAC ATCTTTTACA TCATTCGGAA CAAACTCAGT CTGAACTTAT CTAACTCCAA AGAGACAGGT GCATTTTATG GACGGGAGTT CAAGACGGCT AAGTCCTTGT TTCTGGTTCT TTTCTTGTTT GCTCTGTCAT GGCTGCCTTT ATCTCTCATC AACTGCATCA TCTACTTTAA TGGTGAGGTA CCACAGCTTG TGCTGTACAT GGGCATCCTG CTGTCCCATG CCAACTCCAT GATGAACCCT ATCGTCTATG CCTATAAAAT AAAGAAGTTC AAGGAAACCT ACCTTTTGAT CCTCAAAGCC TGTGTGGTCT GCCATCCCTC TGATTCTTTG GACACAAGCA TTGAGAAGAA TTCTGAGTAG TTATCCATCA GAGATGACTC TGTCTCATTG ACCTTCAGAT TCCCCATCAA CAAACACTTG AGGGCCTGTA TGCCTGGGCC AAGGGATTTT TACATCCTTG ATTACTTCCA CTGAGGTGGG AGCATCTCCA GTGCTCCCCA ATTATATCTC CCCCACTCCA CTACTCTCTT CCTCCACTTC ATTTTTCCTT TGTCCTTTCT CTCTAATTCA GTGTTTTGGA GGCCTGACTT GGGGACAACG TATTATTGAT ATTATTGTCT GTTTTCCTTC TTCCCAATAG AAGAATAAGT CATGGAGCCT GAAGGGTGCC TAGTTGACTT ACTGACAAAA GGCTCTAGTT GGGCTGAACA TGTGTGTGGT GGTGACTCAT TTCCATGCCA TTGTGGAATT GAGCAGAGAA CCTGCTCTCG GAGGATGCCT AGGAGATGTT GGGAACAGAA GAAATAAACT GAGTTTAAGG GGGACTTAAA CTGCTGAATT C -3' **(FRAG. NO:_) (SEQ. ID NO:2427)**

5'-CTGCTGAATT TTATTTTGGA CTGTACATAT TTAGATGCTT AAGGTAAAAA TGATAAAGCC CTCAAGCCAC TGTGTGGGTT GGGTCCAAGT GTTCCTTGCT GCTGCCTCTC TAACACGCCT GGTTAAAATA ATCCCTTTGG ATGGTGCTGA GAAGCACCTG AACCAAGTGG GTCCCCAAAT AACTATGGCG TGCAAGTGTC TGGTTCCCAG AAGTTGGTGA CTAGGTAAGC GACTCAGGGA GAGGGGCTGA TTCCCAGACA GTCGCCTGTT CCTGCTGGGA TGGGGCTGAG GCTTGGGGAA TGTGGGCAGG AGGATATGCC ATTTGATTCT GTTGCACACG TTCTTTTCCC TTCTTTCTGT ATGTCTGGTC ATTCTGCTAT TCTGTCGTTC CTCACATAGG TTGGACATTG GCCGGCTGCC AGCATAAGTG CCAGTGTGAT TTTGCTAGGG TGTGAGCTGA GAAAGAGAGG TGGAGGCTAA

GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTTGCCCT TCTGAGCAGG GAATCTTTGC TTATCCCTTT GACCAAGGAT CTTTGCTCCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT AAGGTTAGGA GGCTGCCACC AAAGTCTCTT TTTTGTTCCT CTGCTTCTCC CGTTTGCCTC CTTATCATGA GATCTTTTTG CTAAGCTGGC AGAAAGATTG CATAATCAGT GCTTCCAGCT CCGCTCCCAC CTGATCCTGC ACTGTCCTCT GGTCCCTGAA TGAATGAACT CTGATACCCA ATCTTGTCTC GAGCCTTCTC TATGCCACTC ATGGCTCCTC TTCTGCTCTT TCCATCTTTT TGCTGAGAGT TACTGAGCTC TGTACTTCCT CTTGGCCCAT CTCACTTCCT GAAACACCCC TGAAGAGGGT TGCTTATCTT GATGGAACTC AAAAAGCCAA AAAGCTGCAG GCAGAGGCGT TGAGGACATC TGTTTGGGGA ACTAAGAGCA GCAGCACTTT CAGATTCAGT CCATATAGAG CTGTCCTACA GCATTCTGGA AACTTGAGGA TGTGCGGTGC ATAAAGGGGC TGGAAGTGAC CCACCTGTGA TGAGCCCTTT CTAAGGAGAA GGGTTTCCAA GAGATCACCC CACCAGAAAA GGGTAGGAAT GAGCAAGTTG GGAATTTTAG ACTGTCACTG CACATGGACC TCTGGGAAGA CGTCTGGCGA GAGCTAGGCC CACTGGCCCT ACAGACGGAT CTTGCTGGCT CACCTGTCCC TGTGGAGGTT CCCCTGGGAA GGCAAGATGC CCAACAACAG CACTGCTCTG-3' **(FRAG. NO:_) (SEQ. ID NO:2426)**

5'-GAATTCCCAG ATGGGCAGAG GTGGCTGGGC TGGTGACCCT AAGTGTGTCT CCTGCCTTTA TTCTCTCTAG TGGGTTATTC TTTCATGTGG TATCTTGCCT ACAGCATGCT GTGTTTGGAC ACAAACCCCT TTCCTTGGTT TCTCTGACCC AGCTGAGATG GACTGATTCC AAAAGAACTC ACCTATGTAC TGGGGTAGGG GAGGGAGGGT TTTTTGCAGT ATTTAACTAA GGTTCAAAGA GTGCTATATA GTGAGAAAGG CTTCTTTTTT TTTTTTTTTT TTTTTTGGCA GAGTGCTGCC TCCTAGAAAT TTCTCTTGGT AACTTCCTTC TCTGAAGCAC AGATAAAGAA AACAATTACA GTAGAAACAT TTATGAGGGA CACATTGGAG GCCGATGAAG CTTTTCAAGT TCCAGCAGTG CAGGGATGTG GGCAGAACTG ACATTGGAAA ATACTAGAAT GATGGAAATT CAGTTGGAGA GGACTGCCCT TTTTAATGTC TGGGGAGTCT GCTCAGGGAG AAATGACAAG TCTGGCGGGG ACAAGTATGG GATTTGGTAA GACTTGGATC AACTTGGGAT ACAGGGTGGG GGTCGGGAGT GGAATCAATG AATGATGCCA GAGCAGATCA ACTAACAAGA GGACCCTGAT GAGCCCCAGG CAGAGGCGTC TCCCTTATGC CCCACTCTGA AGTGTTTGTT AGTAAACACC AGAACGCCAT TGTTGTTACT GCTGAATTTT ATTTTGGGCT GTACATATTT AGATGCTTAA GGTAAAAATG ATAAAGCCCT CAAGCCACTG TGTGGGTTTG GGTCCAAGTG TTCCTTCTTG CTGCCTCTCT AACACGCCTG GTTAAAATAA TCCCTTTGGA TGGTGCTGAG AAGCACCTGA ACCAAGTGGG TCCCCAAATA ACAATGGCGT GCAAGTGTCT GGTTCCCAGA AGTTGGTGAC TAGGTAAGCA GCTTCAGGGA GAGGGGGCTG ATTCCCAGAC AGTCGCCTGT TCCTGCGGGG ATGGGGCTGA GGCTTGGGGA ATGTGGGCAG GAGGATATGC CATTTGATTC TGTTGCACAC GTTCTTTTCC CTTCTTTCTG TATGTCTGGT CATTCTGCTA TTCTGTCGTT CCTCACATAG GTTGGACATT GGCCGGCTGC CAGCATAAGT GCCAGTGTGA TTTTGCTAGG TGTGAGCTGA GAAAGAGAGG TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTTGCCCT TCTGAGCAGG GAATCTTTGC TTATCCCTTT GACCAAGGAT CTTTGCTGCA AAGGCTGGGT ATCGGCTGTG CTCAGCAAAG CGTCAACTCG TGCAAGAACT TAGCAGGAAT AGTTCTGGCT AAGGTTAGGA GGCTGCCACC AAAGTCTCTT TTTTGTTCCT CTGCTTCTCC CGTTTGCCTC CTTATCATGA GATCTTTTTG CTAAGCTGGC AGAAAGATTG CATAGTCAGT GCTTCCAGCT CTGCTCCCAC CTGATCCTGC ACTGTCCTCT GGTCCCTGAA TGAATGAACT CTGATACCCA ATCTTGTCTC GAGCCTTCTC TATGCCACTC ATGGCTCCTC TTCTGCTCTT TCCATCTTTT TGCTGAGAGT TCTGAGCTCT GTACTTCCTC TTGGCCCATC TCACTTCCTG AAACACCCCT GAAGAGGGTT GCTTATCTTG ATGGAACTCA AAAAGCCAAA AAGCTGCAGG CAGAGGCGTT GAGGACATCT GTTTGGGGAA CTAAGAGCAG CAGCACTTTC AGATTCAGTC CATATAGAGC TGTCCTACAG CATTCTGGAA ACTTGAGGAT GTGCGGTGCA TAAAGGGGCT GGAAGTGACC CACCTGTGAT GAGCCCTTTC TAAGGAGAAG GGTTTCCAAG AGATCACCCC ACCAGAAAAG GGTAGGAATG AGCAAGTTGG GAATTTTAGA CTGTCACTGC ACATGGACCT CTGGGAAGAC GTCTGGCGAG AGCTAGGCCC ACTGGCCCTA CAGACGGATC TTGCTGGCTC ACCTGTCCCT GTGGAGGTTC CCCTGGGAAG GCAAGATGCC CAACAACAGC ACTGCTCTGT CATTGGCCAA TGTTACCTAC ATCACCATGG AAATTTTCAT TGGACTCTGC GCCATAGTGG GCAACGTGCT GGTCATCTGC GTGGTCAAGC TGAACCCCAG CCTGCAGACC ACCACCTTCT ATTTCATTGT CTCTCTAGCC CTGGCTGACA TTGCTGTTGG GGTGCTGGTC ATGCCTTTGG CCATTGTTGT CAGCCTGGGC ATCACAATCC ACTTCTACAG CTGCCTTTTT ATGACTTGCC TACTGCTTAT CTTTACCCAC GCCTCCATCA TGTCCTTGCT GGCCATCGCT GTGGACCGAT ACTTGCGGGT CAAGCTTACC GTCAGGTAGC CTGCGGCGTG GGGTGGGCAG CAATTGAGGC AGCTGGGAAA TGAGGCTACA AAGCCAGAGC-3' **(FRAG. NO:_) (SEQ. ID NO:2425)**

5'-GBG CB TGC-3' **(FRAG. NO:1676) (SEQ. ID NO:1689)**
5'-TTG TTG GGC-3' **(FRAG. NO:1677) (SEQ. ID NO:1690)**
5'-TGC CTT CCC BGG G-3' **(FRAG. NO:1678) (SEQ. ID NO:1691)**
5'-GTT GTT GGG CAT CTT GCC-3' **(FRAG. NO:1679) (SEQ ID NO:3)**
5'-GTG GGC CTA GCT CTC GCC-3' **(GRAG. NO:1680) (SEQ ID NO:5)**
5'-ACA GAG CA TGC TGT TGT TGG GCA TCT TGC CTT CCC AGG G-3' **(FRAG 982) (SEQ. ID NO: 992)**
5'-BCB GBG CB TGC TGT TGT TGG GCB TCT TGC CTT CCC BGG G-3' **(FRAG 983) (SEQ. ID NO: 993)**
5'-CCC TTT TCT GGT GGG GTG-3' **(FRAG 984) (SEQ. ID NO: 994)**
5'-GTG CTG TTG TTG GGC-3' **(FRAG 985) (SEQ. ID NO: 995)**
5'-TTT CTT CTG TTC CC-3' **(FRAG 986) (SEQ. ID NO: 996)**
5'-CCC TTT TCT GGT GGG GTG-3' **(FRAG 987) (SEQ. ID NO: 997)**
5'-GTG CTG TTG TTG GGC-3' **(FRAG 988) (SEQ. ID NO: 998)**
5'-TTT CTT CTG TTC CC-3' **(FRAG 989) (SEQ. ID NO: 999)**

Human IgE Receptor β Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TTT CCC CTG GGT CTT CC CTC CTG CTC TTT TTT C ATT TGC TCT CCT ATT ACT TTC TGT GTC CAT TTT TTC ATT AAC CGA GCT GT BTT TGC TCT CCT BTT BCT TTC TGT GTC CBT TTT TTC BTT BBC CGB GCT GT-3' **(FRAG. NO:1681) (SEQ. ID NO:1692)**
5'-CCC CTG GG-3' **(FRAG. NO:1682) (SEQ. ID NO:1693)**
5'-GCTCTCCTBTT-3' **(FRAG. NO:1683) (SEQ. ID NO:1694)**
5'-CBTTBBCCGBGCTG-3' **(FRAG. NO:1684) (SEQ. ID NO:1695)**
5'-TTT CCC CTG GGT CTT CC-3' **(FRAG 990) (SEQ. ID NO: 1000)**
5'-CTC CTG CTC TTT TTT C-3' **(FRAG 991) (SEQ. ID NO: 1001)**

ATTTGCTCTCCTATTACTTTCTGTGTCCATTTTTTCATTAACCGAGCTGT (FRAG 992) (SEQ. ID NO: 1002)
BTTTGCTCTCCTBTTBCTTTCTGTGTCCBTTTTTTCBTTBBCCGBGCTGT (FRAG 993) (SEQ. ID NO: 1003)

Human Fc-ε Recept r CD23 Antigen (IgE Receptor) Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCC TGT GTC TGT CCT CCT GCT TCG TTC CTC TCG TTC CTG CTT GGT GCC CTT GCC G GTC CTG CTC CTC CGG GCT GTG G GTC GTG GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG C GGG TCT TGC TCT GGG CCT GGC TGT GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC TCT CTG AAT ATT GAC CTT CCT CCA TGG CGG TCC TGC TTG GAT TCT CCC GA TCT CTG BBT BTT GBC CTT CCT CCB TGG CGG TCC TGC TTG GBT TCT CCC GB-3' (FRAG 1685) (SEQ. ID NO:1696)
5'-GT CCT CCT-3' (FRAG 1686) (SEQ. ID NO: 1697)
5'-TGT GTC TGT CCT CC-3' (FRAG 1687) (SEQ. ID NO: 1698)
5'-GTG GCC CTG GC-3' (FRAG 1688) (SEQ. ID NO: 1699)
5'-CGT GGT TGG GG-3' (FRAG 1689) (SEQ. ID NO: 1700)
5'-TCT CTG BBT BTT GBC C-3' (FRAG1690) (SEQ. ID NO:1701)
5'-GCC TGT GTC TGT CCT CCT-3' (FRAG 994) (SEQ. ID NO: 1004)
5'-GCT TCG TTC CTC TCG TTC-3' (FRAG 995) (SEQ. ID NO:1005)
5'-CTG CTT GGT GCC CTT GCC G-3' (FRAG 996) (SEQ. ID NO: 1006)
5'-GTC CTG CTC CTC CGG GCT GTG G-3' (FRAG 997) (SEQ. ID NO: 1007)
5'-GTC GTG GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG-3' (FRAG 998) (SEQ. ID NO: 1008)
5'-CCT TCG CTG GCT GGC GGC GTG C-3' (FRAG 999) (SEQ. ID NO: 1009)
5'-GGG TCT TGC TCT GGG CCT GGC TGT-3' (FRAG 1000) (SEQ. ID NO: 1010)
5'-GGC CGT GGT TGG GGG TCT TC-3' (FRAG 1001) (SEQ. ID NO: 1011)
5'-GCT GCC TCC GTT TGG GTG GC (FRAG 1002) (SEQ. ID NO: 1012)
5'-TCT CTG AAT ATT GAC CTT CCT CCA TGG CGG TCC TGC TTG GAT TCT CCC GA (FRAG 1003) (SEQ. ID NO: 1013)
5'-TCT CTG BBT BTT GBC CTT CCT CCB TGG CGG TCC TGC TTG GBT TCT CCC GB (FRAG 1004) (SEQ. ID NO: 1014)

Human IgE Receptor α Subunit Nucleic Acid and Antisense Oligonucleotide Fragments

5'- GCC TTT CCT GGT TCT CTT GTT GTT TTT GGG GTT TGG CTT ACA GTA GAG TAG GGG ATT CCA TGG CAG GAG CCA TCT TCT TCA TGG ACT CC TTC AAG GAG ACC TTA GGT TTC TGA GGG ACT GCT AAC ACG CCA TCT GGA GC BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCT TCB TGG BCT CC TTC BBG GBG BCC TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC GTT GTT TTT GGG GTT TGG CTT GCC TTT CCT GGT TCT CTT BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCT TCB TGG BCT CC TTC BBG GBG BCC TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC-3'
(FRAG. NO: 1691) (SEQ. ID NO:1702)
5'- TGG BCT CC -3' (FRAG. NO: 1692) (SEQ. ID NO:1703)
5'-CCB TCT GGB-3' (FRAG. NO: 1693) (SEQ. ID NO:1704)
5'-CT GCT BBC BCG-3' (FRAG. NO: 1694) (SEQ. ID NO:1705)
5'-GTT TTT GGG GTT TG-3' (FRAG. NO: 1695) (SEQ. ID NO:1706)
5'-GCC TTT CCT GGT TCT CTT GTT GTT TTT GGG GTT TGG CTT-3' (FRAG. NO:1005) (SEQ. ID NO:1015)
5'-ACAGTAGAGTAGGGGATTCCATGGCAGGAGCCATCTTCTTCATGGACTCC-3' (FRAG. NO:1006) (SEQ. ID NO:1016)
5'-TTC AAG GAG ACC TTA GGT TTC TGA GGG ACT GCT AAC ACG CCA TCT GGA GC-3' (FRAG. NO:1007) (SEQ. ID NO:1017)
5'-BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCT TCB TGG BCT CC TTC BBG GBG BCC TTB GGT TTC TGB GGG-3' (FRAG. NO:1008) (SEQ. ID NO:1018)
5'-BCT GCT BBC BCG CCB TCT GGB GC-3' (FRAG. NO:1009) (SEQ. ID NO:1019)
5'-GTT GTT TTT GGG GTT TGG CTT-3' (FRAG. NO:1010) (SEQ. ID NO:1020)
5'-GCC TTT CCT GGT TCT CTT-3' (FRAG. NO:1011) (SEQ. ID NO:1021)
5'-BCBGTBGBGTBGGGGBTTCCBTGGCBGGBGCCBTCTTCTTCBTGGBCTCC-3' (FRAG. NO:1012) (SEQ. ID NO:1022)
5'-TTC BBG GBG BCC TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC-3' (FRAG. NO:1013) (SEQ. ID NO>1023)

Human IgE Receptor (Fc Epsilon R) Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCC TGT GTC TGT CCT CCT GCT TCG TTC CTC TCG TTC CTG CTT GGT GCC CTT GCC G GTC CTG CTC CTC CGG GCT GTG G GTC CTC GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG C CCC BGB BCG BGB CCC GGB CCG BCB GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC GAT CTC TGA ATA TTGA CCT TCC ATG GCG GTC CTG CTT GGA GBT CTC TGB BTB TTGB CCT TCC BTG GCG GTC CTG CTT GGB-3' (FRAG: 1696) (SEQ. ID NO:1707)
5'-TCG TTC CTC TCG-3' (FRAG: 1697) (SEQ. ID NO:1708)
5'-BGB BCG BGB C-3' (FRAG: 1698) (SEQ. ID NO:1709)
5'-TGB BTB TTGB-3' (FRAG: 1699) (SEQ. ID NO:1710)
5'-GCC TGT GTC TGT CCT CCT-3' (FRAG. NO:1014) (SEQ. ID NO:1024)
5'-GCT TCG TTC CTC TCG TTC-3' (FRAG. NO:1015)(SEQ. ID NO:1025)
5'-CTG CTT GGT GCC CTT GCC G-3' (FRAG. NO:1016)(SEQ. ID NO:1026)
5'-GTC CTG CTC CTC CGG GCT GTG G-3' (FRAG. NO:1017)(SEQ. ID NO:1027)
5'-GTC CTC GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG-3' (FRAG. NO:1018) (SEQ. ID NO:1028)
5'-CCT TCG CTG GCT GGC GGC GTG C-3' (FRAG. NO:1019) (SEQ. ID NO:1029)
5'-CCC BGB BCG BGB CCC GGB CCG BCB-3' (FRAG. NO:1020) (SEQ. ID NO:1030)
5'-GGC CGT GGT TGG GGG TCT TC-3' (FRAG. NO:1021) (SEQ. ID NO:1031)
5'-GCT GCC TCC GTT TGG GTG GC-3' (FRAG. NO:1022) (SEQ. ID NO:1032)
5'-GBT CTC TGB BTB TTGB CCT TCC BTG GCG GTC CTG CTT GGB-3' (FRAG. NO:1023) (SEQ. ID NO:1033)

Human High Affinity IgE Receptor Oligonucleotide Fragments

5'-AACAAGAAAA GCGTTGGTAG CTCTGGTGAA TCCCAAAAGA ATGTGGCAGT TGCTAGCCAT GCTCCTGAAT
ATGTATAAAC AGTACATCAT ATGACTAAGA GTTTGACTTA GGGGTTAGAT TTTATGTGTT TGAACCCCAA ATTAGTTATT
TAATAGTTGG CACCCCAAAA CAAGTTACTT AACCTCACTA AGGTTCAGTT TTCCTGTTTA TAAAATGTAG ATAGTGATAG
TATGTACTTT ATAGGATTAT TGTGAAAAAT AAATGAAATA TCAGATTTAT TTAGGATAAC ACCTGGCATA TGTTTGGTAT
TCAGAATTAG TTGCTGCTGT TTTATTCTGC TCTCCCTTGC ATCCCACTTT TCTAAGTTGT AAACTAAATA GTTGTACACA
GATTGACAGA TTAAGAAAGG CTTGTGATTG TGCTAGACCT ATGCCTATGC CTCTGTCTCA CCAGATTCCA GGTGTATATG
TGGAGGTGGG ATAGGGAGTG GAGTAAGTGG GTAAATATTA AATTGCCCAG TTGGGCACCA TCCTGAATAT TATCTCTAAA
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5'-AACAAGAAAA GCGTTGGTAG CTCTGGTGAA TCCCAAAAGA ATGTGGCAGT TGCTAGCCAT GCTCCTGAAT ATGTATAAAC AGTACATCAT ATGACTAAGA GTTTGACTTA GGGGTTAGAT TTTATGTGTT TGAACCCCAA ATTAGTTATT TAATAGTTGG CACCCCAAAA CAAGTTACTT AACCTCACTA AGGTTCAGTT TTCCTGTTTA TAAAATGTAG ATAGTGATAG TATGTACTTT ATAGGATTAT TGTGAAAAAT AAATGAAATA TCAGATTTAT TTAGGATAAC ACCTGGCATA TGTTTGGTAT TCAGAATTAG TTGCTGCTGT TTTATTCTGC TCTCCCTTGC ATCCCACTTT TCTAAGTTGT AAACTAAATA GTTGTACACA GATTGACAGA TTAAGAAAGG CTTGTGATTG TGCTAGACCT ATGCCTATGC CTCTGTCTCA CCAGATTCCA GGTGTATATG TGGAGGTGGG ATAGGGAGTG GAGTAAGTGG GTAAATATTA AATTGCCCAG TTGGGCACCA TCCTGAATAT TATCTCTAAA GAAAGAAGCA AAACCAGGCA CAGCTGATGG GTTAACCAGA TATGATACAG AAAACATTTC CTTCTGCTTT TTGGTTTTAA GCCTATATTT GAAGCCTTAG ATCTCTCCAG CACAGTAAGC ACCAGGAGTC CATGAAGAAG ATG-3' (FRAG. NO:_)(SEQ. ID NO:2500)

5'-GATCTTCATG TGGAATGACT GGTTTCATTC AATAGACTTA ATTCAGCAGT CTGTGGGGAA GAGCAAGGTA TGATAGAATG GTTCCTCAAG TGCTTCAGAT GTGAAGTGGG TTTAAATATA CTGTCCCTGT CTTCTTCAGA GTTTTGGTAA AGATAAAATA GGACACTCAT TTAAAAGCAA TCTTTGCAAA TGACAAGCCA CTATAGACAT TAATAGAGTT TTCATTTCCA GTATTATCAT TAATATCAGA TCCTGGAAGA AGGTTGAGCC TTGACCTAGA GCAAAAAAAC AGAAGAATTA GTAAAGGAAT CCTGGAGAAA GCCCCTGCTG TGTATTTAAA GGAGAAAGGG AGATCATGTT GGGAAATTAT AATATTAAAA GTAAACAAAA GCTAGGAAGT AAAATAAAAT AAATTATATG GCCTAGATCC CCATAAGTAA TGGTTTAACT TCTGCCTTCC TGTGTTCTGA GCCAGATTAG GGCACAGTAG AGAAAGAGGA GTCTCTGAAA ATGTTTCCAA TTTCGCTGGT CAGACAGCGG ATCATCAGTG AATCAGATGA AAATTTGTGG ATTTATGCAC TAACTGATCA GCAGGAAATT AAACAAGAAA AGCGTTGGTA GCTCTGGTGA ATCCCAAAAG AATTTGGCAG TTGCTAGCCA TGCTCCTGAA TATGTATAAA CAGTACATCA TATGACTAAG AGTTTGACTT AGGGGTTAGA TTTTATGTGT TTGAACCCCA AATTAGTTAT TTAATAGTTG GCACCCCAAA ACAAGTTACT TAACCTCACT AAGATTCAGT TTTCCTGTTT ATAAAATGTA GATAGTGATA GTATGTACTT TATAGGATTA TTGTGAAAAA TAAATGAAAT ATCAGATTTA TTTAGGATAA CACCTGGCAT ATGTTTGGTA TTCAGTAATT AGTTGCTGCT GTTTTATTCT GCTCTCCCTT GCATCCCACT TTTCTAAGTT GTAAACTAAA TAGTTGTACA CAGATTGACA GATTAAGAAA GGCTTGTGAT TGTGCTAGAC CTATGCCTCT CTCTCACCAG ATTCCAGGTG TATATGTGGA GGTGGGATAG GGAGTGGAGT AAGTGGGTAA ATATTAAATT GCCCAGTTGG GCACCATCCT GAATATTATC TCTAAAGAAA GAAGCAAAAC CAGGCACAGC TGATGGGTTA ACCAGATATG ATACAGAAAA CATTTCCTTC TGCTTTTTGG TTTTAAGCCT ATATTTGAAG CCTTAGATCT CTCCAGCACA GTAAGCACCA GGAGTCCATG AAGAAGATGG CTCCTGCCAT GGAATCCCCT ACTCTACTGT GTGTAGCCTT ACTGTTCTTC GGTAAGTAGA GATTCAATTA CCCCTCCCAG GGAGGCCCAA ATGAATTTGG GGAGCAGCTG GGGTAGGAAC CTTTACTGTG GGTGGTGACT TTTTCTAGGA CATGTGCAAA CTATTGGGCA TTTCCCAGGG ACTCTGTAGT GGAGCCAAGC TAGAAAGCAG AGGCAAGTGG GCTGAGCAAC ACCTAAGGAG GAAGCCAGAC TGAAAGCTTG GTTCCTTGCA TTTGCTCTGG CATCTTCCAG AGTGCAAATT TCCTACCAAG GTAATGAGGG TAGAGGAGAG AAAGAAGCTC TTTCTTCCCC TGATTCTCAT TCCTGAAAAG ACGGTTGGTC CTTAAAATTC CATGGATGTA GATCTTATCC CCACACCCAG ATTCTAGTCC TCTGGAGATA AAGAAGACTG CTGGACACTA ATGTATCCTC TCTGGACTTT TGCAGCTCCA GATGGCGTGT TAGCAGGTGA GTCCTCTGTT CTTGTTCCCT TGGTGTATCA ACATGTCTGG GCATTGCTTT CCTCTCACTA TTTTCTTCGT CCCATCACTT CTGCTTTCTA ATGAGCATGA ATCTGTTCCT TGGCCAGACT ACTTTCCCTC TCCACCTTGC CTTGTCTTTC TTTTTTTCCC TGATTCATTG CATTCTCTCA AGTCATTCTC TCCTCTGTTT TAGTCAATAA CCATGTCTGT TGCACATATA CATGTCTCAT TCTCTCTCCT AGACACTTTG GCATGATCTC GCTCAATAAT TACATTATTA TTATTATTGC CATTTTATAA TTGAGGATGC TGAAACTCAG TGATTTTCTG GTGGTTACAT GGCTAAGGAA CTGGATTTCA ACGTAAGTTC CTTGGATCTA AGTCCAGTTC TCTTCTGACT ATATCACCCT TTTGTTATCA CCATGTATCT ACTTCTTTGG TCTCTGTTCA AATTTGCACT ACATCCCCTT GTTCCAGGAA GCCATTCAAG ACTGACTTTC TTAGTGCCTC TCACTACTTT CTGGAACTGA CATATGTTTT TCACTCTGTA TATACTTACA ATTAAATAGT CATAAATATT CAGAGCTTGG AGAAACCTTA TATTTCATCC AGTCCAGTAA ATTTATCCAT CCATAATTCA CTCATTCATT CACATAATAA ATATTTAATG TAACAATGGT TGAACATGGC AGACAGTGTT TCTACCTCAA AAGAGATTGC AGTCCTCATT TACAGATACT GAATTGAAAT TAACAGAAGT AGAGTGAGTC AGCTCAAATC ACATAGTGAA TTGGTTTCTT TGTTTTTAAA TCTCCTGCAT ATGTGTCCTG TCTTTCTCCC TGTGTTGGGC GTTCCCTGGG GCACCAATAC TAATTTCTCC TTCCCCTAGA AATCAAAACA GGGTCTTATC ACCAACAGAA TAAGGACAGG TTGACCACTG ATTGTCAGAA TATTGCTTCG TTTGTACTTT TAAGCCTAGA CAGTTTTCAA TGACTTTTTT TCTCTCTACA TGTCTTTTCA TATTTTTATC TTCTTGAAGT CCCTCAGAAA CCTAAGGTCT CCTTGAACCC TCCATGGAAT AGAATATTTA AAGGAGAGAA TGTGACTCTT ACATGTAATG GGAACAATTT CTTTGAAGTC AGTTCCACCA AATGGTTCCA CAATGGCAGC CTTTCAGAAG AGACAAATTC AAGTTTGAAT ATTGTGAATG CCAAATTTGA AGACAGTGGA GAATACAAAT GTCAGCACCA ACAAGTTAAT GAGAGTGAAC CTGTGTACCT GGAAGTCTTC AGTGGTAAGT TCCAGGGATA TGGAAATACA GATCTCTCAT GTGAGGGATG GCTCATCTGA AGATGGGAAA AAACAGGTTA TTCCAAGGGT TAGGACACCA GAGTGGGATT CAAGGCCTCT CATTTTTAAG ACCCCTGCAT TGGCTGGGCA CAGTGGCTCA CGCCTGTAAT CCCAGCACTT TGGGAGGCTG AGGCAGGTGG ATCACGAGGT CAGGAGATCG AGACCATCCG GCTAACATGG TGAAACCCCA TCTCTGCTAA AAAATATATA TATATAAAAT TAGCCGGGCG TAGTGGTGGG CACCTGTAGT CCCAGGTACT CGGGAGGCTG AGGCAGGAGA ATGGTGTGAA CCCAGGAGGT GGAGGTTGCA GTGAGCTGAG ATCACGCCAC TGCCCTCCAG CCTGGGCTAC AGAGCAAGAC TCCGTCTCAA AAAATAAATA AATAAATAAA AAAGACCCCT GCATCTCTTT TCTTCTACCC CCTTCCCTTT TGATTACTTG TATGCCTTCT TTCAATATTC TAGTCATCTC TCAATATTAT TCCTCCACCC TATTTTCCTC TATCTTTTCT GCCTAGATTC AGGTATATAT TATGTGGTCA AACAGCATGA CATATATGTG AACATTTCAA AGAGCTGTGT ATCTGGAATA GGATCAAAAG GTTTGACTTA AAGTTTTGCT CTGCATAATC CATATGGCAG GACCTGAATA TTAGGTTGTA CTCTTCGTTA TGAAACATAT CTGGGTACAT TTCCTTATGT CCTCTGTTGT TACTTAAGAA CACATATTTC ATGCTTGTTT CATTTTTATC ACTCCTACTG CCAACAAATA GCATAGCATG CTTAGGCACA TGTGGCTTAA TTAGCAAATG TTGAATAAAC AAATTAATGA TTTTGAATAG TGACCAATAG GTCTCTTTTA TACTCTATAT TTTTCTCTTG AGTGAAAAAA AATGTTTCAA CCTCCATATG

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5'-TACTAAGAGT CTCCAGCATC CTCCACCTGT CTACCACCGA GCATGGGCCT ATATTTGAAG CCTTAGATCT CTCCAGCACA GTAAGCACCA GGAGTCCATG AAGAAGATGG CTCCTGCCAT GGAATCCCCT ACTCTACTGT GTGTAGCCTT ACTGTTCTTC GCTCCAGATG GCGTGTTAGC AGTCCCTCAG AAACCTAAGG TCTCCTTGAA CCCTCCATGG AATAGAATAT TTAAAGGAGA GAATGTGACT CTTACATGTA ATGGGAACAA TTTCTTTGAA GTCAGTTCCA CCAAATGGTT CCACAATGGC AGCCTTTCAG AAGAGACAAA TTCAAGTTTG AATATTGTGA ATGCCAAATT TGAAGACAGT GGAGAATACA AATGTCAGCA CCAACAAGTT AATGAGAGTG AACCTGTGTA CCTGGAAGTC TTCAGTGACT GGCTGCTCCT TCAGGCCTCT GCTGAGGTGG TGATGGAGGG CCAGCCCCTC TTCCTCAGGT GCCATGGTTG GAGGAACTGG GATGTGTACA AGGTGATCTA TTATAAGGAT GGTGAAGCTC TCAAGTACTG GTATGAGAAC CACAACATCT CCATTACAAA TGCCACAGTT GAAGACAGTG GAACCTACTA CTGTACGGGC AAAGTGTGGC AGCTGGACTA TGAGTCTGAG CCCCTCAACA TTACTGTAAT AAAAGCTCCG CGTGAGAAGT ACTGGCTACA ATTTTTTATC CCATTGTTGG TGGTGATTCT GTTTGCTGTG GACACAGGAT TATTTATCTC AACTCAGCAG CAGGTCACAT TTCTCTTGAA GATTAAGAGA ACCAGGAAAG GCTTCAGACT TCTGAACCCA CATCCTAAGC CAAACCCCAA AAACAACTGA TATAATTACT CAAGAAATAT TTGCAACATT AGTTTTTTTC CAGCATCAGC AATTGCTACT CAATTGTCAA ACACAGCTTG CAATATACAT AGAAACGTCT GTGCTCAAGG ATTTATAGAA ATGCTTCATT AAACTGAGTG AAACTGGTTA AGTGGCATGT AATAGTAAGT GCTCAATTAA CATTGGTTGA ATAAATGAGA GAATGAATAG ATTCATTTAT TAGCATTTGT AAAAGAGATG TTCAATTTCA ATAAAATAAA TATAAAACCA TGTAACAGAA TGCTTCTGAG TAAAAAAAAA AAAAAAAAAA AAAAAAAA-

3' (FRAG. NO:_) (SEQ. ID NO:2502)
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CTTCAGGCAG ACTATTGAAG TCGGCCTCAT CCCCACCACT GCATACATGG CTGACAGTTT TGAAAAAAGA GCAGGAGTTC
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CATTGAGGGA GACATTTTTT CATCATTTAA AGCAGGTTAT CCATTCTGGG GAGCCATATT TTTTTCTATT TCTGGAATGT
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GGGGGAACGG GAATTACCAT CCTGATCATC AACCTGAAGA AGAGCTTGGC CTATATCCAC ATCCACAGTT GCCAGAAATT
TTTTGAGACC AAGTGCTTTA TGGCTTCCTT TTCCACTGAA ATTGTAGTGA TGATGCTGTT TCTCACCATT CTGGGACTTG
GTAGTGCTGT GTCACTCACA ATCTGTGGAG CTGGGGAAGA ACTCAAAGGA AACAAGGTTC CAGAGGATCG TGTTTATGAA
GAATTAAACA TATATTCAGC TACTTACAGT GAGTTGGAAG ACCCAGGGGA AATGTCTCCT CCCATTGATT TATAAGAATC
ACGTGTCCAG AACACTCTGA TTCACAGCCA AGGATCCAGA AGGCCAAGGT CTTGTTAAGG GGCTACTGGA AAAATTTCTA
TTCTCTCCAC AGCCTGCTGG TTTT-3' (FRAG. NO:_)(SEQ. ID NO: 2503)
5'-AAGCTTTTCA AAGGTGCAAT TGGATAACTT CTGCCATGAG AAATGGCTGA ATTGGGACAC AAGTGGGGAC
AATTCCAGAA GAAGGGCACA TCTCTTTCTT TTCTGCAGTT CTTTCTCACC TTCTCAACTC CTACTAAAAT GTCTCATTTT
CAGGTTCTGT AAATCCTGCT AGTCTCAGGC AAAATTATGC TCCAGGAGTC TCAAATTTTC TTATTTCATA TTAGTCTTTA
TTTAGTAGAC TTCTCAATTT TTCTATTCAT CACAAGTAAA AGCCTGTTGA TCTTAATCAG CCAAGAAACT TATCTGTCTG
GCAAATGACT TATGTATAAA GAGAATCATC AATGTCATGA GGTAACCCAT TTCAACTGCC TATTCAGAGC ATGCAGTAAG
AGGAAATCCA CCAAGTCTCA ATATAATAAT ATTCTTTATT CCTGGACAGC TCGGTTAATG AAAAAATGGA CACAGAAAGT
AATAGGAGAG CAAATCTTGC TCTCCCACAG GAGCCTTCCA GGTAGGTACA AGGTATTATT TTTTTCTACC CTCAGTCACT
TGTGGCAGGG GAAGTCATAG TCACGGTGCT TAGGAGATGA AACTTTATTG ATTTAGGCAT GGATCCATCT AGTTTAATTA
ATATATTGGG TATGAGGAAG CTACTTGCTG TACTTTCCAT GTGGTTCTCT CTCCCTGGAG AGGAACATTT TTACTCAGCT
TGCAAACTGG AAATAGATTT TCTCACATTA GAAGCTCATT TTCTGGGTAT GAGACAGGAG AGTTCATACT GTGTATGTAG
ATCTCTGGCT TCTGGGTCTG ACATGTGCTG AGGGACACAT ATCCTTCACA CATGCTTTTA TAAATACTTG ATAAAGTAAC
CTGCTTCTTG ATTGGTCTTT ATAATCCATA AGCTGTGGGA TGCTTCTCTG AAGATGAAAA TAGTAATAGA GTCCCATCTA
GCTATTCAAA GCCATTCCTT CATTGTATTC TGTGCACATG AAGTTGGGGT TTGTTACTGA CAAAATATAT TCAGATACAT
TTCTATGTTA AAAGGATTGT GAGATGCATA GGTAAATGTG TTTATTTTCA GTTTTACTTG TCAACATAGA TGAATGAGAA
AGAACTTGAA AGTAACACTG GATTAAGAAT AGGAAAATTT GGCATGGATT TTGCTCCATT TTGTCCCATC TAATCACTTG
GATAGTGTTC AGGTGTTCTT GGTCAGTTAC TTGGATGCTC TGAGCTTTAG TTTCTTGGTG ATTACAATGA AGATTTGAAT
TACAGGATGG CTTTGAAAAA ATAAACAAAA CTCCCCTTTC TGTCTGTCGA GAATGTTGCA CAGGGAGTTA CAGAATGTTC
TCATGACTGA ATTGCTTTTA AATTTCACAG TGTGCCTGCA TTTGAAGTCT TGGAAATATC TCCCCAGGAA GTATCTTCAG
GCAGACTATT GAAGTCGGCC TCATCCCCAC CACTGCATAC ATGGCTGACA GTTTTGAAAA AAGAGCAGGA GTTCCTGGGG
GTGAGTGAGC CTCCTCCAAC TTTGACTAGA GTAAGGGTTG GGTCTAGAAA AGAATATTGA GTTGCATCAA CTGTTTTCCC
ACTTGGATTC ATGAGAGGTG TTAGGTCCTT TAAAAAACAT GGTAGATAAA GAGTTGACAC TAACTGGGTC CTTTTGGGAA
GAGCCAGAAG CATTTCCTCA TAAAGACTTT AAATTGCTAG GACGAGAATG GCCAACAGGA GTGAAGGATT CATAACTTTA
TCTTTACTTA GATGTAAAGA ACAATTACTG ATGTTCAACA TGACTACATA CATAAAGGCG CATGGAGAAA AGTATTGGCC
TTCCATGCAT TAGGTAGTGC TTGTATCAAT TCTTATAGTG GCTAGGGTAT CCTGGAAAAT CTTACGTGTG GATCATTTCT
CAGGACAGTC TAGGACACTA ACGCAGTTTC TCATGTTTGG CTTCTATTAT TAAAAAATGA TACAATCTCG GGAAAATTTT
TTTGATTTTC ATGAAATTCA TGTGTTTTTC TATAGGTAAC ACAAATTCTG ACTGCTATGA TATGCCTTTG TTTTGGAACA
GTTGTCTGCT CTGTACTTGA TATTTCACAC ATTGAGGGAG ACATTTTTTC ATCATTTAAA GCAGGTTATC CATTCTGGGG
AGCCATATTT GTGAGTATAT ATCTATAATT GTTTCTGAAA TAACACTGAA CATAGGTTTT TCTCTTTCTC AGATCTAACC
AGTTGTTTAT TCCCAGTATT AAGATGATAT TTATAATTCT TAATTATAAA TATATGTGAG CATATATAAC ATAGATATGC
TCATTAACAA CAACAAAAGA TTCTTTTTAC AATTAACGGT GGGTTAAACA TTTAGCCCAC AGTTTTATCC CATGAGAAAC
CTGAATCTAA TACAAGTTAA ATGACTTGCC TAAGGGCCAC TTGACTAATA GTAATTGAAC CTAAACTTTC AGAATCCAAC
TCCAGGAACA TACTTCTAGC ACTATTCATC AATAAAGTTA TATGATAAAT ACATACAACT TTATCTGTCA ACTAAAAATA
ACAACAGAGG CTGGGCATGG TGGCTCACAC CCGTAATCCC AGCACTTTGG GAGGCTGAGG CAGGTGGATC ACCTGAGGTC
AGGAGTTTGA GACCAGCCTG ACCAACATGG TGAAACCTCA TCTCTACTAA ATATAAAAAA TTAGCTGAGT GTGATAGTGC
ATACCTGTAA TCCAGCTACT TAAGAGGCTG AGGCAGGAGG CTTGTTTGAA CCTGGAAGGC AGAGGTTGCA GTGAGCTGAG
ATTGTGCCAT TGCACTCCAG CCTGGGCAAT AAGTGCGAAC TCTGTCTCAA AATAATAATA ATAATAATAG AAAATAAAGT
TGTCTTCATG AAAAATGAGG AAAGAGATTG CTGGGGTGAG AAACATTAAG ATCAATGGGC ATATGGTGAC CTTCTATGCC
CTAGAAACTC TTTTANGGTA TTTTCTCCTG GTATCTCTTT TACNCATCGT TCTATCTGGA AAAATAGGTG GATGAGTGAG
ATAATAACGG TATATACTTT TTAAAGGTCT AATTGACATA TATAAATTGC AAGTATTTCA GATGTCAATT TGCTAACCTT
GACACACATA GACACACATG AAAACATCAC CACATTAATA CAATGTATGT ATCCATCATT CCAAAAGCTT CCCTGTGTAT
CTTTGTAACT CTTTCTTCCT CCCTCCACTC CTTGTCCTCT CGTTCCCAAG AAAACATTGA TCTGCTTCCT GTGAATATAA
ATTAACTTAC ATTTTTTAGA GCTTTATATA AGTATGTTCT CTTTACTGTT TGTCTTCCTT CGCTGCACAG TTATTTTGAG
ATTCTTCAAG TTTTTTCTTT ATATCGATAC TTCATTCACA AGAATATATT TTAATTCTAG ACTATGTCAC ATTGACTTTG
TCGTCTGCTA AATCCTTAGT GCTCAGATGA CTTGTTCAGG ACTCTCCTTG AACCTGTACC TCTGTTANAT TGAAACTTGT
CTCTACTGTC TTTTTATTTC AAACACAGCT TATTAGGTGT CTCTCAACCC ATCAAACNCA CAATCTGAGT CTTTAGGAGA
TTGCTTTGAA TTTGTGCTAT TGACTTATAT NTATATNAAA TNTGTAAATG TTTGGTAAAA ATATCATCAT GTACNTTTTC
ATAATTACGC TATNTNCACA TGATATATGT CAGACTCTGG AAATATGCAT GCCACAGACA CGTGTTTCTT GCCTAAAGGG
GCTGATGGAA GACNCACATA CNAATAGACG ATTGCAGTAG AATGAGAGTG GTGGTCTAAN CAGTACATGT CCTGATGTTG
CTCGGACAGT TACTACNCCA AGAGTACCCC CTGCATTGTC AGGGTTAGCA TCTCCTGGAA GCCTCATGTA AATGAAGAAT
TTCATGCTCC ATCCAGGACC TAATGAATAA GAATCTGCAT TTTAGCAAGA CCCTCATATG ATTCATATAC ACTTTTTTTT
TTTTTTTTTA GATGGAGTCT CACTCTTGTC GCCCAGGCTG GAGTGCAATG GCATGATCTT GGCTCACTGC AACCTCTGCC
TCCCGGGTTC AAGTGATTCT CCTGTCTCAG CCTCCCTAGT AGCTGGGACT ACAGGTGCAT GCCACAGTGG CTGGCTAATT
TTTGTATTTT TAGTAGAGAC AGGGTTTCAC CATTTTGGTC AGGCTGGTCT TGAACTCATG ACCTCCGGTG ATTCCCCCGC
CTCGGCTTCC CAAAGTGCTG GGATTACAGA CATGAGCCAC CACACCCGCC TTATTCGTAT ACNCATTTAA TTCTGAGAAG
CACTCTATAG AAAATAAGAA TAAGAAAATA TTGGGCTCAC AGGTGACATT AATAAGTAAC TTTATCGAGT ACCCCAAATT
TTACCTATGT TTGGAAGATG GGGTTAAAAG GACACATTGA AAACAAGAAC TCATTGTGGC TTTTTTTTCC TCCTTTTTGA

ACAGTTTTCT ATTTCTGGAA TGTTGTCAAT TATATCTGAA AGGAGAAATG CAACATATCT GGTGAGTTGC CCGTTTCTGT
CTTTGTCCAT CCTTGAAAAG ATAAGAAGAA CAGAGTTTTA AGAGTCTTAA GGGAAACACA TCTTTGTCTC CTATATTACT
TGTGAATGTG GATATATGAT TTTGTTTCAA TCTATTTTGT GTCCTAAGGC TTTTTGCAAC AGAAGTTGGA TATATCATTA
GAAACATAAA TTGTACCATT TAACATACAT GAAGTTTATG TTTACCTTGA CGTTCTTCTA AAAAGTGTCC TACACCGGCA
TTGTCCTTGT AGGCATATTC ACATGATCAA ATAAAATAAT TAGTTTTCAA TTAAGGAGAA TATTTGAGGA AAGACCGTAC
GTGTTCATGT GGTTCCTGAA GGCAGTCCAG TGAGAAAGTA ATATATGCTT CATTAAACAA TGCGGACATT TTCAGGGTTT
CCCTTTTTAA CCAAAATTTG GAAGCAATGT GGAATTTACT GGATGCATCC AGCCCTGAAA TGAAGATAGG TTTATTGAAT
GTGCCAGCAA GTGCAGGCCC AGGTCTGAGT GTTCTTCATT ATTATCAGGT GAGAGGAAGC CTGGGAGCAA ACACTGCCAG
CAGCATAGCT GGGGGAACGG GAATTACCAT CCTGATCATC AACCTGAAGA AGAGCTTGGC CTATATCCAC ATCCACAGTT
GCCAGAAATT TTTTGAGACC AAGTGCTTTA TGGCTTCCTT TTCCACTGTA TGTATTTTTT TTTGTGTGGG AAGACTAAGA
TTCTGGGTCC TAATGTAAGT AAGAAGCCCT CTTCTCCTGT TCCATGAACA CCATCCTTTT CTGTAACTTC TATTACACAG
TATAGTGGTT CTGTAAGTTC ACACAGCCCA GGGAGATGCT GGCTGCCCAC TCCCCTCAAC CCAGGCAAAT TCCTCGGGGT
TAAAGTTATC TACTGCAAGT GACGATCTCT GGGTTTTTCT GTGCCTGTGT TTGTGTGTGT GTGTGTGTGT GTGTGTGTGT
GTATGTGTCA CTTTAAAAGG ACTGGTCAGA TGGTAGGGAG ATGAAAACAG GAGATGCTAT AAGAAAATAA ACTTTTGGGG
CGAATACCAA TGTGACTCTT TTTGTTTGTC ATTTGTTGCT GTTCAATAGG AAATTGTAGT GATGATGCTG TTTCTCACCA
TTCTGGGACT TGGTAGTGCT GTGTCACTCA CAATCTGTGG AGCTGGGGAA GAACTCAAAG GAAACAAGGT AGATAGAAGC
CCGATATAAA ATCTTGAATG ACAGGTTAAC GAATTGGAGC TTTATTCCTT AAAATATGGC CTGGGTTTTC TGAAACATTT
CTTCCAGAAA ATAGTTTCTC CAAGTTTTAT TACTTTGGTT TACAAATCTC ACATTTAAAT CACATTTTAT ACCATAAGTA
GCACACATTT CATAATATTC CTCTGAATGA GGGTTGGGAT AATAGGACTG ATATGTTAGA AATGCCTTAA AGTGTGTGGA
GCATGAGAGA TGGATGTACA GAAGGCTTGT GAGGAAACCA CCCAGGTATC TGGCCTTGTT TTCTGCCCCA GAACTAGCCG
CCTATTCCTG TTTCTGTTTT ATTCCTTTGT TTCTTGACTT TTCCTTTCCA ACTTGCTCTA AAACCTCAGT TTTCTTTCCT
TTCTGATTCA TGACTACCAA ATGTTTTCAC TTGCCTCACC CGTCCATTAC ACCTTTGATA AGAACCACCA GACCTTGTGC
TCATGTACTT GCCCATGTCT GATGGAAGAA ACATACTCTC TCCATCTGTC CACTTTCCTG AGGCATTCAA GTCTAGCCAC
CTTTTAAAAT CACTCTCCTC CAGGCTGGGC ACGGTGTCAC GCCTGTAATC TCAGCACTTT GTGAGGCTGA GGAGGGCGGA
TCACTTGAAG TCAGGAGTTC AAAACCAGCC TGGCCAAATG GCAAAACCAA ATCTTCTTCA ATTATAACCA AATCTTAAAC
CAAATCTCTA CTAAAAAATA CAACAAAACA AAACAACAAC AACAAAAACA GAAAAGGAAA CATTAGCCCA GCGTGGTGGC
AGGTACCTGA GGTTCCAGAT ACTTGGGAGG CTGAAGCAGG AGAATCGCTT GAGCCCAAGA GATGGAGGTT GCAGTGAGCC
GAGATCATGC CACTGCACCA CAGCCAGGGT GACAGAGCCA TACTTCCCAG CACATTGGGA GGCCAAAGCT GAAGAATAAT
TTGAGGTGAG GATTTGGAGA CCAGCCTGGC CAACATGGTG AAACTCCGTC TGTACTAAAA ATATAAAACT TAGTGGGGCA
TGGGGGCACA CACCTGTAAT TTCAGCTACT TAGGAGGCTG AGGCAGGAGA ATTGCTTGAA CCCGGGAGGC GGAAGTTGCA
GTGAGCCAAG ATCGTGGCCA CTGCACTCCA GCCTGGGTGA CATAGTGAGA TTCTGTCTCA AAAAAAATAA AAGAAATTTA
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ACATGATTTC TTTTGGCCCA CTTGGCCAGC TAGTCTGGTT TGGTTTTCTG GAAATGAAAG AAATAATCAG AGTTTAATGA
CAGAGAGCGT GAGACCCAGA AAGACAAAAG TAGATGAGGT AAGTCTCTTG AGCGAGACTT CTAGGGATGG GAAATTTGTG
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TTACAGTGAG TTGGAAGACC CAGGGGAAAT GTCTCCTCCC ATTGATTTAT AAGAATCACG TGTCCAGAAC ACTCTGATTC
ACAGCCAAGG ATCCAGAAGG CCAAGGTTTT GTTAAGGGGC TACTGGAAAA ATTTCTATTC TCTCCACAGC CTGCTGGTTT
TACATTAGAT TTATTCGCCT GATAAGAATA TTTTGTTTCT GCTGCTTCTG TCCACCTTAA TATGCTCCTT CTATTTGTAG
ATATGATAGA CTCCTATTTT TCTTGTTTTA TATTATGACC ACACACATCT CTGCTGGAAA GTCAACATGT AGTAAGCAAG
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ATAATATTTG GTTCTTAGGG TTTTTTTTTT TTTTAGCATT CTTAATAGTT ACAGTTGGGC ATGATTTGTA CCATCCACCC
ATACCCACAC AGTCACAGTC ACACACACAT ATGTATTACT TACACTATAT ATAACTTCCT ATGCAAATAT TTTACCACCA
GTCAATAATA CATTTTTGCC AAGACATGAA GTTTTATAAA GATCTGTATA ATTGCCTGAA TCACCAGCAC ATTCACTGAC
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TAAGACCTGA GCTGAAATAA AGTGACGTGG AAATGGAAAT AATGGTTATA TCTAAAACAT GTAGAAAAAG AGTAACTGGT
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AAGGAGAACA CTGGTTATGT TGATAGAATG ATAAAAAGGG TCGGGCGCGG AGGCTCACGC CTGTAATCCC AGCCCTTTGG
GAGGCCGAGG TGGGCAGATC ACGAAGTCAG TAGTTTGAGA CCAGCCTGGC CAACATAGTG AAACCCCGTC TCTACTAAAA
ATACAAAAAA AAAATTAGCT GGGTGTGGTG GCAGTCACCT GTAGTCCCAG CTACTTGGGA GGATGAGGCA GGAGAATCGC
TTGAACCTGG GAGGCGGAGG TTGCAGTGAG CCGAGATCGC ACCAGTGCAC TCCAGCCTTG GTGACAATGG GAGACTCCAT
CTCAAAAAAA AAAAAAAAAA AAAAAAGATA AAAAGTCAGA AATCTGAAAA GTGGAGGAAG AGTACAAATA
GACCTAAATT AAGTCTCATT TTTTGGCTTT GATTTTGGGG AGACAAAGGG AAATGCAGCC ATAGAGGGCC TGATGACATC
CAATACATGA GTTCTGGTAA AGATAAAATT TGATACACGG TTTGGTGTCA TTATAAGAGA AATCATTATT AAATGAAGCA
AGTTAACACT CTAAGAGAAT TATTTTGAGA TAGAAGTGAA GCTAAGCTAA ACTTCACATG CCTATAATTG GAGGGAAAAA
CTAAGGATAA AATCTAGCCT AGAAGATACA ATAATTAGTC ATAAACATGC ATTGTGAAAC TGTAGAGAGC AGGTAGCCCA
AAATAGAGAA AGATTAGATA AAGAGAAAAT AAGTATCCAT CAGAGACAGT ATCTCTAGGC TTGGGCAAGA GAAAAGTCCA
CAGTGATAAG CAACTCCACC TAAGGCATGA ATATGCGGCA GAGAAAACAG CAATAGTGAA TGAATGCAAA AGGTGCTGAG
CAAATTCCAC ACATGAGTAT TGTGCATGAG TAAATGAATA AAACATTTGC AAAGACCTTT AGAGAAAGAG AATGGGAGCA
TATGTGCGAA ATAAGATAGT TGATTATGAA TAGAAGGTAG TGAAGAAAAG CAAGCTAAGA AAAAATTCTG TTTATAAAAG
AAGGAAAAGA TAGTTTATGT TTTTAGCCTA AGTATAAGAG TCCTACAGAT GGACTGAAAA AAATCAGTCT GAGAGTATTA
GTCACAATTA ATGAAATAAT TACATTTTAT GTATTGAGGA TGCCAAGATT AAAAGGTGAC AGGTAGATGT TAATTTCCCT
AGATTGTGAA AGTGATCACG ACAATCACAC AACAAATAAT TAAGTGACTT GGTATGCTTT ATTTAATTGT AGGGCCTGAG
GTTTTCCATT CTCATTTTTC TAAAATACAA TTTTGTTTCT CCAAATTTGA CAGCAGAATA AAAACCCTAC CCTTTCACTG
TGTATCATGC TAAGCTGCAT CTCTACTCTT GATCATCTGT AGGTATTAAT CACATCACTT CCATGGCATG GATGTTCACA
TACAGACTCT TAACCCTGGT TTACCAGGAC CTCTAGGAGT GGATCCAATC TATATCTTTA CAGTTGTATA GTATATGATA
TCTCTTTTAT TTCACTCAAT TTATATTTTC ATCATTGACT ACATATTTCT TATACACAAC ACACAATTTA TGAATTTTTT
CTCAAGATCA TTCTGAGAGT TGCCCCACCC TACCTGCCTT TTATAGTACG CCCACCTCAG GCAGACACAG AGCACAATGC
TGGGGTTCTC TTCACACTAT CACTGCCCCA AATTGTCTTT CTAAATTTCA ACTTCAATGT CATCTTCTCC ATGAAGACCA

CTGAATGAAC ACCTTTTCAT CCAGCCTTAA TTTCTTGCTC CATAACTACT CTATCCCACG ATGCAGTATT GTATCATTAA TTATTAGTGT GCTTGTGACC TCCTTATGTA TTCTCAATTA CCTGTATTTG TGCAATAAAT TGGAATAATG TAACTTGATT TCTTATCTGT GTTTGTGTTG GCATGCAAGA TTTAGGTACT TATCAAGATA ATGGGGAATT AAGGCATCAA TAAAATGATG CCAAAGACCA AGAGCAGTTT CTGAAGTCCT CCTTTTCATC AGCTCTTTAT CAAACAGAAC ACTCTATAAA CAACCCATAG CCAGAAAACA GGATGTAGGA ACAATCACCA GCACACTCTA TAAACAACCC ATAGCCAGAA AACAGAATGT AAGGACAATC ACCAGCCATC TTTTGTCAAT AATTGATGGA ATAGAGTTGA AAGGAACTGG AGCATGAGTC ATATTTGACC AGTCAGTCCT CACTCTTATT TACTTGCTAT GTAAACTTGA GAAAGCTTTT TTCTCTTTGT GAACCTCAGG TTTTACATCT GAAAATGAGA AATTTGGAAC AAAAGATTCC TAACTGGTCT TTCTGTTCCC ATATTCTGTG ATTTTTCAAT ATTTAGGATT TTTGGTAATC ACAATTACTT AGTTTGTGGT TGAGATAGCA ACACGAATCA GAACTATTTG GTGGACATAT TTTCAAAGGA GTAGCTCTCC ACTTTGGGTA AAGAAGTGAT GCNGGTCGTG GTGGCTCACG CCTGTAATCC CAGCACTTTA GGGAGGCCAA GGCGGGTGGA TCACGAGGTC AGGAGATCGA GACCATCCTG GCTAACACGG TGAAACCCCG TCTCTACTAA AAAATACAAA AAATTAGCCA GGCGTGGTGG CGGGCGCCTG TAGTCCCACG TACTCGGGAG GCTGAGGCAG GAGAATGGCA TGAACCAGGG AGGCGGAGCT TGCCGTGAGC CGAGATAGCG CCACTGCAGT CCCTCCTGGG CAAAAGAGCA AGACTGCGTC TCAAAAAAAA AAAAAAAAAA AAAAAAAGAA GTGTGTGGAG TAGCAGGACA CCTGCAACAA TAATATTTTT CTAAATCCCT CTGAAAAATG CTAATCAAAG GGTTTTTTTC CTAAAAATTG TCTTAGAAAT AAAATTTCCC CTTTGGGAGA CCGAGGCTGG CAGATCACGA GGTCAGGAGA TAGAGACCAC GGTGAAACCC CGTCTCTACT AAAAATACTA AAAATTAGCC GGGGNGTGGT GGTGGGTACA CCTGTAGTCC CAGCTACTTG GAGGCTGAGG CTGGAGAATC ACGTGAAC-3' (FRAG. NO:_)(SEQ. ID NO:2504)

Human Histidine Decarboxvlase Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TCT CCC TTG GGC TCT GGC TCC TTC TC TCT CTC TCC CTC TCT CTC TGT CGC CTC CGC CCT GGC TGC TGG GGT GGT GGT GC TTT TGT TCT TCC TTG CTG CC GCC CCG CTG CTT GTC T TC CTC G CTC TGT CCC TCT CTC TCT GTB CTC CTC BGG CTC CBT CBT CTC CCT TGG GC-3' **(FRAG. NO:1700) (SEQ. ID NO:1711)**

5'-GGC TCT GGC **(FRAG. NO:1701) (SEQ. ID NO: 1712)**

5'-CCC TTG G **(FRAG. NO:1702) (SEQ. ID NO: 1713)**

5'- TT TGT TCT TCC **(FRAG. NO:1703) (SEQ. ID NO: 1714)**

5'- TCT CCC TTG GGC TCT GGC TCC TTC TC-3' **(FRAG. NO:1024) (SEQ. ID NO: 1034)**

5'- TCT CTC TCC CTC TCT CTC TGT -3' **(FRAG. NO:1025) (SEQ. ID NO:1035)**

5'- CGC CTC CGC CCT GGC TGC TGG GGT GGT GGT GC-3' **(FRAG. NO:1026) (SEQ. ID NO:1036)**

5'- TTT TGT TCT TCC TTG CTG CC-3' **(FRAG. NO:1027) (SEQ. ID NO:1037)**

5'- GCC CCG CTG CTT GTC T TC CTC G-3' **(FRAG. NO:1028) (SEQ. ID NO:1038)**

5'-CTC TGT CCC TCT CTC TCT GTB CTC CTC BGG CTC CBT CBT CTC CCT TGG GC **(FRAG. NO:1029) (SEQ. ID NO:1039)**

Human Beta Trvptase Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTT GCT CCT GGG GGC CTC CTG GTC CCT CCG GGT GTT CCC GGC GGG CCT GGC CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GBT TCB GCB TCC TGG-3' **(FRAG. NO:1704) (SEQ. ID NO: 1715)**

5'- GCT CCT GGG GGC CT-3' **(FRAG. NO:1705) (SEQ. ID NO: 1716)**

5'-CGT BGG CGC-3' **(FRAG. NO:1706) (SEQ. ID NO: 1717)**

5'-T GGC CTG GGG-3' **(FRAG. NO:1707) (SEQ. ID NO: 1718)**

5'-CTT GCT CCT GGG GGC CTC CTG-3' **(FRAG. NO:1030) (SEQ. ID NO:1040)**

5'-GTC CCT CCG GGT GTT CCC GGC-3' **(FRAG. NO:1031) (SEQ. ID NO:1041)**

5'-GGG CCT GGC CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GBT TCB GCB TCC TGG-3' **(FRAG. NO:1032) (SEQ. ID NO:1042)**

Human Trvptase-I Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTT GCT CCT GGG GGC CTC CTG GTC CCT CTG GCT G TT CCC GGC CCT GGB CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GGC TCB GCB TCC TGG CCB CGG BBT TCC-3' **(FRAG. NO: 1708) (SEQ. ID NO:1719)**

5'-CT CCT GGG GGC CTC CTG-3' **(FRAG. NO:1709) (SEQ. ID NO:1720)**

5'-B TCC TGG CCB CGG BBT TCC -3' **(FRAG. NO:1710) (SEQ. ID NO:1721)**

5'-GTC CCT C-3' **(FRAG. NO:1711) (SEQ. ID NO:1722)**

5'-CTT GCT CCT GGG GGC CTC CTG-3' **(FRAG. NO:1033) (SEQ. ID NO:1043)**

5'-GTC CCT CTG GCT G TT CCC GGC-3' **(FRAG. NO:1034) (SEQ. ID NO:1044)**

5'-CCT GGB CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GGC TCB GCB TCC TGG CCB CGG BBT TCC -3' **(FRAG. NO:1035) (SEQ. ID NO:1045)**

Human Prostaglandin D Svnthase Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGT GTG CGG GGC CTG GTG CC CCT GGG CCT CGG GTG CTG CCT GT GCG CTG CCT TCT TCT CCT GG GTC CTC GCC GGG GCC CTT GCT GCC CTG GCT GT GCC CTG GGG GTC TGG GTT CGG CTG T CCC CBG CBG GBC CBG TCC CBT CCB CBG CGT GTG BTG BGT BGC CBT TCT CCT GCB GCC GBG-3' **(FRAG. NO:1712) (SEQ. ID NO:1723)**

5'-T TCT CCT GCB GCC GBG -3' **(FRAG. NO:1713) (SEQ. ID NO:1724)**

5'-CTT GCT GCC CTG GCT GT-3' **(FRAG. NO:1714) (SEQ. ID NO:1725)**

5'- TCT TCT CCT GG-3' **(FRAG. NO:1715) (SEQ. ID NO:1726)**

5'-GGT GTG CGG GGC CTG GTG CC-3' **(FRAG. NO:1036) (SEQ. ID NO:1046)**

5'-CCT GGG CCT CGG GTG CTG CCT GT-3' **(FRAG. NO:1037) (SEQ. ID NO:1047)**

5'-GCG CTG CCT TCT TCT CCT GG-3' **(FRAG. NO:1038) (SEQ. ID NO:1048)**

5'-GTC CTC GCC GGG GCC CTT GCT GCC CTG GCT GT-3' **(FRAG. NO:1039) (SEQ. ID NO:1049)**

5'-GCC CTG GGG GTC TGG GTT CGG CTG T-3' **(FRAG. NO:1040) (SEQ. ID NO:1050)**

5'-CCC CBG CBG GBC CBG TCC CBT CCB CBG CGT GTG BTG BGT BGC CBT TCT CCT GCB GCC GBG -3'

(FRAG. NO:1041) (SEQ. ID NO:1051)

Human Cyclooxygenase-2 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGG CGC GGG CGB GCB TCG C TTT GGG CTT TTC TCC TTT GGT T TGB GCG CCB GGB CCG CGC BCB GCB GCB GGG CGC GGG CGB GCB TCG CBG CGG CGG GCB GGG-3' (FRAG. NO: 1716) (SEQ. ID NO:1727)

5'-G GCB GGG -3' (FRAG. NO: 1717) (SEQ. ID NO: 1728)

5'-TCC TTT GGT T-3' (FRAG. NO:1718) (SEQ. ID NO:1729)

5'- GGG CGC GGG CGB GCB TCG C-3' (FRAG. NO:1042) (SEQ. ID NO:1052)

5'- TTT GGG CTT TTC TCC TTT GGT T-3' (FRAG. NO:1043) (SEQ. ID NO:1053)

5'-TGB GCG CCB GGB CCG CGC BCB GCB GCB GGG CGC GGG CGB GCB TCG CBG CGG CGG GCB GGG -3' (FRAG. NO:1044) (SEQ. ID NO:1054)

Human Eosinophil Cationic Protein Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CCT CCT TCC TGG TCT GTC TGC CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC CBG TCT CTG BGC TGT GGC-3' (FRAG. NO: 1719) (SEQ. ID NO: 1730)

5'-TTC TCC TTT GGT T-3' (FRAG. NO:1720) (SEQ. ID NO: 1731)

5'-T TTC TCC TTT GGT T-3' (FRAG. NO:1721) (SEQ. ID NO:1732)

5'- GGG CGC GGG CGB GCB TCG C-3' (FRAG. NO:1042) (SEQ. ID NO:1052)

5'- TTT GGG CTT TTC TCC TTT GGT T-3' (FRAG. NO:1043) (SEQ. ID NO:1053)

5'-TGB GCG CCB GGB CCG CGC BCB GCB GCB GGG CGC GGG CGB GCB TCG CBG CGG CGG GCB GGG -3' (FRAG. NO:1044) (SEQ. ID NO:1054)

Human Eosinophil Derived Neurotoxin Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCC CTG CTG CTC TTT CTG CT TCC CTT GGT GGG TTG GGC C GCT GGT TGT TCT GGG GTT C TTG CTG CCC CTT CTG TCC C TGT TTG CTG GTG TCT GCG C 5'- CCC CBB CBG BBG BBG CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC TGT-3'
(FRAG. NO: 1722) (SEQ. ID NO: 1733)

5'-TTC CTG T-3' (FRAG. NO:1723) (SEQ. ID NO: 1734)

5'-CTC TTT CTG CT-3' (FRAG. NO: 1724) (SEQ. ID NO:1735)

5'-CCC CTT CTG TCC C-3' (FRAG. NO:1725) (SEQ. ID NO: 1736)

5'- GCC CTG CTG CTC TTT CTG CT-3' (FRAG. NO:1047) (SEQ. ID NO:1057)

5'- TCC CTT GGT GGG TTG GGC C-3' (FRAG. NO:1048) (SEQ. ID NO:1058)

5'- GCT GGT TGT TCT GGG GTT C-3' (FRAG. NO:1049) (SEQ. ID NO:1059)

5'- TTG CTG CCC CTT CTG TCC C-3' (FRAG. NO:1050) (SEQ. ID NO:1060)

5'- TGT TTG CTG GTG TCT GCG C -3' (FRAG. NO:1051) (SEQ. ID NO:1061)

5'- CCC CBB CBG BBG BBG CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC TGT-3' (FRAG. NO:1052) (SEQ. ID NO:1062)

Human Eosinophil Peroxidase Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCG CTC GGC CTG GTC CCG G GGG TCT CCT CTT GTT GTT GC TTG CGC CTC CTG CTG GGG GT CC CTC TGT TCT TGT TTT GGG GGC GGG CCC GGC CGT TGT CTT G GTT TGG GGG TTT CCG TTG GGG TTC TCC TGG CCC GGG CCT TGC CC GGC CGT GGT CCC GGC TTC GTTCCT GTC TCC GTC TCG GCT CTT CTG GGG CCT TGC GCT GTC TTT GGT G 5'-GCB CCG TCC BGT GBT GGT GCG GTB CTT GTC GCT GCB GCG CTC GGC CTG GTC CCG GBG BGC CACCGCTCCT GTCAGCCAAC AAATATCCAT TGAGCGACAC CTGTGTCCCA GGTGCTGCTC TGGGCCCTGG GAGAAGTGCA TCAGTGGGCT TGGTAGTAGA GGGTAGGGAT GGAGTGAAGG GTAGGCAGGA AGAATGTCCC CAGGCTGGTA GGAGGTGGGG TGGGGGGTTT CAGTCTCAAA ACTCCCATGA AAACCAGAGA GAAGTTTCAG AACTCCACCC AAGAGGCTGG GTTTCTAGGG CCCAGAGCTG CCCTCCCCCA CCCTAGAATG GGCTATAAAA GTCCCTTCCC AGCTACGTCC AGAGAAGAGC TGGAGGAAGT GAGAGGTCGG CTGGGGGTCC TCAAAGTGAG AGGGGAGCAG AGGATCCTCC CGTGCAGGCT GTGGATGTCA CTCACTTCCC AGCTGGTGAA GCCTCGCTGC AGAGATGCAT CTGCTCCCAG CCCTGGCAGG GGTCCTGGCC ACACTCGTCC TCGCCCAGCC CTGTGAGGGC ACTGACCCAG GTAATAGTCC CCTAGACAGG CAAGGAGGAG GGAGGGGAAA TGGAAGGGGA AGCACTTGGG TCTTGGAGGG GGTCTTGTGG CTTGCTGAAC CCTGAGTCCC CATCTCTTTG AACAGCCTCC CCTGGGGCAG TGGAGACCTC GGTCCTGCGA GACTGCATAG CAGAGGCCAA GTTGCTGGTG GATGCTGCCT ACAATTGGAC CCAGAAGAGG TGGACTTGGG TCTGGGGGCT GCATGGGCCT GGGAGGATCA GT TAATACCTTG TGGGGTCAGG GAGCCCATGT CCCGTGCTGA TGTTATTTCC CCACCAGGTC CGGGCTGTCT CCAACCAGAT TGTGCGCTTC CCCAATGAGA GACTGACCTC CGACCGTGGC CGAGCCCTCA TGTTCATGCA GTGGGGCCAG TTCATTGACC ATGACCTGGA CTTCTCCCCG GAGTCCCCGG CCAGAGTGGC CTTCACTGCA GGCGTTGACT GTGAGAGGAC CTGCGCCCAG CTGCCCCCCT GCTTTCCCAT CAAGGTACCT ACCCTCAGCC AATCTCCCAT GCCCTTGTGT GGCCTCCCCC AAAGGCAAGG TGCTGGGGGT GGGGATCTGG AAGACTGGAG CACCATCCTT AAGGAGCTGC CTGTGGAGCT AGGGTATGAG ACAGAGACAC AAG CACTGTCTCC TCTTCCATCT CAGATCCCAC CCAATGACCC CCGCATCAAG AACCAGCGTG ACTGCATCCC TTTCTTCCGC TCGGCACCCT CATGCCCCCA AAACAAGAAC AGAGTCCGCA ACCAGATCAA CGCGCTCACC TCCTTTGTGG ACGCCAGCAT GGTGTATGGC AGTGAGGTCT CCCTCTCGCT GCGGCTCCGC AACCGGACCA ACTACCTGGG GCTGCTGGCC ATCAACCAGC GCTTTCAAGA CAACGGCCGG GCCCTGCTGC CCTTCGACAA CCTGCACGAT GACCCCTGTC TCCTCACCAA CCGCTCGGCG CGCATCCCCT GCTTCCTGGC AGGTCAGACA GGGAGGAAGG TGGTGTCTTC CCAGGAAACA GCCATCCCTG GGGTCCCAAC TGGGAAGCAA TGGTGGGATG TGGTGAAGGT ACATGGTTTG GGACCTCAGT ATTAGGCACA CCATAAGCAT GGATCTGTGC AC TGAAGAGATG GAGGTCCAGT GAGGGCCAGG AGTTTGGCCC ACCCCGTCTC TCCCATCCCC AGCCCTGGGT CTACCCTGGT AGAAAGACAT TTCTCTGGGA AAGGCTGCAG TAAATCTGAG CTTGGGGTTT TCAAGGTGAC ACCCGATCAA CGGAAACCCC CAAACTGGCA GCCATGCACA CCCTCTTTAT GCGAGAGCAC AACCGGCTGG CCACCGAGCT GAGACGCCTG AATCCCCGGT GGAATGGAGA CAAACTGTAC AATGAGGCTC GGAAGATCAT GGGGGCCATG GTCCAGGTAA GGAGCTCTGC ATCCCAGCAT CCCCC CTTTGTATCT CCACCCACCA ATAGTAAATT AATGTTGTCA CATTTGACGT GATGACAATA AAGAATATGT CTGAGCCACC CTTTGAAAAG GCAAGGGTAT GGGTGAGTAG CCTCTGGGGA ATGTTCCTCC TGTCTTCCCT TCCAGATCAT CACCTACCGA GACTTTCTGC CCCTGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCCTGGG GCACTACAGG GGGTACTGCT CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCCTGGC

CTTCCGCTTT GGCCACACAA TGCTCCAGCC CTTCATGTTC CGCTTGGACA GTCAGTACCG GGCCTCCGCA CCCAACTCGC ATGTCCCACT TAGCTCTGCC TTCTTTGCCA GCTGGCGGAT CGTGTATGAA GGTGACCAGG TTTTCCAGGG GGCAAATGGG GGTGAGGGTG GGGAGCATGC CCTCCCCTAG GTGG TCCAGCTGCT TCATGTCTCT CCAGAACTCT GTTTCCTGAC AAACGTTACT AACATACCCG ACTGGCTTGT CCAGCTCTGG GCTAGCTTGG CATCATGTGA TAACCCAAGT AGCTTCCCAG AGGCTGGTCC AATCTGTGCT GCTCACATTC CCTGCCACCA GGGGGCATCG ACCCCATCCT CCGGGGCCTC ATGGCCACCC CTGCCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC CGGCTGTTTC GGCAAGTGAG GAGGATTGGG CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC ACGGCCTTCC AGGTGAGGGG GCTGTCCACC TCTTCTCCCA GCTTTGCTCG GGCCAGGCTG CTCAAGGGGT TCTGGGAAGA CCCTGGTACC CGACTGCCTG GTAGGTTCTG GTGGCAGAAA CGAGGTGTTT TCACCAAAAG ACAGCGCAAG GCCCTGAGCA GAATTTCCTT GTCTCGAATT ATATGTGACA ATACCGGTAT CACCACGGTT TCAAGGGACA TCTTCAGAGC CAACATCTAC CCTCGGGGCT TTGTGAACTG CAGCCGTATC CCCAGGTTGA ACCTATCAGC CTGGCGAGGG ACATGAGGCT TCTGCAGGTA AGGGGAGGCC ACCTCCAGCA CCCTGGGCTG GTTAAGCCTC ACATCCTTCC CTGGATGGAT GGCTGAGTCC TCTTAGGTCT CTAAGCAGAG AAAACAGAAC TTGTCACTAG GTACTCTTTC CAAGTGGCTT CCCAATGTGC TAGTTTCTGG GCTGACAGTC AATTCCAGGC CCTAGGACTT TGGGGGGAAA TTAGGAGCAT CCAACTA GAATTCCGTG GCCAGGACCC CTGCCAGGGC ACTGACCCAG CCTCCCCTGG GGCAGTGGAG ACCTCGGTCC TGCGAGACTG CATAGCAGAG GCCAAGTTGC TGGTGGATGC TGCCTACAAT TGGACCCAGA AGAGCATCAA GCAGCGGCTT CGCAGCGGTT CAGCCAGCCC CATGGACCTC CTGTCCTACT TCAAACAACC GGTAGCAGCC ACCAGGACAG TTGTTCGGGC CGCAGATTAT ATGCATGTGG CTTTGGGGCT GCTTGAAGAG AAGTTACAAC CCCAGCGGTC CGGACCCTTC ATTGTCACTG ATGTGCTAAC AGAACCACAG CTGCGGCTGC TGTCCCAGGC CAGTGGCTGT GCTCTCCGGG ACCAGGCCGA GCGCTGCAGC GACAAGTACC GCACCATCAC TGGACGGTGC AACAACAAGA GGAGACCCTT GCTAGGGGCC TCCAACCAGG CTCTGGCTCG CTGGCTGCCC GCCGAGTATG AGGATGGGCT GTCGCTCCCC TTCGGCTGGA CCCCCAGCAG GAGGCGCAAT GGCTTCCTTC TCCCTCTTGT CCGGGCTGTC TCCAACCAGA TTGTGCGCTT CCCCAATGAG AGACTGACCT CCGACCGTGG CCGAGCCCTC ATGTTCATGC AGTGGGGCCA GTTCATTGAC CATGACCTGG ACTTCTCCCC GGAGTCCCCG GCCAGAGTGG CCTTCACTGC AGGCGTTGAC TGTGAGAGGA CCTGCGCCCA GCTGCCCCCC TGCTTTCCCA TCAAGATCCC ACCCAATGAC CCCCGCATCA AGAACCAGCG TGACTGCATC CCTTTCTTCC GCTCGGCACC CTCATGCCCC CAAAACAAGA ACAGAGTCCG CAACCAGATC AACGCGCTCA CCTCCTTTGT GGACGCCAGC ATGGTGTATG GCAGTGAGGT CTCCCTCTCG CTGCGGCTCC GCAACCGGAC CAACTACCTG GGGCTGCTGG CCATCAACCA GCGCTTTCAA GACAACGGCC GGGCCCTGCT GCCCTTCGAC AACCTGCACG ATGACCCCTG TCTCCTCACC AACCGCTCGG CGCGCATCCC CTGCTTCCTG GCAGGTGACA CCCGATCAAC GGAAACCCCC AAACTGGCAG CCATGCACAC CCTCTTTATG CGAGAGCACA ACCGGCTGGC CACCGAGCTG AGACGCCTGA ATCCCCGGTG GAATGGAGAC AAACTGTACA ATGAGGCTCG GAAGATCATG GGGGCCATGG TCCAGATCAT CACCTACCGA GACTTTCTGC CCCTGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCCTGGG GCACTACAGG GGGTACTGCT CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCCTGGC CTTCCGCTTT GGCCACACAA TGCTCCAGCC CTTCATGTTC CGCTTGGACA GTCAGTACCG GGCCTCCGCA CCCAACTCGC ATGTCCCACT TAGCTCTGCC TTCTTTGCCA GCTGGCGGAT CGTGTATGAA GGGGGCATCG ACCCCATCCT CCGGGGCCTC ATGGCCACCC CTGCCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC CGGCTGTTTC GGCAAGTGAG GAGGATTGGG CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC ACGGCCTTCC AGGGTACAAT GCTTGGAGGC GCTTCTGTGG GCTCTCCCAG CCCCGGAATT TGGCACAGCT TAGCCGGGTG CTGAAAAACC AGGACTTGGC AAGGAAGTTC CTGAATTTGT ATGGAACACC TGACAACATT GACATCTGGA TTGGGGCCAT CGCTGAGCCT CTTTTGCCGG GGCTCGAGT GGGGCCTCTT CTGGCTTGTC TGTTCGAGAA CCAGTTCAGA AGAGCCGAGA CGGAGACAGG TTCTGGTGGC AGAACGAGGT GTTTTCACCA AAGACAGCGC AAGGCCCTGA GCAGAATTTC CTTGTCTCGA ATTATATGTG ACAATACCGG TATCACCACG GTTTCAAGGG ACATCTTCAG AGCCAACATC TACCCTCGGG GCTTTGTGAA CTGCAGCCGT ATCCCCAGGT TGAACCTATC AGCCTGGCGA GGGACATGAG GCTTCTGCAG GAGTCTATCC CAAGTCTCCA ACTTTTGGAG ACAAGGGGAA GGGGAGGACC ATGAGGCTGC CTTGTCTCCC TGGAGCAAGT GCAGGCTCGT GACGCTTCTG CTGGCTACAG CTCAGAGCTG GGTTCCCCAG CCAGGAGTGA AGGCTGGGGG CTCCTATCAG CAATGGACCT TCCGCCTTGG GAGCCTCTTA GGTATTAGGC TATGAATCAG CGCCACGTGC AAAGGCTTGG GAGCCAAGCC ATGTGGTCTT GCACCCCAGG CAAGAAAAGT CAGCTGGAGG GTTTACAGCA CTTTCTACTG TTTCCCAGCC CTCCCTCCCC TCCCTCACCA TGACTAAGAG ACCACTCGGT CCTAGCCTCC AGACACCCCA CAATACTCCT CTGAGCCTGA GGCCAGGCAG CATGCTCTGC TTCTACCAAT AAAGCACTGC CGGAATTC-3' **(FRAG. NO: 1726) (SEQ. ID NO: 1737)**

5'-CACCGCTCCT GTCAGCCAAC AAATATCCAT TGAGCGACAC CTGTGTCCCA GGTGCTGCTC TGGGCCCTGG GAGAAGTGCA TCAGTGGGCT TGGTAGTAGA GGGTAGGGAT GGAGTGAAGG GTAGGCAGGA AGAATGTCCC CAGGCTGGTA GGAGGTGGGG TGGGGGGTTT CAGTCTCAAA ACTCCCATGA AAACCAGAGA GAAGTTTCAG AACTCCACCC AAGAGGCTGG GTTTCTAGGG CCCAGAGCTG CCCTCCCCCA CCCTAGAATG GGCTATAAAA GTCCCTTCCC AGCTACGTCC AGAGAAGAGC TGGAGGAAGT GAGAGGTCGG CTGGGGGTCC TCAAAGTGAG AGGGGAGCAG AGGATCCTCC CGTGCAGGCT GTGGATGTCA CTCACTTCCC AGCTGGTGAA GCCTCGCTGC AGAGATGCAT CTGCTCCCAG CCCTGGCAGG GGTCCTGGCC ACACTCGTCC TCGCCCAGCC CTGTGAGGGC ACTGACCCAG GTAATAGTCC CCTAGACAGG CAAGGAGGAG GGAGGGGAAA TGGAAGGGGA AGCACTTGGG TCTTGGAGGG GGTCTTGTGG CTTGCTGAAC CCTGAGTCCC CATCTCTTTG AACAGCCTCC CCTGGGGCAG TGGAGACCTC GGTCCTGCGA GACTGCATAG CAGAGGCCAA GTTGCTGGTG GATGCTGCCT ACAATTGGAC CCAGAAGAGG TGGACTTGGG TCTGGGGGCT GCATGGGCCT GGGAGGATCA GT-3' (FRAG. NO:_)(SEQ. ID NO:2483)

5'-TAATACCTTG TGGGGTCAGG GAGCCCATGT CCCGTGCTGA TGTTATTTCC CCACCAGGTC CGGGCTGTCT CCAACCAGAT TGTGCGCTTC CCCAATGAGA GACTGACCTC CGACCGTGGC CGAGCCCTCA TGTTCATGCA GTGGGGCCAG TTCATTGACC ATGACCTGGA CTTCTCCCCG GAGTCCCCGG CCAGAGTGGC CTTCACTGCA GGCGTTGACT GTGAGAGGAC CTGCGCCCAG CTGCCCCCCT GCTTTCCCAT CAAGGTACCT ACCCTCAGCC AATCTCCCAT GCCCTTGTGT GGCCTCCCCC AAAGGCAAGG TGCTGGGGGT GGGGATCTGG AAGACTGGAG CACCATCCTT AAGGAGCTGC CTGTGGAGCT AGGGTATGAG ACAGAGACAC AAG-3' (FRAG.NO:_)(SEQ.ID NO:2484)

5'-CACTGTCTCC TCTTCCATCT CAGATCCCAC CCAATGACCC CCGCATCAAG AACCAGCGTG ACTGCATCCC TTTCTTCCGC TCGGCACCCT CATGCCCCCA AAACAAGAAC AGAGTCCGCA ACCAGATCAA CGCGCTCACC TCCTTTGTGG ACGCCAGCAT GGTGTATGGC AGTGAGGTCT CCCTCTCGCT GCGGCTCCGC AACCGGACCA ACTACCTGGG GCTGCTGGCC ATCAACCAGC GCTTTCAAGA CAACGGCCGG GCCCTGCTGC CCTTCGACAA CCTGCACGAT GACCCCTGTC TCCTCACCAA CCGCTCGGCG CGCATCCCCT GCTTCCTGGC AGGTCAGACA GGGAGGAAGG TGGTGTCTTC CCAGGAAACA GCCATCCCTG GGGTCCCAAC TGGGAAGCAA TGGTGGGATG TGGTGAAGGT ACATGGTTTG GGACCTCAGT ATTAGGCACA CCATAAGCAT GGATCTGTGC AC-3' (FRAG.NO:_)(SEQ.ID NO:2485)

5'-TGAAGAGATG GAGGTCCAGT GAGGGCCAGG AGTTTGGCCC ACCCCGTCTC TCCCATCCCC AGCCCTGGGT CTACCCTGGT AGAAAGACAT TTCTCTGGGA AAGGCTGCAG TAAATCTGAG CTTGGGGTTT TCAAGGTGAC ACCCGATCAA CGGAAACCCC CAAACTGGCA GCCATGCACA CCCTCTTTAT GCGAGAGCAC AACCGGCTGG CCACCGAGCT GAGACGCCTG AATCCCCGGT GGAATGGAGA CAAACTGTAC AATGAGGCTC GGAAGATCAT GGGGGCCATG GTCCAGGTAA GGAGCTCTGC ATCCCAGCAT CCCCC-3' (FRAG.NO:_)(SEQ.IDNO:2486)

5'-CTTTGTATCT CCACCCACCA ATAGTAAATT AATGTTGTCA CATTTGACGT GATGACAATA AAGAATATGT CTGAGCCACC CTTTGAAAAG GCAAGGGTAT GGGTGAGTAG CCTCTGGGGA ATGTTCCTCC TGTCTTCCCT TCCAGATCAT CACCTACCGA GACTTTCTGC CCCTGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCCTGGG GCACTACAGG GGGTACTGCT CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCCTGGC CTTCCGCTTT GGCCACACAA TGCTCCAGCC CTTCATGTTC CGCTTGGACA GTCAGTACCG GGCCTCCGCA CCCAACTCGC ATGTCCCACT TAGCTCTGCC TTCTTTGCCA GCTGGCGGAT CGTGTATGAA GGTGACCAGG TTTTCCAGGG GGCAAATGGG GGTGAGGGTG GGGAGCATGC CCTCCCCTAG GTGG-3' (FRAG.NO:_)(SEQ.ID NO:2487)

5'-TCCAGCTGCT TCATGTCTCT CCAGAACTCT GTTTCCTGAC AAACGTTACT AACATACCCG ACTGGCTTGT CCAGCTCTGG GCTAGCTTGG CATCATGTGA TAACCCAAGT AGCTTCCCAG AGGCTGGTCC AATCTGTGCT GCTCACATTC CCTGCCACCA GGGGGCATCG ACCCCATCCT CCGGGGCCTC ATGGCCACCC CTGCCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC CGGCTGTTTC GGCAAGTGAG GAGGATTGGG CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC ACGGCCTTCC AGGTGAGGGG GCTGTCCACC TCTTCTCCCA GCTTTGCTCG GGCCAGGCTG CTCAAGGGGT TCTGGGAAGA CCCTGGTACC-3' (FRAG.NO:_)(SEQ.ID NO:3488)

5'-CGACTGCCTG GTAGGTTCTG GTGGCAGAAA CGAGGTGTTT TCACCAAAAG ACAGCGCAAG GCCCTGAGCA GAATTTCCTT GTCTCGAATT ATATGTGACA ATACCGGTAT CACCACGGTT TCAAGGGACA TCTTCAGAGC CAACATCTAC CCTCGGGGCT TTGTGAACTG CAGCCGTATC CCCAGGTTGA ACCTATCAGC CTGGCGAGGG ACATGAGGCT TCTGCAGGTA AGGGGAGGCC ACCTCCAGCA CCCTGGGCTG GTTAAGCCTC ACATCCTTCC CTGGATGGAT GGCTGAGTCC TCTTAGGTCT CTAAGCAGAG AAAACAGAAC TTGTCACTAG GTACTCTTTC CAAGTGGCTT CCCAATGTGC TAGTTTCTGG GCTGACAGTC AATTCCAGGC CCTAGGACTT TGGGGGGAAA TTAGGAGCAT CCAACTA-3' (FRAG.NO:_)(SEQ.ID NO:2489)

5'-GAATTCCGTG GCCAGGACCC CTGCCAGGGC ACTGACCCAG CCTCCCCTGG GGCAGTGGAG ACCTCGGTCC TGCGAGACTG CATAGCAGAG GCCAAGTTGC TGGTGGATGC TGCCTACAAT TGGACCCAGA AGAGCATCAA GCAGCGGCTT CGCAGCGGTT CAGCCAGCCC CATGGACCTC CTGTCCTACT TCAAACAACC GGTAGCAGCC ACCAGGACAG TTGTTCGGGC CGCAGATTAT ATGCATGTGG CTTTGGGGCT GCTTGAAGAG AAGTTACAAC CCCAGCGGTC CGGACCCTTC ATTGTCACTG ATGTGCTAAC AGAACCACAG CTGCGGCTGC TGTCCCAGGC CAGTGGCTGT GCTCTCCGGG ACCAGGCCGA GCGCTGCAGC GACAAGTACC GCACCATCAC TGGACGGTGC AACAACAAGA GGAGACCCTT GCTAGGGGCC TCCAACCAGG CTCTGGCTCG CTGGCTGCCC GCCGAGTATG AGGATGGGCT GTCGCTCCCC TTCGGCTGGA CCCCCAGCAG GAGGCGCAAT GGCTTCCTTC TCCCTCTTGT CCGGGCTGTC TCCAACCAGA TTGTGCGCTT CCCCAATGAG AGACTGACCT CCGACCGTGG CCGAGCCCTC ATGTTCATGC AGTGGGGCCA GTTCATTGAC CATGACCTGG ACTTCTCCCC GGAGTCCCCG GCCAGAGTGG CCTTCACTGC AGGCGTTGAC TGTGAGAGGA CCTGCGCCCA GCTGCCCCCC TGCTTTCCCA TCAAGATCCC ACCCAATGAC CCCCGCATCA AGAACCAGCG TGACTGCATC CCTTTCTTCC GCTCGGCACC CTCATGCCCC CAAAACAAGA ACAGAGTCCG CAACCAGATC AACGCGCTCA CCTCCTTTGT GGACGCCAGC ATGGTGTATG GCAGTGAGGT CTCCCTCTCG CTGCGGCTCC GCAACCGGAC CAACTACCTG GGGCTGCTGG CCATCAACCA GCGCTTTCAA GACAACGGCC GGGCCCTGCT GCCCTTCGAC AACCTGCACG ATGACCCCTG TCTCCTCACC AACCGCTCGG CGCGCATCCC CTGCTTCCTG GCAGGTGACA CCCGATCAAC GGAAACCCCC AAACTGGCAG CCATGCACAC CCTCTTTATG CGAGAGCACA ACCGGCTGGC CACCGAGCTG AGACGCCTGA ATCCCCGGTG GAATGGAGAC AAACTGTACA ATGAGGCTCG GAAGATCATG GGGGCCATGG TCCAGATCAT CACCTACCGA GACTTTCTGC CCCTGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCCTGGG GCACTACAGG GGGTACTGCT CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCCTGGC CTTCCGCTTT GGCCACACAA TGCTCCAGCC CTTCATGTTC CGCTTGGACA GTCAGTACCG GGCCTCCGCA CCCAACTCGC ATGTCCCACT TAGCTCTGCC TTCTTTGCCA GCTGGCGGAT CGTGTATGAA GGGGGCATCG ACCCCATCCT CCGGGGCCTC ATGGCCACCC CTGCCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC CGGCTGTTTC GGCAAGTGAG GAGGATTGGG CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC ACGGCCTTCC AGGGTACAAT GCTTGGAGGC GCTTCTGTGG GCTCTCCCAG CCCCGGAATT TGGCACAGCT TAGCCGGGTG CTGAAAAACC AGGACTTGGC AAGGAAGTTC CTGAATTTGT ATGGAACACC TGACAACATT GACATCTGGA TTGGGGCCAT CGCTGAGCCT CTTTTGCCGG GGGCTCGAGT GGGGCCTCTT CTGGCTTGTC TGTTCGAGAA CCAGTTCAGA AGAGCCGAGA CGGAGACAGG TTCTGGTGGC AGAACGAGGT GTTTTCACCA AAGACAGCGC AAGGCCCTGA GCAGAATTTC CTTGTCTCGA ATTATATGTG ACAATACCGG TATCACCACG GTTTCAAGGG ACATCTTCAG AGCCAACATC TACCCTCGGG GCTTTGTGAA CTGCAGCCGT ATCCCCAGGT TGAACCTATC AGCCTGGCGA GGGACATGAG GCTTCTGCAG GAGTCTATCC CAAGTCTCCA ACTTTTGGAG ACAAGGGGAA GGGGAGGACC ATGAGGCTGC CTTGTCTCCC TGGAGCAAGT GCAGGCTCGT GACGCTTCTG CTGGCTACAG CTCAGAGCTG GGTTCCCCAG CCAGGAGTGA AGGCTGGGGG CTCCTATCAG CAATGGACCT TCCGCCTTGG GAGCCTCTTA GGTATTAGGC TATGAATCAG CGCCACGTGC AAAGGCTTGG GAGCCAAGCC ATGTGGTCTT GCACCCCAGG CAAGAAAAGT CAGCTGGAGG GTTTACAGCA CTTTCTACTG TTTCCCAGCC CTCCCTCCCC TCCCTCACCA TGACTAAGAG ACCACTCGGT CCTAGCCTCC AGACACCCCA CAATACTCCT CTGAGCCTGA GGCCAGGCAG CATGCTCTGC TTCTACCAAT AAAGCACTGC CGGAATTC-3' (FRAG.NO:_)(SEQ.ID no:2490)

5'-TC GGC CTG GTC CCG G-3' (FRAG. NO: 1727) (SEQ. ID NO:1738)
5'-TGG GGG TTT CCG TTG-3' (FRAG. NO: 1728) (SEQ. ID NO: 1739)
5'-TG GTC CCG GBG BGC -3' (FRAG. NO: 1729) (SEQ. ID NO: 1740)
5'-GCG CTC GGC CTG GTC CCG G-3' (FRAG. NO:1053) (SEQ. ID NO:1063)
5'-GGG TCT CCT CTT GTT GTT GC-3' (FRAG. NO:1054) (SEQ. ID NO:1064)
5'- TTG CGC CTC CTG CTG GGG GT CC-3' (FRAG. NO:1055) (SEQ. ID NO:1065)
5'-CTC TGT TCT TGT TTT GGG GGC-3' (FRAG. NO:1056) (SEQ. ID NO:1066)
5'-GGG CCC GGC CGT TGT CTT G-3' (FRAG. NO:1057) (SEQ. ID NO:1067)
5'-GTT TGG GGG TTT CCG TTG-3' (FRAG. NO:1058) (SEQ. ID NO:1068)
5'-GGG TTC TCC TGG CCC GGG CCT TGC CC-3' (FRAG. NO:1059)(SEQ. ID NO:1069)
5'-GGC CGT GGT CCC GGC TTC GTT GC-3' (FRAG. NO:1060) (SEQ. ID NO:1070)
5'-CCT GTC TCC GTC TCG GCT CTT CTG-3' (FRAG. NO:1061) (SEQ. ID NO:1071)

5'-GGG CCT TGC GCT GTC TTT GGT G-3' (FRAG. NO:1062) (SEQ. ID NO:1072)

5'-GCB CCG TCC BGT GBT GGT GCG GTB CTT GTC GCT GCB GCG CTC GGC CTG GTC CCG GBG BGC -3' (FRAG. NO:1063) (SEQ. ID NO:1073)

Human Intercellular Adhesion Molecule-1 (ICAM-1) Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCG CGG GCC GGG GGC TGC TGG G GGT TGG CCC GGG GTG CCC C GCC GCT GGG TGC CCT CGT CCT CTG CGG TC GTG TCT CCT GGC TCT GGT TCC CC GCT GCG CCC GTT GTC CTC TGG GGT GGC CTT C GCT CCC GGG TCT GGT TCT TGT GT TGG GGG TCC CTT TTT GGG CCT GTT GT GGC GTG GCT TGT GTG TTC GGT TTC TGC CCT GTC CTC CGG CGT CCC CGG BGC CTC CCC GGG GCB GGB TGB CTT TTG BGG GGG BCB CBG BTG TCT GGG CBT TGC CBG GTC CTG GGB BCB GBG CCC CGB GCB GGB CCB GGB GTG CGG GCB GCG CGG GCC GGG GGC TGC TGG GBG CCB TBG CGB GGC TGB G-3'
(FRAG. NO: 1730)
(SEQ. ID NO: 1741)

5'-GGG GGC TGC TGG G-3' (FRAG. NO: 1731) (SEQ. ID NO:1742)
5'-T GTC CTC CGG CGT CCC-3' (FRAG. NO:1732) (SEQ. ID NO:1743)
5'-G CCB TBG CGB GGC TGB G-3' (FRAG. NO: 1733) (SEQ. ID NO: 1744)
5'-CTC TGG GGT GGC CTT C-3' (FRAG. NO:1734) (SEQ. ID NO:1745)
5'-GCG CGG GCC GGG GGC TGC TGG G-3' (FRAG. NO:1064) (SEQ. ID NO:1074)
5'-GGT TGG CCC GGG GTG CCC C-3' (FRAG. NO:1065) (SEQ. ID NO:1075)
5'-GCC GCT GGG TGC CCT CGT CCT CTG CGG TC-3' (FRAG. NO:1066) (SEQ. ID NO:1076)
5'-GTG TCT CCT GGC TCT GGT TCC CC-3' (FRAG. NO:1067) (SEQ. ID NO:1077)
5'-GCT GCG CCC GTT GTC CTC TGG GGT GGC CTT C-3' (FRAG. NO:1068) (SEQ. ID NO:1078)
5'-GCT CCC GGG TCT GGT TCT TGT GT-3' (FRAG. NO:1069) (SEQ. ID NO:1079)
5'-TGG GGG TCC CTT TTT GGG CCT GTT GT-3' (FRAG. NO:1070) (SEQ. ID NO:1080)
5'-GGC GTG GCT TGT GTG TTC GGT TTC-3' (FRAG. NO:1071) (SEQ. ID NO:1081)
5'-TGC CCT GTC CTC CGG CGT CCC-3' (FRAG. NO:1072) (SEQ. ID NO:1082)
5'- CGG BGC CTC CCC GGG GCB GGB TGB CTT TTG BGG GGG BCB CBG BTG TCT GGG CBT TGC CBG GTC CTG GGB BCB GBG CCC CGB GCB GGB CCB GGB GTG CGG GCB GCG CGG GCC GGG GGC TGC TGG GBG CCB TBG CGB GGC TGB G-3' (FRAG. NO:1073) (SEQ. ID NO:1083)

Human Vascular Cell Adhesion Molecule 1 (VCAM-1)

Nucleic Acid and Oligonucleotide Fragments

5'-CCT CTT TTC TGT TTT TCC C CTC TGC CTT TGT TTG GGT TCG CTT CCT TTC TGC TTC TTC C CTG TGT CTC CTG TCT CCG CTT TTT TCT TC GTC TTT GTT GTT TTC TCT TCC TTG CTG BGC BBG BTB TCT BGB TTC TGG GGT GGT CTC GBT TTT BBBB GCT TGB GBB GCT GCB BBC BTT BTC CBB BGT BTB TTT GBG GCT CCB BGG BTC BCG BCC BTC TTC CCB GGC BTT TTB BGT TGC TGT CGT-3' (FRAG. NO: 1735) (SEQ. ID NO: 1746)
5'-C TGT CGT-3' (FRAG. NO:1736) (SEQ. ID NO:1747)
5'-TGC TTC TTC C-3' (FRAG. NO:1737) (SEQ. ID NO:1748)
HSVCAM1AS1: 5'-CCT CTT TTC TGT TTT TCC C-3' (FRAG. NO:1074) (SEQ. ID NO:1084)
HSVCAM1AS2: 5'-CTC TGC CTT TGT TTG GGT TCG-3' (FRAG. NO:1075) (SEQ. ID NO:1085)
HSVCAM1AS3: 5'-CTT CCT TTC TGC TTC TTC C-3' (FRAG. NO:1076) (SEQ. ID NO:1086)
HSVCAM1AS4: 5'-CTG TGT CTC CTG TCT CCG CTT TTT TCT TC-3' (FRAG. NO:1077) (SEQ. ID NO:1087)
HSVCAM1AS5: 5'-GTC TTT GTT GTT TTC TCT TCC TTG-3' (FRAG. NO:1078) (SEQ. ID NO:1088)
CTG BGC BBG BTB TCT BGB TTC TGG GGT GGT CTC GBT TTT BBBB GCT TGB GBB GCT GCB BBC BTT BTC CBB BGT BTB TTT GBG GCT CCB BGG BTC BCG BCC BTC TTC CCB GGC BTT TTB BGT TGC TGT CGT (FRAG. NO:1079) (SEQ. ID NO:1089)

Human Endothelial Leukocyte Adhesion Molecule(ELAM-1)

Nucleic Acid and Antisense Oligonucleotide Fragments

5'-BBG TGB GBG CTG BGB GBB BCT GTG BBG CBB TCB TGB CTT CBB GBG TTC TTT TCB CCC GTT CTT GGC TTC TTC TGT C CGT TGG CTT CTC GTT GTC CC TGT GGG CTT CTC GTT GTC CC CCC TTC GGG GGC TGG TGG GGC CGT CCT TGC CTG CTG G GTT CTT GGC TTC TTC TGT CCG T TGG CTT CTC GTT GTC CC TGT GGG CTT CTC GTT GTC CC CCC TTC GGG GGC TGG TGG GGC CGT CCT TGC CTG CTG G CCTGAGACAG AGGCAGCAGT GATACCCACC TGAGAGATCC TGTGTTTGAA CAACTGCTTC CCAAAACGGA AAGTATTTCA AGCCTAAACC TTTGGGTGAA AAGAACTCTT GAAGTCATGA TTGCTTCACA GTTTCTCTCA GCTCTCACTT TGGTGCTTCT CATTAAAGAG AGTGGAGCCT GGTCTTACAA CACCTCCACG GAAGCTATGA CTTATGATGA GGCCAGTGCT TATTGTCAGC AAAGGTACAC ACACCTGGTT GCAATTCAAA ACAAAGAAGA GATTGAGTAC CTAAACTCCA TATTGAGCTA TTCACCAAGT TATTACTGGA TTGGAATCAG AAAAGTCAAC AATGTGTGGG TCTGGGTAGG AACCCAGAAA CCTCTGACAG AAGAAGCCAA GAACTGGGCT CCAGGTGAAC CCAACAATAG GCAAAAAGAT GAGGACTGCG TGGAGATCTA CATCAAGAGA GAAAAAGATG TGGGCATGTG GAATGATGAG AGGTGCAGCA AGAAGAAGCT TGCCCTATGC TACACAGCTG CCTGTACCAA TACATCCTGC AGTGGCCACG GTGAATGTGT AGAGACCATC AATAATTACA CTTGCAAGTG TGACCCTGGC TTCAGTGGAC TCAAGTGTGA GCAAATTGTG AACTGTACAG CCCTGGAATC CCCTGAGCAT GGAAGCCTGG TTTGCAGTCA CCCACTGGGA AACTTCAGCT ACAATTCTTC CTGCTCTATC AGCTGTGATA GGGGTTACCT GCCAAGCAGC ATGGAGACCA TGCAGTGTAT GTCCTCTGGA GAATGGAGTG CTCCTATTCC AGCCTGCAAT GTGGTTGAGT GTGATGCTGT GACAAATCCA GCCAATGGGT TCGTGGAATG TTTCCAAAAC CCTGGAAGCT TCCCATGGAA CACAACCTGT ACATTTGACT GTGAAGAAGG ATTTGAACTA ATGGGAGCCC AGAGCCTTCA GTGTACCTCA TCTGGGAATT GGGACAACGA GAAGCCAACG TGTAAAGCTG TGACATGCAG GGCCGTCCGC CAGCCTCAGA ATGGCTCTGT GAGGTGCAGC CATTCCCCTG CTGGAGAGTT CACCTTCAAA TCATCCTGCA ACTTCACCTG TGAGGAAGGC TTCATGTTGC AGGGACCAGC CCAGGTTGAA TGCACCACTC AAGGGCAGTG GACACAGCAA ATCCCAGTTT GTGAAGCTTT CCAGTGCACA GCCTTGTCCA ACCCCGAGCG AGGCTACATG AATTGTCTTC CTAGTGCTTC TGGCAGTTTC CGTTATGGGT CCAGCTGTGA GTTCTCCTGT GAGCAGGGTT TTGTGTTGAA GGGATCCAAA AGGCTCCAAT GTGGCCCCAC AGGGGAGTGG GACAACGAGA AGCCCACATG TGAAGCTGTG AGATGCGATG CTGTCCACCA GCCCCCGAAG GGTTTGGTGA GGTGTGCTCA TTCCCCTATT GGAGAATTCA CCTACAAGTC CTCTTGTGCC TTCAGCTGTG AGGAGGGATT TGAATTATAT GGATCAACTC AACTTGAGTG CACATCTCAG GGACAATGGA CAGAAGAGGT TCCTTCCTGC CAAGTGGTAA AATGTTCAAG CCTGGCAGTT CCGGGAAAGA TCAACATGAG CTGCAGTGGG GAGCCCGTGT

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-3' (FRAG. NO: 1738) (SEQ. ID NO: 1749)

5'-GCCACCATGG AAACCCTTTG CCTCAGGGCA TCCTTTTGGC TGGCACTGGT TGGATGTGTA ATCAGTGATA ATCCTGAGAG
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CCCATGAACG GAACAAGCAT CCAGTGGAAG AACCACGATC AAAACAACCA CAACACAGAC CGGAGCAGCC ATAAGGACAG
CATGAACTGA CCACCCTTAG AAGCACTCCT-3' (FRAG. NO: ___) (SEQ. ID NO: 2481)

5'-GATCAAAATT TTTACCTATT ATGCATTTGA TATATAAATA AGTATATAAA TGCACACACA GACACAGCAA TGATGGTGAA
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AAGTTGCCAT TCAGTGGTTA AGAGTGTTGC CTGGGAGCTG TATCACATGT GCTTAAATCC ATTCTTGAAA TCATTTACTC
CTTCTGAGCC CTTGGGCTAT TTGGTTAATT TCTCTGAACG TTAGTTTGCT CATCTGAAAA TGGAAATAAT AATAGCAACT
TCTTGACAGG GTTATAGTGA GAATTGAGTT CATCACTGTG AAATGCTTAG AAATGTGCAT GACACATAGT TAATACTCAA
GGAATTAGCC ACATCACTAT CATCATCACT GATTATCTTC CACTCTTACC CTCTTCCAGT TCATTTTCTG CCCAGCAGAA
TGATCTTTTA AAAAGTAAAT CAGATCATGT TACTCTATTG CTTGAAGTCT ATCCCATTTG ATTAAGAATA ACAACCTAAT
CCTCTGTGGA TGCTGCCTCC TTCACCAGCC TGTCTCATGC TGCTCTCCCT ACTCTTAGTT CCTCAAACAT ACCAAACTCT
CCTGTCCCAG AGTCTTTTCG TGGTTTTTCC ATCTGCCTAG GATGCTTCTC TCTCCTATTT TGTGTACCTT GCTAACTCCT
GCTTACTGTC TTTCAGTTCT CAGCTTAAGA GTTATATCTT CATGATAACA TTCTTTGATA TCCTTACCCT AAGATTAAGT
TAGATTGATA TCCTTACCCT AAGAATAAGT TAGATTAGGT CTCTCTATTG TAGCACCTTA GACTCTGTCA TTTGACAAAT
CACAGCCCTA ATTAATTATT CTTAAAATTA TTTAACATTC TCTCTCATGC TAGACCACAA GTTTCATGCA GGTAAGGCGG
AGATTGTGTC CATTTGTTTG ACCCCTTTGT CTCCAGGGCC TGGTAGAATG CCTCATACAT AGTAAGAATT CAATTAATAT
TTTACACAGA GAAAAAATTA GCAACTTATT TAAACAAATA TAACTGCTTC AGAGGTAAAC TGGGCACATC TTAGTTATAT

TATGTGATAT ATGATGCTTT TTGATTGTTT TTTTAAATGT TCTACAAGGT AGATATTGTT AGAGGTCCTA AGTTACTTGA TGTGTTACTT GTGGTGATTG TATTCTTTTC TTTTTATTCA TTTAGGCAGA GCCTTAAGCA CCAGTCCATA ATAAAAAGCC AGTTGAAACA CAAAGATATA ATTACTAGCT TGTGTGAAGA CATTCTTTTC TCCTTCCATT CTTGTTTACA GTTAGCTGAG CAGATGACAC AGTCAGATGC ACAGGTAAAA TTTGGGCTAA TAGCATTTTA AACAGCAACT CTTATTTTCT TTGGCAGTTA GTAAATCTCA TTTGAATGTC TGGGTCAGTC TATTTAAGAG GATTTTAATT TATTTCATTT GGGTGTTTTT TTTTGATCTG TGGGATTATT TATATCCCAT AATTACTTTT CACCCAGAGC ATTGTATTAG ATTCCTAACT GCTGTCATTG CCTCTGGGGT CTGCCTGGCT CCCTCTTTGC TTGGTAACTG GTTGGTCACA GCATTCTTCT CAGAATCCTT TCATTCTTTT CTGCATGAGA ACAAAAATTC TTTTGTTCAT ATTTGTATAA GATCTGATAT AGCTGCAATC AATCTTGCAT TTTTTCTTCA CCAACGCATT GCGACCTTTA GGGATACAAG TATGTTTGTG CATGTATATG TATGTATCAG TCTTTTAAAT TTGATATAGT CATACATTTG TTTTTATTTT GAAAAGTTAG AGTGTTGAAT TGGTATCCCA TTTATGAAAC ATTATATTCT AAAAATTTGT AGTACGATTA TTGGGAATTA TAACTCATTT TCCTGTAACA CTGTTATACA TAGTACCTTT TGCTTTCAGA CTAGCCCTCA ATTTTATTTA ACTATAGTAG TCCTAAATTA TAAGATTAAT AGTACTCAGG ACCTAACAGT TATATGTCAT TTGTTTTTTT TTTTTTTGAG ATGGCGTCTC ACTCTGTCAC CCAAGCTGGA GTGCAGTGGT ATGACCTTGG CTCACTGCAG CCTCTGCCTC ACGGGTTCAA GGGATCGTTC TGCCTTAGCC TCCTGAGTAG CTGGGATTAT AGGCGCCTGC CACCACGCCT GGCTAATTTT TTTAGTAGAG ACGGGGTTTC GCCATGTTGG CCAGGCTGGT CTCGAACTCC TGACCTCAGG TGGTCCACCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGTGTGAGCC ACCGCGCCCA GCCTATATGT AATAATTTTA ATGGGACCAT GAATTGAATA TTTCTTCCTT GAATAGCAAT GACATAGCCC CTTCTATTGT ACATCTGCAA GCTGATACAG GGAATTCCTT TGTACCTGCG CTCTTCCCTG CCAGTCAGCT ATGGGGGTGA AAGTGTAGGG GTTCATCCAA GTCCTAAAAC TGGTAGCAAC TCCTAGGGCA GGGCTGATCT GGAAGGACAG ACCCTAGGGG AGGGTGGAAC TTTAAAAAGA AGTTCTGAAG GTAGTAAGAA GGAAATGAGG AGTAGTGTTA GGAAGGGGCT AACTTTTTTC TTCTTGCTTC TCTTCTTTAT CTCACCTGCC CCTCCCCTTG TATCCCTTCT TCCTTTTTCC CTTTCCTTTT TTGTCCTCAC TTCATTCGTG CATCCTTTCT GATTCCTCTT ACCTTGCTAA AAGGAGAAGT TTGTTTGGGT ATCCTATATC AATGGCAGGA AGGTTGTTTT CTTCTTTACC TTTATCCTAT AGATTCATAT TCTCAACACC AACCTCCTCC TTTTTCAGTT TCCTTCTTGC TTCTCTTGAC ACCACAGAGT TTGCAGCTAG TACTTGGAGA GGAAAATTAA ACAGAGATAC TTGGACCAAG AGTAAGATGA AGAAAGTCTA AACAACAGTA TAGTCTATAG TGGCAAGAGA GAGTATGGGG GCTGCTTAGC CAGGGTGGCT GTACATAAAG TATATCTTCA GTTTATATAA ACTGCTTATA GATGGAAATC AGAAAATTTA AATTCTCTTA ACTGTCCAAG AAAATTCTCA TTTTTTCAAA TTTGGGACTG ATAAATGTGA CCAGTTCTGC TTACTGTCCA TTGCCTGAAA TGGAGCTTTG AGGTGGACTG TATAATTTCT TCAATCTTAA CTCCAAATTC TGATCAGCGA CGCCCTCTGC TGTTCACTAT TAATATTTAT TTACCAATCA AAGTAAAGTA TTGAAGTTTT CCTGGCAGTT TTCACTTTGT GTTTTAGTCC ATTTAGGCTG CTATAACAAA ATCCCTTAAA CTGGGTAAGG GATTATAAAT ATTAGAAATT TATCTCTCAC AGTTCTGGAA GCTGGGAAGC CCAATATCAA GGCACCAGTA GATTTGGTGT CTAACGAGGG TGTGCCGTCT GCTTCAAAAA TGGCCCCTTG TTGCTGCATC CTCACTTAGT GCAAGGGGCA AGACAGCTCC CTTCAACCTC TTTTATAAGG GCACTTATGT CATTCATGAG GGCAGAGCCC TCATGACTTA ATCACTTCCC CAAAGGCCCC ACCTCTTAAT AGTATCACAT TGGGTGTTAG GTGTCTGGGA GGACACCAAT CTTCAAGCCA TATCATCTCA CTTGGAAAAA AGTCAAAATA AAACCAGTAG ATTTAATTAA TATTACACTA TTTATAGAAG CATGTGATGT ATCATTCCTT GTATTAATTT CCTGGGGTTG CCGTAACAAG TTACCACAAA CTAGGTGGCT TAAAACAATA GAATTTTATT CTCTCACATT TCTAGAGGCA GAAGTTCACA GTGTGTCAAT AGGGCCATGT TCTCTGGAAG GCTTTAGGGG AGAATATATT TCATATCTTT CTCTTAGCTT CTCGGTGTCA CTGGCAATCC TTAGCTTACT TTGGCTTTCT GTGTCTTCAC ATCATCTTTT TATAAGAACA CCAGTGATAG TGATTAAGGG CATACCTTAC TTTAATATGA CCTCATCTTA ACTAATTATG TCTTCAATAA CCCTATTTCC AAATAAGGCC ACATTCTGAA GTATTGGGAG TTAGAACTTA AAGCTTTTTG GGAGGGACAC AGTTCAACCC ATAACAACCC CTAAAATCGA TATTTATTCT CAATTAAGTC TTGAAATTGG TTTCAAAAAG AGAATATTCT ATTAGAGTTT TTAATGTATA GTTTTAACAT ATAGTTCTTT AGCCCCCAAT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTGAGAC GGAGTCTCGC TCTGTCGCCC AGGCCGGACT GCGGACTGCA GTGGCGCAAT CTCGGCTCAC TGCAAGCTCC GCTTCCCGGG TTCACGCCAT TCCCCTGCCT CAGCCTCCCG AGTAGCTGGG ACTACAGGCG CCTGCCACCG CGCCCGGCTA ATTTTTTTGT ATTTTTAGTA GAGACGGGGT TTCACCTTGT TAGCCAGGAT GGTCTCGATC TCCTGACCTC ATGATCCACC CGCCTCGGCC TCCCAAAGTG CTGGGATTAC AGGCGTGAGC CACCGCGCCC GGCCTGCCCC CAATTATTTA GTTTTTCTAT AAACAGGGAA ATTTATTTGT GTGGCCCTTA GAACTAATTT AATTTCCACT CTAATTCCTA CTTATGTTTA TATAATGCTT TTAGAAATTT GTATTATTCA GAAAATAAAC ATATACTATT GTATCTGTTG CCTACACTTA GATTTTATTG CCTGCTATAT TTAAATTTTA TTAGTATTTT AATTGTTTTA TTAAAGAAAG AATGTGCCTG TAATCTCAGC ACTTTTGAGA GGCCAAGGCA GAAGGATTGC TTGAGCCCAG GAGTTTGAGA CCAGACTGAG CAACACAGGG AGACCCCCAT CTCTACAAAA AATAAAAAAA TTCTCCAGGC CTCATGGCAC ATACCTGTAG TTCTAGTTAC TTGGGAGACT GGGGTGGGAG GATGCATTGA GCCCAGGAGA TTGAGGCTGC AGTGAGCCAT GATCAGGCCA CTGTACTCCA GCTTGGACAA CAGAGTGAGA GCTTGTCTAG ATAGATAGAT AGATAGATAA TCTAAATAGA TAATAGACAG ATTATCTAAA TAGATAATAG ACAGATTATC TAAATAGATA ATAGACAGAT TATCTAAATA GATAATAGAC AGATTATCTA AATAGATAAT AGACAGATTA TCTAAATAGA TAATAGACAG ATTATCTATC TAAATAGATA ATAGATTATC TAAATAGATA ATAGATAGAT AGATTAGATA GATAGATAGA TAGATAGAGC TTGGACAACA GAGTGAGAGC CTGTCTAGAT AGATAGAAAC AAAGAAAGAA AGAAAGAATG GTGCTCATAT TTTAAAGCAT TGAAAAATGG TCTTCCTTGC TTATATTACC CACACCTTCT TTGTTGGCAT TAAGATGCAA ACTTTGTTTT AAACAGTTGA GTAAATCAAA GATGGGACTG TTAAGTTATT TGTGTTATTT ACCTGCTTTT TGAAAATGTA AAAATAAAAC TCTAGGTTTA ATTAGTAGTA TGCTATTTAG TAATGAAGTA AAGCTAGAGG CTTCGAACAA ATCTTGTGTA ATTTCCTCTT GAATGAGAGA GAAAATTTAA AGTAAGCAAA CAAATAAGTT GTGTGTCACC ACTCATTCAG TCATTTAACA AGTATTTCCA GAGTACTTAT TCTGTGCCAG GAAATGTTGT AGGTGCCCTC AACAACTTAG AGTCTAGCCT GAGACACAAG TAAGTAGGTA ATTATTATAG AATGGTATGA TCTTTGGAGG ACTGGGTATT GGCTGGCTCA TGGGAGTACA AGATAGGTAC CCAGTGATGA AGTCAGGAAA GGTTTCTTAT GGTGATATGA TGACGTCTAT GCTGATTATA AGGTCAGTGT AGAATAAACT TTGTGCTTTT AAATTTGCAT AGCACTGTAT TAGAGAGTTC ATCTTCAAAA TAATCGAAAA GGCTGAGTGT GGTGACCCAT GGCTGTAATC CCAGCACTTT GGGAGGCCGA GGTGGGCAGA TTGCTTGAGC TAGGAGTTCG AGACCAGGCT GGCCAACATG GTGAAACCCC GTCTCTACTA AAAATACAAA AATTAGCCAG GAGTGATGGT GCGCACCTGT AATGCCAGCT ACTTGGGAGG CTGAGGCAGG AGGATCACTT GAACCCAGGA GGTGGAGGTT GAAGTAAGCC GAGGTCATGC CACTGCACTC CAGCCTGGGC AACAGAGTGA GACTCCATCT CAAAAAAAAA AAAAATGATC AAAGAAAGGT GAATTTTCAT CTACCCTATT TCTGCTGAGG AAAATGGACT ATTTTCAAAT ATTTTTAATA AGGGTCAAAA TGAGGGATC-3' **(FRAG. NO: ___) (SEQ. ID NO: 2480)**

5'-CCTGAGACAG AGGCAGCAGT GATACCCACC TGAGAGATCC TGTGTTTGAA CAACTGCTTC CCAAAACGGA AAGTATTTCA AGCCTAAACC TTTGGGTGAA AAGAACTCTT GAAGTCATGA TTGCTTCACA GTTTCTCTCA GCTCTCACTT TGGTGCTTCT CATTAAAGAG AGTGGAGCCT GGTCTTACAA CACCTCCACG GAAGCTATGA CTTATGATGA GGCCAGTGCT TATTGTCAGC AAAGGTACAC ACACCTGGTT GCAATTCAAA ACAAAGAAGA GATTGAGTAC CTAAACTCCA TATTGAGCTA TTCACCAAGT TATTACTGGA TTGGAATCAG AAAAGTCAAC AATGTGTGGG TCTGGGTAGG AACCCAGAAA CCTCTGACAG AAGAAGCCAA GAACTGGGCT CCAGGTGAAC CCAACAATAG GCAAAAAGAT GAGGACTGCG TGGAGATCTA CATCAAGAGA GAAAAAGATG TGGGCATGTG GAATGATGAG AGGTGCAGCA AGAAGAAGCT TGCCCTATGC TACACAGCTG CCTGTACCAA TACATCCTGC AGTGGCCACG GTGAATGTGT AGAGACCATC AATAATTACA CTTGCAAGTG TGACCCTGGC TTCAGTGGAC

TCAAGTGTGA GCAAATTGTG AACTGTACAG CCCTGGAATC CCCTGAGCAT GGAAGCCTGG TTTGCAGTCA CCCACTGGGA
AACTTCAGCT ACAATTCTTC CTGCTCTATC AGCTGTGATA GGGGTTACCT GCCAAGCAGC ATGGAGACCA TGCAGTGTAT
GTCCTCTGGA GAATGGAGTG CTCCTATTCC AGCCTGCAAT GTGGTTGAGT GTGATGCTGT GACAAATCCA GCCAATGGGT
TCGTGGAATG TTTCCAAAAC CCTGGAAGCT TCCCATGGAA CACAACCTGT ACATTTGACT GTGAAGAAGG ATTTGAACTA
ATGGGAGCCC AGAGCCTTCA GTGTACCTCA TCTGGGAATT GGGACAACGA GAAGCCAACG TGTAAAGCTG TGACATGCAG
GGCCGTCCGC CAGCCTCAGA ATGGCTCTGT GAGGTGCAGC CATTCCCCTG CTGGAGAGTT CACCTTCAAA TCATCCTGCA
ACTTCACCTG TGAGGAAGGC TTCATGTTGC AGGGACCAGC CCAGGTTGAA TGCACCACTC AAGGGCAGTG GACACAGCAA
ATCCCAGTTT GTGAAGCTTT CCAGTGCACA GCCTTGTCCA ACCCCGAGCG AGGCTACATG AATTGTCTTC CTAGTGCTTC
TGGCAGTTTC CGTTATGGGT CCAGCTGTGA GTTCTCCTGT GAGCAGGGTT TTGTGTTGAA GGGATCCAAA AGGCTCCAAT
GTGGCCCCAC AGGGGAGTGG GACAACGAGA AGCCCACATG TGAAGCTGTG AGATGCGATG CTGTCCACCA GCCCCCGAAG
GGTTTGGTGA GGTGTGCTCA TTCCCCTATT GGAGAATTCA CCTACAAGTC CTCTTGTGCC TTCAGCTGTG AGGAGGGATT
TGAATTATAT GGATCAACTC AACTTGAGTG CACATCTCAG GGACAATGGA CAGAAGAGGT TCCTTCCTGC CAAGTGGTAA
AATGTTCAAG CCTGGCAGTT CCGGGAAAGA TCAACATGAG CTGCAGTGGG GAGCCCGTGT TTGGCACTGT GTGCAAGTTC
GCCTGTCCTG AAGGATGGAC GCTCAATGGC TCTGCAGCTC GGACATGTGG AGCCACAGGA CACTGGTCTG GCCTGCTACC
TACCTGTGAA GCTCCCACTG AGTCCAACAT TCCCTTGGTA GCTGGACTTT CTGCTGCTGG ACTCTCCCTC CTGACATTAG
CACCATTTCT CCTCTGGCTT CGGAAATGCT TACGGAAAGC AAAGAAATTT GTTCCTGCCA GCAGCTGCCA AAGCCTTGAA
TCAGACGGAA GCTACCAAAA GCCTTCTTAC ATCCTTTAAG TTCAAAAGAA TCAGAAACAG GTGCATCTGG GGAACTAGAG
GGATACACTG AAGTTAACAG AGACAGATAA CTCTCCTCGG GTCTCTGGCC CTTCTTGCCT ACTATGCCAG ATGCCTTTAT
GGCTGAAACC GCAACACCCA TCACCACTTC AATAGATCAA AGTCCAGCAG GCAAGGACGG CCTTCAACTG AAAAGACTCA
GTGTTCCCTT TCCTACTCTC AGGATCAAGA AAGTGTTGGC TAATGAAGGG AAAGGATATT TTCTTCCAAG CAAAGGTGAA
GAGACCAAGA CTCTGAAATC TCAGAATTCC TTTTCTAACT CTCCCTTGCT CGCTGTAAAA TCTTGGCACA GAAACACAAT
ATTTTGTGGC TTTCTTTCTT TTGCCCTTCA CAGTGTTTCG ACAGCTGATT ACACAGTTGC TGTCATAAGA ATGAATAATA
ATTATCCAGA GTTTAGAGGA AAAAAATGAC TAAAAATATT ATAACTTAAA AAAATGACAG ATGTTGAATG CCCACAGGCA
AATGCATGGA GGGTTGTTAA TGGTGCAAAT CCTACTGAAT GCTCTGTGCG AGGGTTACTA TGCACAATTT AATCACTTTC
ATCCCTATGG GATTCAGTGC TTCTTAAAGA GTTCTTAAGG ATTGTGATAT TTTTACTTGC ATTGAATATA TTATAATCTT
CCATACTTCT TCATTCAATA CAAGTGTGGT AGGGACTTAA AAAACTTGTA AATGCTGTCA ACTATGATAT GGTAAAAGTT
ACTTATTCTA GATTACCCCC TCATTGTTTA TTAACAAATT ATGTTACATC TGTTTTAAAT TTATTTCAAA AAGGGAAACT
ATTGTCCCCT AGCAAGGCAT GATGTTAACC AGAATAAAGT TCTGAGTGTT TTTACTACAG TTGTTTTTTG AAAACATGGT
AGAATTGGAG AGTAAAAACT GAATGGAAGG TTTGTATATT GTCAGATATT TTTTCAGAAA TATGTGGTTT CCACGATGAA
AAACTTCCAT GAGGCCAAAC GTTTTGAACT AATAAAAGCA TAAATGCAAA CACACAAAGG TATAATTTTA TGAATGTCTT
TGTTGGAAAA GAATACAGAA AGATGGATGT GCTTTGCATT CCTACAAAGA TGTTTGTCAG ATGTGATATG TAAACATAAT
TCTTGTATAT TATGGAAGAT TTTAAATTCA CAATAGAAAC TCACCATGTA AAAGAGTCAT CTGGTAGATT TTTAACGAAT
GAAGATGTCT AATAGTTATT CCCTATTTGT TTTCTTCTGT ATGTTAGGGT GCTCTGGAAG AGAGGAATGC CTGTGTGAGC
AAGCATTTAT GTTTATTTAT AAGCAGATTT AACAATTCCA AAGGAATCTC CAGTTTTCAG TTGATCACTG GCAATGAAAA
ATTCTCAGTC AGTAATTGCC AAAGCTGCTC TAGCCTTGAG GAGTGTGAGA ATCAAAACTC TCCTACACTT CCATTAACTT
AGCATGTGTT GAAAAAAAAA GTTTCAGAGA AGTTCTGGCT GAACACTGGC AACGACAAAG CCAACAGTCA AAACAGAGAT
GTGATAAGGA TCAGAACAGC AGAGGTTCTT TTAAAGGGGC AGAAAAACTC TGGGAAATAA GAGAGAACAA CTACTGTGAT
CAGGCTATGT ATGGAATACA GTGTTATTTT CTTTGAAATT GTTTAAGTGT TGTAAATATT TATGTAAACT GCATTAGAAA
TTAGCTGTGT GAAATACCAG TGTGGTTTGT GTTTGAGTTT TATTGAGAAT TTTAAATTAT AACTTAAAAT ATTTTATAAT
TTTTAAAGTA TATATTTATT TAAGCTTATG TCAGACCTAT TTGACATAAC ACTATAAAGG TTGACAATAA ATGTGCTTAT
GTTT-3' **(FRAG. NO: ____) (SEQ. ID NO: 2479)**

5'-CCT TGC CTG CTG G-3' **(FRAG. NO: 1739) (SEQ. ID NO: 1750)**
5'-GTT GTC CC-3' **(FRAG. NO: 1740) (SEQ. ID NO:1751)**
5'-GTT CTT GGC TTC TTC TGT C-3' **(FRAG. NO:1080) (SEQ. ID NO:1090)**
5'-GGC TGG TGG-3' **(FRAG. NO:1083) (SEQ. ID NO:1093)**
5'-CGT TGG CTT CTC GTT GTC CC-3' **(FRAG. NO:1081) (SEQ. ID NO:1091)**
5'-TGT GGG CTT CTC GTT GTC CC-3' **(FRAG. NO:1082) (SEQ. ID NO:1092)**
5'-CCC TTC GGG GGC TGG TGG-3' **(FRAG. NO:1083) (SEQ. ID NO:1093)**
5'-GGC CGT CCT TGC CTG CTG G-3' **(FRAG. NO:1084) (SEQ. ID NO:1094)**

Human P Selectin Fragments

5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT CTT TTC-3' **(FRAG. NO: 1741) (SEQ. ID NO: 1752)**
5'-TCC TTT CTT TTC-3' **(FRAG. NO: 1742) (SEQ. ID NO: 1753)**
5'-CTC CTT TT-3' **(FRAG. NO:1743) (SEQ. ID NO:1754)**
5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT-3' **(FRAG. NO:1085) (SEQ. ID NO:1095)**
5'-TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT CTT TTC-3' **(FRAG. NO:1086) (SEQ. ID NO:1096)**

Human Endothelial Monocyte Activating Factor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT CTT TTC-3' **(FRAG. NO: 1744) (SEQ. ID NO: 1755)**
5' -CC TTT CTT TTC **(FRAG. NO: 1745) (SEQ. ID NO: 1756)**
5'-CTG TTC CTC CTT TT-3' **(FRAG. NO:1746) (SEQ. ID NO:1757)**
5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT-3' **(FRAG. NO:1087) (SEQ. ID NO:1097)**
5'-TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT CTT TTC-3' **(FRAG. NO:1088) (SEQ. ID NO:1098)**

Human IL3* Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTC TGT CTT GTT CTG GTC CTT CGT GGG GCT CTG TGT CGC GTG G GTG CGG CCG TGG CC GGC GGB CCB GGB GTT GGB GCB GGB GCB GGB CGG GCB GGC GGC TCB TGT TTG GBT CGG CBG GBG GCB CTC **(FRAG. NO: 1747) (SEQ. ID NO: 1758)**
5'-G GBG GCB CTC-3' **(FRAG. NO: 1748) (SEQ. ID NO: 1759)**

5'-GT GGG GCT CTG-3' (FRAG. NO:1749) (SEQ. ID NO:1760)
HUMIL3AAS1: 5'-CTC TGT CTT GTT CTG GTC CTT CGT GGG GCT CTG-3' (FRAG. NO:1089) (SEQ. ID NO:1099)
HUMIL3AAS2: 5'-TGT CGC GTG G GTG CGG CCG TGG CC-3' (FRAG. NO:1090) (SEQ. ID NO:1100)
GGC GGB CCB GGB GTT GGB GCB GGB GCB GGB CGG GCB GGC GGC TCB TGT TTG GBT CGG CBG GBG GCB CTC (FRAG. NO:1091) (SEQ. ID NO:1101)

Human IL3 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TCT GGG GTG TCC TGG CCT TCG TGG TTC CTC TTC CTT CGT TTG CCG TCC GCG GGG GCC CCC GGG CCT GGC TGC GCT CCT GCC CCG CCT CTT TCC CGG GCT CTT GCG CTG GGG GGT GCT CC CGT GTG TTT GCG CCC TC CTC CTG GTC GCG CTT GTC GTT TTG GGG CCG GCT TTG CCC GCC TCC CGG CGC CTG GCC CGG CC TTC CTG GGC TGC GTG CGC GTT CTG TTC TTC TTC CTG GCT CTG GGG TGT CCT GGC CTT CGT GGT TCC TCT TCC TTC GTT TGC CGT CCG CGG GGG CCC CCG GGC CT GGC TGC GCT CCT GCC CCG CCT CTT TCC CGG GCT CTT GCG CTG GGG GGT GCT CCC GTG TGT TTG CGC CCT CCT CCT GGT CGC GCT TGT CGT TTT GG GGC CGG CTT TGC CCG CCT CCC GGC GCC TGG CCC GGC CTT CCT GGG CTG CGT GCG CGT TCT GTT CTT CTT CCT GGC GCA GGA GAC AGG GCA GGG CGA TCA GGA GCA GCG TGA GCC AAA GGA GGA CCA TCG GGA ACG CAG CTC CGG AAC GCA GGA CAG AGG TGC C GC BGG BGB CBG GGC BGG GCG BTC BGG BGC BGC GTG BGC CBB BGG BGG BCC BTC GGG BBC GCB GCT CCG GBB CGC BGG BCB GBG GTG CC-3' (FRAG. NO: 1750) (SEQ. ID NO: 1761)
GBG GTG CC-3' (FRAG. NO: 1751) (SEQ. ID NO: 1762)
5'- GCC CCG C-3' (FRAG. NO:1752) (SEQ. ID NO:1763)
5'-TCTGGGGTGTCCTG (FRAG. NO:1092) (SEQ. ID NO:1102)
5'-GCCTTCGTGGTTCC (FRAG. NO:1093) (SEQ. ID NO:1103)
5'-TCTTCCTTCGTTTGC (FRAG. NO:1094) (SEQ. ID NO:1104)
5'-CGTCCGCGGGGGCCCCCGGGCCT (FRAG. NO:1095) (SEQ. ID NO:1105)
5'-GGC TGC GCT CCT GCC CCG C (FRAG. NO:1096) (SEQ. ID NO:1106)
5'-CTCTTTCCCGGGCTCTT (FRAG. NO:1097) (SEQ. ID NO:1107)
5'-GCGCTGGGGGGTGCTCC (FRAG. NO:1098) (SEQ. ID NO:1108)
5'-CGTGTGTTTGCGCCCTCCTCCTGGTCGC (FRAG. NO:1099) (SEQ. ID NO:1109)
5'-GCTTGTCGTTTTGG (FRAG. NO:1100) (SEQ. ID NO:1110)
5'-GGCCGGCTTTGCCCGCCTCCC (FRAG. NO:1101) (SEQ. ID NO:1111)
5'-GGCGCCTGGCCCGGCC (FRAG. NO:1102) (SEQ. ID NO:1112)
5'-TTCCTGGGCTGCGTGCGC (FRAG. NO:1103) (SEQ. ID NO:1113)
5'-GTTCTGTTCTTCTTCCTGGC (FRAG. NO:1104) (SEQ. ID NO:1114)
5'-GCB GGB GBC BGG GCB GGG CGB TCB GGB GCB GCG TGB GCC BBB GGB GGB CCB TCG GGB BCG CBG CTC CGG BBC GCB GGB 5'-CBG BGG TGC C (FRAG. NO:1105) (SEQ. ID NO:1115)

Human IL-4 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTC TGG TTG GCT TCC TTC GCC GGC BCB TGC TBG CBG GBB GBB CBG BGG GGG BBG CBG TTG GGB GGT GBG BCC CBT TBB TBG GTG TCG B-3' (FRAG. NO: 1753) (SEQ. ID NO: 1764)
5'-GCC GGC BCB-3' (FRAG. NO: 1754) (SEQ. ID NO: 1765)
5'-T TCC TTC-3' (FRAG. NO:1755) (SEQ. ID NO:1766)
5'-CTC TGG TTG GCT TCC TTC-3' (FRAG. NO:1106) (SEQ. ID NO:1116)
5'-GCCGGCBCBTGCTBGCBGGBBGBBCBGBGGGGGBBGCBGTTGGGBGGTGBGBCCCBTTBBTBGGTGTCGB-3' (FRAG. NO:1107) (SEQ. ID NO:1117)

Human IL4 Receptor Nucleic Acid and Antisense Oligonucleotide Fragment

5'-TCT GCC CTG TCC GCC GGC TCT TCG GTG GCT CGG CCC CGC TCC TTG TCT TGC CGC GGG TTG GTT CCT GGG CCT GGT TCT TGC GGG CGT TTC GGT CTG CTG GCT GGT CTG GGC CCG CGG TGC GGC GGG TGG CTT GCT GTT CTG CCT GGG CTC TCC CCT CTC CTC CTT TTC TCC CTT CCT CTG TCT TGC CTC CTT CCT CTG GGT CCT CTT GGC CTG GGC GCT CTT CCC CTC GGG CGG CTG CGG GCG CTC GTG CTG CCT GGT CCG CTC CCT GGG GGT GCT CCT TCC CTT TCC CCG CTC GTG GGG TTT GCG GGG CTG GGC TGC CCT GGG GGG TCT GGG CCT TTT GGG GTC GGC TGG CTG CTG CTT CGG GCC GCC TGG GCT TCC CTG TGC CCC TTT CCT CTG CTG GGT CCC CCT CCC GTT CCA AGC TGC ACC GCA CAG ACC GGC GCT ACA GGA CAG AGC CAG GCA AGC ACC CAT GGG GAT CCA GGC CCA GCT GTT CCB BGC TGC BCC GCB CBG BCC GGC GCT BCB GGB CBG BGC CBG GCB BGC BCC CBT GGG GBT CCB GGC CCB GCT G -3' (FRAG. NO: 1756) (SEQ ID NO: 1767)
5'-TCTGCGC-3' (FRAG. NO: 1757) (SEQ ID NO: 1768)
5'-CCT GCT CCT GGG G (FRAG. NO:1758) (SEQ. ID NO:1769)
5'-TCTGCGCGCCCCTGCTCC (FRAG. NO:1108) (SEQ. ID NO:1118)
5'-CGCCCGGCTTCTCT (FRAG. NO:1109) (SEQ. ID NO:1119)
5'-CGTGTGGGCTTCGG (FRAG. NO:1110) (SEQ. ID NO:1120)
5'-CCCCGCGCCTCCGTTGTTCTC (FRAG. NO:1111) (SEQ. ID NO:1121)
5'-TGCTCGCTGGGCTTG (FRAG. NO:1112) (SEQ. ID NO:1122)
5'-GGTTTCCTGGGGCCCTGGGTTTC (FRAG. NO:1113) (SEQ. ID NO:1123)
5'-TCTGCCGGGTCGTTTTC (FRAG. NO:1114) (SEQ. ID NO:1124)
5'-GGGTGCTGGCTGCG (FRAG. NO:1115) (SEQ. ID NO:1125)
5'-CTTGGTGCTGGGGCTCC (FRAG. NO:1116) (SEQ. ID NO:1126)
5'-GGCGGCTGCGGGCTGGGTTGGG (FRAG. NO:1117) (SEQ. ID NO:1127)
5'-CTTGGCTGGTTCCTGGCCTCGGG (FRAG. NO:1118) (SEQ. ID NO:1128)
5'-CCTCCTCCTCCTCCTCGCTCCCTTTTTCTTCCTCT (FRAG. NO:1119) (SEQ. ID NO:1129)
5'-TCCCTGCTGCTCTC (FRAG. NO:1120) (SEQ. ID NO:1130)
5'-TGCCCTCCCTTCCCTCCTGG (FRAG. NO:1121) (SEQ. ID NO:1131)
5'-GGTGCCTCCTTGGGCCCTGC (FRAG. NO:1122) (SEQ. ID NO:1132)
5'-GGCTGCTCCTTGCCCC (FRAG. NO:1123) (SEQ. ID NO:1133)

5'-CTCTGGGTCGGGCTGGC (FRAG. NO:1124) (SEQ. ID NO:1134)
5'-GGGGCGTCTCTGTGC (FRAG. NO:1125) (SEQ. ID NO:1135)
5'-CTGGCCTGGGTGCC (FRAG. NO:1126) (SEQ. ID NO:1136)
5'-GCCTCTCCTGGGGGGGTGGCTCCCTGTCC (FRAG. NO:1127) (SEQ. ID NO:1137)
5'-CCTTTTCCCCCGGCTCC (FRAG. NO:1128) (SEQ. ID NO:1138)
5'-GTGGGGGCTTTGGC (FRAG. NO:1129) (SEQ. ID NO:1139)
5'-GGG GGT CTG TGG CCT GCT CCT GGG G (FRAG. NO:1130) (SEQ. ID NO:1140)
5'-AGGGGTCTGGGGCCCTC (FRAG. NO:1131) (SEQ. ID NO:1141)
5'-TTTTGGGGGTCTGGCTTG (FRAG. NO:1132) (SEQ. ID NO:1142)
5'-GCCTGGCTGCCTTCC (FRAG. NO:1133) (SEQ. ID NO:1143)
5'-GGGGCCTGCCGTGGGGC (FRAG. NO:1134) (SEQ. ID NO:1144)
5'-TGTCCTCTGTTGCTCCCCTT (FRAG. NO:1135) (SEQ. ID NO:1145)
5'-TGCCTGCTGTCTGG (FRAG. NO:1136) (SEQ. ID NO:1146)
5'-GGTTCCCGCCTTCCCT (FRAG. NO:1137) (SEQ. ID NO:1147)
5'-GTT CCC AGA GCT TGC CAC CTG CAG CAG GAC CAG GCA GCT CAC AGG GAA CAG GAG CCC AGA GCA AAG CCA CCC CAT TGG GAG ATG CCA AGG CAC CAG GCT G (FRAG. NO:1138) (SEQ. ID NO:1148)
5'-GTT CCC BGB GCT TGC CBC CTG CBG CBG GBC CBG GCB GCT CBC BGG GBB CBG GBG CCC BGB GCB BBG CCB CCC CBT TGG GBG BTG CCB BGG CBC CBG GCT G-3' (FRAG. NO:1139) (SEQ. ID NO:1149)

Human IL5* Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TCCCTGTTTC CCCCCTTTCG TTCTGCGTTT GCCTTTGGCG TTTTTTGTTT GTTTTCTCTC TCCGTCTTTC TTCTCCCCT GTGGGBBTTT CTGTGGGGBT GGCBTBCBCG TBGGCBGCTC CBBGBGCTBG CBBBCTCBBB TGCBGBBGCB TCCTCBTGGC TCTGBBBCGG TGGGAATTTC TGTGGGGBTG GCATACACGT AGGCAGCTCC AAGAGCTAGC AAACTCAAAT GCAGAAGCATC CTCATGGCTC TGAAACG-3' (FRAG. NO: 1759) (SEQ. ID NO: 1770)
5'-GCC CCG GG-3' (FRAG. NO: 1760) (SEQ. ID NO: 1771)
5'-G GGT TTC T-3' (FRAG. NO: 1761) (SEQ. ID NO: 1772)
5'-GTG GGG BTG GC-3' (FRAG. NO: 1762) (SEQ. ID NO:1773_)
5'-CCB BGB GCT BGC-3' (FRAG. NO: 1763) (SEQ. ID NO: 1774)
5'-TCC CTG TTT CCC CCC TTT-3' (FRAG. NO:1140) (SEQ. ID NO:1150)
5'-CGT TCT GCG TTT GCC TTT GGC-3' (FRAG. NO:1141)(SEQ. ID NO:1151)
5'-GTT TTT TGT TTG TTT TCT-3' (FRAG. NO:1142)(SEQ. ID NO:1152)
5'-CTC TCC GTC TTT CTT CTC C-3' (FRAG. NO:1143) (SEQ. ID NO:1153)
5'-CCT CCT GCC TGT GTC CCT GCT CCC C-3' (FRAG. NO:1144) (SEQ. ID NO:1154)
5'-GAG GGT TTC TGG CTT CCT CTC T-3' (FRAG. NO:1145) (SEQ. ID NO:1155)
5'-TGT CTC TCT GTC CTT TTG TT-3' (FRAG. NO:1146) (SEQ. ID NO:1156)
5'-TGT TGT GCG GCC TGG TGC TGC CCT GCC CCG GG-3' (FRAG. NO:1147) (SEQ. ID NO:1157)
5'-GTG GGA ATT TCT GTG GGG BTG GCA TAC ACG TAG GCA GCT CCA AGA GCT AGC AAA CTC AAA TGC AGA AGC ATC CTC ATG GCT CTG AAA CG-3' (FRAG. NO: 1764) (SEQ. ID NO: 1775)
5'-GTG GGB BTT TCT GTG GGG BTG GCB TBC BCG TBG GCB GCT CCB BGB GCT BGC BBB CTC BBB TGC BGB BGC BTC CTC BTG GCT CTG BBB CG-3' (FRAG. NO:1148) (SEQ. ID NO:1158)

Human IL-5 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTCAGTGGCC CCCAAAAGGA TGAGTAATAC ATGCGCCACG ATGATCATAT CCTTTTTACT ATGAGGCCGT GTCTGTCGTG TCTTTCCTTT GCTCTTGGTG TGTCTTTGCT GTGCCCTGCC TCTCTGCCCG TGTCTGTCGT GTCTTTCCTT TGCTCTTGGT GTGTCTTTGC TGTGCCCTGC CTCTCTGCCC CGTGTCTGTC GTGTCTTTCC TTTGCTCTTG GTGTGTCTTT GCTGTGCCCT GCCTCTCTGC-3' (FRAG. NO: 1765) (SEQ. ID NO: 1776)
5'-CCG TGT C-3' (FRAG. NO: 1766) (SEQ. ID NO: 1777)
5'-GCCCTGCC-3' (FRAG. NO: 1767) (SEQ. ID NO: 1778)
5'-CCG TGT CTG TCG TGT CT-3' (FRAG. NO:1149) (SEQ. ID NO:1159)
5'-TTCCTTTGCTCTTG-3' (FRAG. NO:1150) (SEQ. ID NO:1160)
5'-GTGTGTCTTTGCTGT-3' (FRAG. NO:1151) (SEQ. ID NO:1161)
5'-GCCCTGCCTCTCTGC-3' (FRAG. NO:1152) (SEQ. ID NO:1162)
5'-CT CBGTGGCCCC CBBBBGGBTG BGTBBTBCBT GCGCCBCGBT GBTCBTBTCC TTTTTBCTBT GBGG (FRAG. NO: 1768) (SEQ. ID NO: 1779)

Human IL-6 Receptor Fragments

5'-GGGGGTGGCT TCCTGCCGCG TCTCTGGGCC GTCCCGTCCC TCGGCCCCGC GCCGCGCTCG GCTCCTCTCC CTCTGGCCCG GCTCGGGGCG GGGCGGGGCG GTGGGCGGGC GGCGCTGCCC TGCGCGCGGC GCTGGCCCCT GCTGGCCGTC GGCTGCGCGC TGCTGGCTGC CCTGCTGGCC GCGCCGGGGC CTGTCCGCCT CTGCGGGCGC TGTCTCCTGG CTTGTCTTCC GGCTCTTCTG CTGGGGTGGG GCTGGGCGGC CGGCCCGGTG CTGGGGCTCC TCGGGGGGGG GGGCTCTTCC GGGCTGTCTC CCTCCGGGGC GGGGGTTTCT GGCCGTGGGG GTCTTGCCTG GCCTCCGGGC TCCTGCTTGT CTTGCCTTCC TTCTCTGGTC GGTTGTGGCT CGGGGCTCCG TGGGTCCCTG GCGCCCGTTT GTGTTTTGTC TTTTCCCCTG GCGTCCCTGT GCCCCTCTCC TCTCCTTCCT CTGCTTCTCG CTCTCCTTTG TGGGGCCCTC CCTGCTGCTC TTGGTTTTGG GCTTTTTTTC TCTTCCTCCT TTTTCGTGCG TGGGCCTCCG CACGCCTCTT GCCACCTCCT GCGCAGGGCA GCGCCTTGG GGCCAGCGCC GCTCCCGGCG CGGCCAGCAG GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCCT CCTCGGCTAC CACTCCATGG TCCCGCAGAG GCGGACAGGC GCBCGCCTC TTGCCBCCTC CTGCGCBGGG CBGCGCCTTG GGGCCBGCGC CGCTCCCGGC GCGGCCBGCB GGGCBGCCBG CBGCGCGCBG CCGBCGGCCB GCBTGCTTCC TCCTCGGCTB CCBCTCCBTG GTCCCGCBGB GGCGGBCBGG C-3' (FRAG. NO: 1769) (SEQ. ID NO: 1780)
5'-CCCGGCGC-3' (FRAG. NO:1184) (SEQ. ID NO:1194)
5'-GGCCBGCBGG-3' (FRAG. NO:1186) (SEQ. ID NO:1196)
5'-GCBGCCBGCBGCG-3' (FRAG. NO: 1770) (SEQ. ID NO: 1781)

5'-C GCBGCCGBCGGCC -3' **(FRAG. NO: 1771) (SEQ. ID NO: 1782)**
5'-GGGGGTGGCTTCCTGCC3'- **(FRAG. NO:1153) (SEQ. ID NO:1163)**
5'-GCGTCTCTGGGCCGTCCC-3' **(FRAG. NO:1154) (SEQ. ID NO:1164)**
5'-GTCCCTCGGCCCCGCGCCGCGCTCGGCTCCTCTCCC-3' **(FRAG. NO:1155) (SEQ. ID NO:1165)**
5'-TCTGGCCCGGCTC-3' **(FRAG. NO:1156) (SEQ. ID NO:1166)**
5'-GGGGCGGGGCGGGGCGGTGGGCGGGC-3' **(FRAG. NO:1157) (SEQ. ID NO:1167)**
5'-GGCGCTGCCCTGCGC-3' **(FRAG. NO:1158) (SEQ. ID NO:1168)**
5'-GCGGCGCTGGCCCC-3' **(FRAG. NO:1159) (SEQ. ID NO:1169)**
5'-TGCTGGCCGTCGGCTGCGCGCTGCTGGCTGCCCT-3' **(FRAG. NO:1160) (SEQ. ID NO:1170)**
5'-GCTGGCCGCGCCGGG-3' **(FRAG. NO:1161) (SEQ. ID NO:1171)**
5'-GCCTGTCCGCCTCTGCGGG-3' **(FRAG. NO:1162) (SEQ. ID NO:1172)**
5'-CGCTGTCTCCTGGC-3' **(FRAG. NO:1163) (SEQ. ID NO:1173)**
5'-TTGTCTTCCGGCTCT-3' **(FRAG. NO:1164) (SEQ. ID NO:1174)**
5'-TCTGCTGGGGTGGG-3' **(FRAG. NO:1165) (SEQ. ID NO:1175)**
5'-GCTGGGCGGCCGGCCCGGT-3' **(FRAG. NO:1166) (SEQ. ID NO:1176)**
5'-GCTGGGGCTCCTCGGGGGG-3' **(FRAG. NO:1167) (SEQ. ID NO:1177)**
5'-GGGGGCTCTTCCGG-3' **(FRAG. NO:1168) (SEQ. ID NO:1178)**
5'-GCTGTCTCCCTCCGGG-3' **(FRAG. NO:1169) (SEQ. ID NO:1179)**
5'-GCGGGGGTTTCTGGCC-3' **(FRAG. NO:1170) (SEQ. ID NO:1180)**
5'-GTGGGGGTCTTGCC-3' **(FRAG. NO:1171) (SEQ. ID NO:1181)**
5'-TGGCCTCCGGGCTCC-3' **(FRAG. NO:1172) (SEQ. ID NO:1182)**
5'-TGCTTGTCTTGCCTTCCTTC-3' **(FRAG. NO:1173) (SEQ. ID NO:1183)**
5'-TCTGGTCGGTTGTGGCTCG-3' **(FRAG. NO:1174) (SEQ. ID NO:1184)**
5'-GGGCTCCGTGGGTCCCTGGC-3' **(FRAG. NO:1175) (SEQ. ID NO:1185)**
5'-GCCCGTTTGTGTTTTGTC-3' **(FRAG. NO:1176) (SEQ. ID NO:1186)**
5'-TTTTCCCCTGGCGT-3' **(FRAG. NO:1177) (SEQ. ID NO:1187)**
5'-CCCTGTGCCCCTCTCCTCTCCTTCCTCTGCTTCTC-3' **(FRAG. NO:1178) (SEQ. ID NO:1188)**
5'-GCTCTCCTTTGTGGG-3' **(FRAG. NO:1179) (SEQ. ID NO:1189)**
5'-GCCCTCCCTGCTGCT-3' **(FRAG. NO:1180) (SEQ. ID NO:1190)**
5'-CTTGGTTTTGGGCT-3' **(FRAG. NO:1181) (SEQ. ID NO:1191)**
5'-TTTTTTCTCTTCCTCCTTTTTC-3' **(FRAG. NO:1182) (SEQ. ID NO:1192)**
5'-GTGCGTGGGCCTCC-3' **(FRAG. NO:1183) (SEQ. ID NO:1193)**
5'-
GCACGCCTCTTGCCACCTCCTGCGCAGGGCAGCGCCTTGGGGCCAGCGCCGCTCCCGGCGCGGCCAGCAGGGCAGCCAGCAGCG
CGCAGCCGACGGCCAGCATGCTTCCTCCTCGGCTACCACTCCATGGTCCCGCAGAGGCGGACAGGC-3'
(FRAG. NO:1185) (SEQ. ID NO:1195)
5'-
GCBCGCCTCTTGCCBCCTCCTGCGCBGGGCBGCGCCTTGGGGCCBGCGCCGCTCCCGGCGCGGCCBGCBGGGCBGCCBGCBGCGC
GCBGCCGBCGGCCBGCBTGCTTCCTCCTCGGCTBCCBCTCCBTGGTCCCGCBGBGGCGGBCBGGC-3'
(FRAG. NO:1187) (SEQ. ID NO:1197)

Human IL-6 Nucleic Acid and Antisense Oligonucleotide Fragments

5'–GGGGGTGGCT TCCTGCCGCG TCTCTGGGCC GTCCCGTCCC TCGGCCCCGC GCCGCGCTCG GCTCCTCTCC CTCTGGCCCG GCTCGGGGCG GGGCGGGGCG GTGGGCGGGC GGCGCTGCCC TGCGCGCGGC GCTGGCCCCT GCTGGCCGTC GGCTGCGCGC TGCTGGCTGC CCTGCTGGCC GCGCCGGGGC CTGTCCGCCT CTGCGGGCGC TGTCTCCTGG CTTGTCTTCC GGCTCTTCTG CTGGGGTGGG GCTGGGCGGC CGGCCCGGTG CTGGGGCTCC TCGGGGGGGG GGGCTCTTCC GGGCTGTCTC CCTCCGGGGC GGGGGTTTCT GGCCGTGGGG GTCTTGCCTG GCCTCCGGGC TCCTGCTTGT CTTGCCTTCC TTCTCTGGTC GGTTGTGGCT CGGGGCTCCG TGGGTCCCTG GCGCCCGTTT GTGTTTTGTC TTTTCCCCTG GCGTCCCTGT GCCCCTCTCC TCTCCTTCCT CTGCTTCTCG CTCTCCTTTG TGGGGCCCTC CCTGCTGCTC TTGGTTTTGG GCTTTTTTTC TCTTCCTCCT TTTTCGTGCG TGGGCCTCC GCACGCCTCT TGCCACCTCC TGCGCAGGGC AGCGCCTTGG GGCCAGCGCC GCTCCCGGCG CGGCCAGCAG GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCCT CCTCGGCTAC CACTCCATGG TCCCGCAGAG GCGGACAGGC GCBCGCCTC TTGCCBCCTC CTGCGCBGGG CBGCGCCTTG GGGCCBGCGC CGCTCCCGGC GCGGCCBGCB GGGCBGCCBG CBGCGCGCBG CCGBCGGCCB GCBTGCTTCC TCCTCGGCTB CCBCTCCBTG GTCCCGCBGB GGCGGBCBGG C-3' **(FRAG. NO:1772) (SEQ. ID NO:1783)**

5'-GGGGCBGG-3' **(FRAG. NO:1773) (SEQ. ID NO:1784)**
5'-GBBGGCBG CBGGC-3' **(FRAG. NO:1774) (SEQ. ID NO:1785)**
5'-CCBGGBGCBG CCCC-3' **(FRAG. NO:1775) (SEQ. ID NO:1786)**
5'-BGGG BGBBGGCBBC-3' **(FRAG. NO:1776) (SEQ. ID NO:1787)**
5'-GCT TCT CTT TCG TTC CCG GTG GGC TCG-3' **(FRAG. NO:1188) (SEQ. ID NO:1198)**
5'-GTG GCT GTC TGT GTG GGG CGG CT-3' **(FRAG. NO:1189) (SEQ. ID NO:1199)**
5'-GTG CCT CTT TGC TGC TTT C-3' **(FRAG. NO:1190) (SEQ. ID NO:1200)**
5'-GAT TCT TTG CCT TTT TCT GC-3' **(FRAG. NO:1191) (SEQ. ID NO:1201)**
5'-CTCCTGGGGG TBCTGGGGCB GGGBBGGCBG CBGGCBBCBC CBGGBGCBGC CCCBGGGBGB BGGCBBCTGG BCCGBBGGCG CTTGTGGBGB BGGBGTTCBT BGCTGGGCTC CTGGBGGGGB GBTBGBGC-3' **(FRAG. NO:1777) (SEQ. ID NO:1788)**

Human Monocyte-derived Neutr phil Chemotactic Factor
Nucleic Acid and Antisense Olig nucleotide Fragments

5'-GGGGTGGBBB GGTTTGGBGT BTGTCTTTBT GCBCTGBCBT CTBBGTTCTT TBGCBCTCCT TGGCBBBBCT GCBCCTTCBC BCBGBGCTGC BGBBBTCBGG BBGGCTGCCB BGBGBGCCBC GGCCBGCTTG GBBGTCBTGT TTBCBCBCBG TGBGBTGGTT CCTTCCGGGC TTGTGTGCTC TGCTGTCTCT TGGTTCCTTC CGGTGGTTTC TTCCTGGCTC TTGTCCTTTC TCTTGG CCCT TGGC-3' **(FRAG. NO:1778) (SEQ. ID NO: 1789)**

5'-GGBGT BTG-3' (FRAG. NO:1779) (SEQ. ID NO: 1790)
5'-GCBCTGBCBT CT-3' (FRAG. NO:1780) (SEQ. ID NO:1791)
5'-CCG GTG G-3' (FRAG. NO:1781) (SEQ. ID NO: 1792)
5'-GG CCC TTG GC-3' (FRAG. NO:1782) (SEQ. ID NO: 1793)
5'-GCT TGT GTG CTC TGC TGT CTC T-3' (FRAG. NO:1192) (SEQ. ID NO:1202)
5'-TGG TTC CTT CCG GTG GTT TCT TCC TGG CTC TTG TCC T-3' (FRAG. NO:1193) (SEQ. ID NO:1203)
5'-TTC TCT TGG CCC TTG GC-3' (FRAG. NO:1194) (SEQ. ID NO:1204)
5'-GGGGTGGBBB GGTTTGGBGT BTGTCTTTBT GCBCTGBCBT CTBBGTTCTT TBGCBCTCCT TGGCBBBBCT GCBCCTTCBC BCBGBGC-3' (FRAG. NO:1783) (SEQ. ID NO: 1794)

Human Neutrophil Elastase (Medullasin) Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGGCTCCCGC CGCGBGBGGT TBTGGGCTCC CBGGBCCBCC CGCBCCGCGC GGBCGTTTBC BTTCGCCBCG CBGTGCGCGG CCGBCBTGBC GBBGTTGGGC GCBBTCBGGG TGGCGCCGCB GBBGTGGCCT CCGCGCBGCT GCBGGGBCBC CBTGBBGGGC CBCGCGTGGG GCCGCGCTCG CCGGCCCCCC BCBBTCTCCG BGGCCBGCGC GGTGCCCCCC BGCBGCBBGG CCGGCBGGBC BCBGGCGBGG BGBCBCGCGB GTCGGCGGCC GBGGGTCBTG GTGGGGCTGG GGCTCCGGGG TCTCTGCCCC TCCGTGCTGG TGGGGCTGGG GCTCCGGGG TCTCTGCCCC TCCGTGCCGC GTGGGGCCGC GCTCGCCGGC CCCCCCCTGC CGGGTGGGCT CCCGCCGCGC GCCGGCCTGC CGGCCCCTCG TGGGTCCTGC TGGCCGGGTC CGGGTCCCGG GGGTGGGGCG CGBGTCGGCG GCCGBGGGTC-3' (FRAG. NO:1784) (SEQ. ID NO: 1795)
5'-GG TGG GGC-3' (FRAG. NO:1785) (SEQ. ID NO: 1796)
5'-G GGG CCG -3' (FRAG. NO:1786) (SEQ. ID NO:1797)
5'- GGC CGG GTC CGG G-3' (FRAG. NO:1787) (SEQ. ID NO: 1798)
5'-TGG TGG GGC TGG GGC TCC GGG GTC TCT GCC CCT CCG TGC-3' (FRAG. NO:1195) (SEQ. ID NO:1205)
5'-CGC GTG GGG CCG CGC TCG CCG GCC CCC C-3' (FRAG. NO:1196) (SEQ. ID NO:1206)
5'-CCT GCC GGG TGG GCT CCC GCC GCG-3' (FRAG. NO:1197) (SEQ. ID NO:1207)
5'-CGC CGG CCT GCC GGC CCC TC-3' (FRAG. NO:1198) (SEQ. ID NO:1208)
5'-GTG GGT CCT GCT GGC CGG GTC CGG GTC CCG GGG GTG GGG-3' (FRAG. NO:1199) (SEQ. ID NO:1209)
5'-CGC GBG TCG GCG GCC GBG GGT C-3' (FRAG. NO:1200) (SEQ. ID NO:1210)
5'-GGGCTCCCGC CGCGBGBGGT TBTGGGCTCC CBGGBCCBCC CGCBCCGCGC GGBCGTTTBC BTTCGCCBCG CBGTGCGCGG CCGBCBTGBC GBBGTTGGGC GCBBTCBGGG TGGCGCCGCB GBBGTGGCCT CCGCGCBGCT GCBGGGBCBC CBTGBBGGGC CBCGCGTGGG GCCGCGCTCG CCGGCCCCCC BCBBTCTCCG BGGCCBGCGC GGTGCCCCCC BGCBGCBBGG CCGGCBGGBC BCBGGCGBGG BGBCBCGCGB GTCGGCGGCC GBGGGTCBTG GTGGGGCTGG GGCTCCGGGG TCTCTGCCCC TCCGTGC-3' (FRAG. NO:1788) (SEQ. ID NO: 1799)

Human Neutrophil Oxidase Factor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CGGGBGTGGG GGTCCTGGBC GGCBCTGBBG GCBTCCBGGG CTCCCTTCCB GTCCTTCTTG TCCGCTGCCB GCBCCCCTTC BTTCCBGBGG CTGBTGGCCT CCBCCBGGGB CBTGBTTBGG TBGBBBCTBG GBGGCCGGCC TCCBCCBGGG BCBTGGTCCT TCTTGTCCGC TGCCTCTCTG GGGTTTTCGG TCTGGGTGGG CTTTCCTCCT GGGGCTGCTG CTGGGCTCTT CTTTTTGTTT CTGGCCTGGT GCTCTCTCGT GCCCTTTCCC TTGGGTGTCT TGTTTTTGTG GCCTCCBCCB GGGBCBTG-3' (FRAG. NO:1789) (SEQ. ID NO: 1800)
5'-CGGGBGTGGG GG-3 ' (FRAG.NO:1790) (SEQ. ID NO: 1801)
5'-GCCBGCBCCCC-3' (FRAG.NO:1791) (SEQ. ID NO: 1802)
5'-C CBC CBG-3' (FRAG.NO:1792) (SEQ. ID NO: 1803)
5'-GGC CTC CBC CBG GGB CBT G-3' (FRAG. NO:1201) (SEQ. ID NO:1211)
5'-GTC CTT CTT GTC CGC TGC C -3' (FRAG. NO:1202) (SEQ. ID NO:1212)
5'-TCT CTG GGG TTT TCG GTC TGG GTG G-3 (FRAG. NO:1203) (SEQ. ID NO:1213)
5'-GCT TTC CTC CTG GGG CTG CTG CTG-3' (FRAG. NO:1204) (SEQ. ID NO:1214)
5'-GGC TCT TCT TTT TGT TTC TGG CCT GGT G-3' (FRAG. NO:1205) (SEQ. ID NO:1215)
5'-CTC TCT CGT GCC CTT TCC-3' (FRAG. NO:1206) (SEQ. ID NO:1216)
5'-CTT GGG TGT CTT GTT TTT GT-3' (FRAG. NO:1207) (SEQ. ID NO:1217)
5'-GGC CTC CBC CBG GGB CBT G-3' (FRAG. NO:1208) (SEQ. ID NO:1218)
5'-CGGGBGTGGG GGTCCTGGBC GGCBCTGBBG GCBTCCBGGG CTCCCTTCCB GTCCTTCTTG TCCGCTGCCB GCBCCCCTTC BTTCCBGBGG CTGBTGGCCT CCBCCBGGGB CBTGBTTBGG TBGBBBCTBG GBGGCC-3' (FRAG. NO:1793) (SEQ. ID NO: 1804)

Human Cathepsin G Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CCCTCCBCBT CTGCTCTGBC CTGCTGGBCT CTGGBTCTGB BGBTBCGCCB TGTBGGGGCG GGBGTGGGGC CTGCTCTCCC GGCCTCCGBT GBTCTCCCCT GCCTCBGCCC CBGTGGGTBG GBGBBBGGCC BGCBGBBGCB GGBGTGGCTG CBTCTTTCCT GGTGGGGCCT GCTCTCCCGG CCTCCGTGTG TTGCTGGGTG TTTTCCCGTC TCTGGTCTGC CTTCGGGGGT CGT-3' (FRAG. NO:1794) (SEQ. ID NO: 1805)
5'-GBBGBTBCGCC-3' (FRAG. NO:1795) (SEQ. ID NO: 1806)
5'-CBGCCCCBG-3' (FRAG. NO:1796) (SEQ. ID NO: 1807)
5'-TCC CGT CTC TGG-3' (FRAG. NO:1797) (SEQ. ID NO: 1808)
5'-GTG GGG CCT GCT CTC CCG GCC TCC G-3' (FRAG. NO:1209) (SEQ. ID NO:1219)
5'-TGT GTT GCT GG GTG TTT TCC CGT CTC TGG-3' (FRAG. NO:1210) (SEQ. ID NO:1220)
5'-TCT GCC TTC GGG GGT CGT-3' (FRAG. NO:1211) (SEQ. ID NO:1221)
5'-CCCTCCBCBT CTGCTCTGBC CTGCTGGBCT CTGGBTCTGB BGBTBCGCCB TGTBGGGGCG GGBGTGGGGC CTGCTCTCCC GGCCTCCGBT GBTCTCCCCT GCCTCBGCCC CBGTGGGTBG GBGBBBGGCC BGCBGBBGCB GGBGTGGCTG-3' (FRAG. NO:1798) (SEQ. ID NO: 1809)

Human Defensin 1 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CCGGGGCTGC BGCBBCCTCB TCBGCTCTTG CCTGGBGTGG CTCBGCCTGG GCCTGCBGGG CCBCCBGGBG BBTGGCBGCB BGGBTGGCGB GGGTCCTCBT GGCTGGGGTC BCBGBTCCTC TBGCTBGGCB GGGTGBCCBG BGBGGGC GGG TCC TCB TGG

CTG GGG GCC TGG GCC TGC BGG GCC GCT CTT GCC TGG BGT GGC TC GCC CBG BGT CTT CCC TGG T GCTCAGCCTC
CAAAGGAGCC AGCCTCTCCC CAGTTCCTGA AATCCTGAGT GTTGCCTGCC AGTCGCCATG AGAACTTCCT ACCTTCTGCT
GTTTACTCTC TGCTTACTTT TGTCTGAGAT GGCCTCAGGT GGTAACTTTC TCACAGGCCT TGGCCACAGA TCTGATCATT
ACAATTGCGT CAGCAGTGGA GGGCAATGTC TCTATTCTGC CTGCCCGATC TTTACCAAAA TTCAAGGCAC CTGTTACAGA
GGGAAGGCCA AGTGCTGCAA GTGAGCTGGG AGTGACCAGA AGAAATGACG CAGAAGTGAA ATGAACTTTT TATAAGCATT
CTTTTAATAA AGGAAAATTG CTTTTGAAGT AT CTGCAGTGGT AAAAAGATTC TATATCTGCT GTTTGATGAA
TGCAGCACCC ACTAGCCACA TAGTGCTCGT GAGCACTTGC AATGCGGCTA GGGTGATTTC AATTAACCTA AAAGAGAACA
GCCACAGGGA GCATGTGGCT GCCATATTGG ATGGTGCTGC TTTGAGAACA AAATGAGAGA AATGAAGCCT CTATTTACCT
TGGTTGGCGG AACACATTGA AGGGACTCTG TATTGATACC AGGCTTCAAA CTTTGGGAAG TGTACTGGCC AACTTAAACA
CATCCACAGG AGAATGAAGA GGTTTGGGAA GGGACCAGAA ACCAGGCATT GAGGACAATG AGAAGAGTTT TTCAAAAGTG
GAATTACTGC AAAAAGTGGA AAAATAGCCT TTGGATGGAA GTTACTGATG AGACAATTTC CATCGGTGTG AAAGCCATCT
TTCCAACAGA GATCTGCAAC ATGAGAATGT ACTGTCTCCT AGGGTAGCGA TGGCCTCTTG TATTAGTCCG CTCAGGCTAC
CAGATTTATC GTTTAAACTG CCCATAAACA GACCAGGCAG TTTAAACAAC AGAAATTTAT TTCCTCGCAG TCCTGGAGGC
AGGAAGTCTG CGATCAAGGT GGAAGCAGGG TTGGCTTCTT CTCAGGTGTC TGTCCTTGGC TGGTAGATGA CCGCCGCCTC
CCTGGGTCCT CACATGGTCT TTCCTCTGTG TGTGTCTGTC CCAATCTCTT CTTATAAGGA TGCAAGTCTT ATGGATCAGA
GCACACCCCA ATGACCGTGT TTAACTTGAA TCACCTCTTT AAAGTTTCTC TCTCCAAATA CAATCACCTC CTGAGGCACT
GTTAGGGCTT CGACACAGGA ATTCTTTTCC TAGGGGATTC AGTTCAGTCC AAAACGCCTA CCAGTGGAGA CTTGCAACAT
GGCGGCCTGC TGGTCCCTCG CCAGGAATAT CACAGGCGAC TGTTCCCTGT TGCATGGAAT AGAAGGCTAT TCCAGAGTAC
TGTCTCTATT TATCAGATCT GGGATACTGG GAGAAGGGCA AAATAAAGTC CAAGTAGAAA AAAAAACTAT GAAAGTTTTA
GAGAGTAACC ATAATTTCAG CCCGATGTGA AACGATCCTA GATTTCAGCT GAAATAGTGA TGTGGGAAGT GAGGGGGCCG
GGATTCAAGG CAGAGGGAAC AGCGTAACTG AAGGCATGGA AGGAGGGAAG TGTAGGCTGT GTTTGAAGAG TGGCAGCTGC
TTCCACATTT CTAAAACACA GGATGTGATT TTGGGGTGTG TTGAGACAAG GCAGAAAACT TGTTTGGAAA AATAACTTGA
ATTCCCTGCA CATTTAAAAT CTCTCAGCAG AAGAAAACCC CACTCAGAAC CCCACTGTTC ATTCCTTGGC TTGTATTTGG
SCACAGCTGG CATAGCCCCA GACTGAGTAA GCTCTTCAGA CACCTCATTT CATGAGTAGC CCCAAAGATC AATCATGGGC
CAATTTCTTG GAAGAGAAGA CTCTCCGGTG TTTTGCAGTT ATTTGTTCTG CTTTCGCGAG ATGTTCTCAA ATCGTTGCAG
CTACAAGCCA TGAGTCTGAA GTGTTTGTGT TCCCTCCTTA CAGGTGGTAA CTTTCTCACA GGCCTTGGCC ACAGATCTGA
TCATTACAAT TGCGTCAGCA GTGGAGGGCA ATGTCTCTAT TCTGCCTGCC CGATCTTTAC CAAAATTCAA GGCACCTGTT
ACAGAGGGAA GGCCAAGTGC TGCAAGTGAG CTGAGAGTGA CCAGAAGAAA TGACGCAGAA GTGAAATGAA CTTTTTATAA
GCATTCTTTT AATAAAGGAA AATTGCTTTT GAAGTATACC TCCTTTGGGC CAAAATGAAT CTTGTGTCTC AATTGGAAGA
GGTAAAGAAG TAGGGGGTTA GGGTGCATGG GTTGGAACGT GAGACAGGTC GAACCACAAA GCCTGCCTGG AAAAGGGGAG
TGACGTCCTA GGCTTCAGTG ATGTCACCTC CACTTTGTTT GATCCACAAA CCAACAGGTG ACTGATTTTG GTCAGCTCAG
CCTCCAAAGG AGCCAGCCTC TCCCCAGTTC CTGAAATCCT GAGTGTTGCC TGCCAGTCGC CATGAGAACT TCCTACCTTC
TGCTGTTTAC TCTCTGCTTA CTTTTGTCTG AGATGGCCTC AGGTGGTAAC TTTCTCACAG GCCTTGGCCA CAGATCTGAT
CATTACAATT GCGTCAGCAG TGGAGGGCAA TGTCTCTATT CTGCCTGCCC GATCTTTACC AAAATTCAAG GCACCTGTTA
CAGAGGGAAG GCCAAGTGCT GCAAGTGAGC TGGGAGTGAC CAGAAGAAAT GACGCAGAAG TGAAATGAAC TT
-3' (FRAG.NO:1799) (SEQ. ID NO: 1810)

5'-GTCAGCTCAG CCTCCAAAGG AGCCAGCCTC TCCCCAGTTC CTGAAATCCT GAGTGTTGCC TGCCAGTCGC CATGAGAACT
TCCTACCTTC TGCTGTTTAC TCTCTGCTTA CTTTTGTCTG AGATGGCCTC AGGTGGTAAC TTTCTCACAG GCCTTGGCCA
CAGATCTGAT CATTACAATT GCGTCAGCAG TGGAGGGCAA TGTCTCTATT CTGCCTGCCC GATCTTTACC AAAATTCAAG
GCACCTGTTA CAGAGGGAAG GCCAAGTGCT GCAAGTGAGC TGGGAGTGAC CAGAAGAAAT GACGCAGAAG TGAAATGAAC
TT-3' **(FRAG.NO:___) (SEQ. ID NO: 2475)**

5'-CTGCAGTGGT AAAAAGATTC TATATCTGCT GTTTGATGAA TGCAGCACCC ACTAGCCACA TAGTGCTCGT GAGCACTTGC
AATGCGGCTA GGGTGATTTC AATTAACCTA AAAGAGAACA GCCACAGGGA GCATGTGGCT GCCATATTGG ATGGTGCTGC
TTTGAGAACA AAATGAGAGA AATGAAGCCT CTATTTACCT TGGTTGGCGG AACACATTGA AGGGACTCTG TATTGATACC
AGGCTTCAAA CTTTGGGAAG TGTACTGGCC AACTTAAACA CATCCACAGG AGAATGAAGA GGTTTGGGAA GGGACCAGAA
ACCAGGCATT GAGGACAATG AGAAGAGTTT TTCAAAAGTG GAATTACTGC AAAAAGTGGA AAAATAGCCT TTGGATGGAA
GTTACTGATG AGACAATTTC CATCGGTGTG AAAGCCATCT TTCCAACAGA GATCTGCAAC ATGAGAATGT ACTGTCTCCT
AGGGTAGCGA TGGCCTCTTG TATTAGTCCG CTCAGGCTAC CAGATTTATC GTTTAAACTG CCCATAAACA GACCAGGCAG
TTTAAACAAC AGAAATTTAT TTCCTCGCAG TCCTGGAGGC AGGAAGTCTG CGATCAAGGT GGAAGCAGGG TTGGCTTCTT
CTCAGGTGTC TGTCCTTGGC TGGTAGATGA CCGCCGCCTC CCTGGGTCCT CACATGGTCT TTCCTCTGTG TGTGTCTGTC
CCAATCTCTT CTTATAAGGA TGCAAGTCTT ATGGATCAGA GCACACCCCA ATGACCGTGT TTAACTTGAA TCACCTCTTT
AAAGTTTCTC TCTCCAAATA CAATCACCTC CTGAGGCACT GTTAGGGCTT CGACACAGGA ATTCTTTTCC TAGGGGATTC
AGTTCAGTCC AAAACGCCTA CCAGTGGAGA CTTGCAACAT GGCGGCCTGC TGGTCCCTCG CCAGGAATAT CACAGGCGAC
TGTTCCCTGT TGCATGGAAT AGAAGGCTAT TCCAGAGTAC TGTCTCTATT TATCAGATCT GGGATACTGG GAGAAGGGCA
AAATAAAGTC CAAGTAGAAA AAAAAACTAT GAAAGTTTTA GAGAGTAACC ATAATTTCAG CCCGATGTGA AACGATCCTA
GATTTCAGCT GAAATAGTGA TGTGGGAAGT GAGGGGGCCG GGATTCAAGG CAGAGGGAAC AGCGTAACTG AAGGCATGGA
AGGAGGGAAG TGTAGGCTGT GTTTGAAGAG TGGCAGCTGC TTCCACATTT CTAAAACACA GGATGTGATT TTGGGGTGTG
TTGAGACAAG GCAGAAAACT TGTTTGGAAA AATAACTTGA ATTCCCTGCA CATTTAAAAT CTCTCAGCAG AAGAAAACCC
CACTCAGAAC CCCACTGTTC ATTCCTTGGC TTGTATTTGG SCACAGCTGG CATAGCCCCA GACTGAGTAA GCTCTTCAGA
CACCTCATTT CATGAGTAGC CCCAAAGATC AATCATGGGC CAATTTCTTG GAAGAGAAGA CTCTCCGGTG TTTTGCAGTT
ATTTGTTCTG CTTTCGCGAG ATGTTCTCAA ATCGTTGCAG CTACAAGCCA TGAGTCTGAA GTGTTTGTGT TCCCTCCTTA
CAGGTGGTAA CTTTCTCACA GGCCTTGGCC ACAGATCTGA TCATTACAAT TGCGTCAGCA GTGGAGGGCA ATGTCTCTAT
TCTGCCTGCC CGATCTTTAC CAAAATTCAA GGCACCTGTT ACAGAGGGAA GGCCAAGTGC TGCAAGTGAG CTGAGAGTGA
CCAGAAGAAA TGACGCAGAA GTGAAATGAA CTTTTTATAA GCATTCTTTT AATAAAGGAA AATTGCTTTT GAAGTATACC
TCCTTTGGGC CAAAATGAAT CTTGTGTCTC AATTGGAAGA GGTAAAGAAG TAGGGGGTTA GGGTGCATGG GTTGGAACGT
GAGACAGGTC GAACCACAAA GCCTGCCTGG AAAAGGGGAG TGACGTCCTA GGCTTCAGTG ATGTCACCTC CACTTTGTTT
GATCCACAAA CCAACAGGTG ACTGATTTTG-3' **(FRAG.NO:___) (SEQ. ID NO: 2474)**

5'-GCTCAGCCTC CAAAGGAGCC AGCCTCTCCC CAGTTCCTGA AATCCTGAGT GTTGCCTGCC AGTCGCCATG AGAACTTCCT
ACCTTCTGCT GTTTACTCTC TGCTTACTTT TGTCTGAGAT GGCCTCAGGT GGTAACTTTC TCACAGGCCT TGGCCACAGA

TCTGATCATT ACAATTGCGT CAGCAGTGGA GGGCAATGTC TCTATTCTGC CTGCCCGATC TTTACCAAAA TTCAAGGCAC CTGTTACAGA GGGAAGGCCA AGTGCTGCAA GTGAGCTGGG AGTGACCAGA AGAAATGACG CAGAAGTGAA ATGAACTTTT TATAAGCATT CTTTTAATAA AGGAAAATTG CTTTTGAAGT AT-3' **(FRAG.NO:___) (SEQ. ID NO: 2472)**

5'-CCGGGGC-3' **(FRAG.NO:1800) (SEQ. ID NO: 1811)**

5'-GG GCCTGCBGGG CC-3' **(FRAG.NO:1801) (SEQ. ID NO: 1812)**

5'-GGCBGCB BGG-3' **(FRAG.NO:1802) (SEQ. ID NO: 1813)**

5'-GGG TCC TCB TGG CTG GGG-3' **(FRAG. NO:1212) (SEQ. ID NO:1222)**

5'-GCC TGG GCC TGC BGG GCC-3' **(FRAG. NO:1213) (SEQ. ID NO:1223)**

5'-GCT CTT GCC TGG BGT GGC TC-3' **(FRAG. NO:1214) (SEQ. ID NO:1224)**

5'-GCC CBG BGT CTT CCC TGG T-3' **(FRAG. NO:1215) (SEQ. ID NO:1225)**

5'-CCGGGGCTGC BGCBBCCTCB TCBGCTCTTG CCTGGBGTGG CTCBGCCTGG GCCTGCBGGG CCBCCBGGBG BBTGGCBGCB BGGBTGGCGB GGGTCCTCBT GGCTGGGGTC BCBGBTCCTC TBGCTBGGCB GGGTGBCCBG BGBGGGC-3' **(FRAG.NO:1803) (SEQ. ID NO: 1814)**

<u>Human Defensin 2 Nucelic Acid and Antisense Oligonucleotide Fragments</u>

5'-ATCCTTTAAG TCAATGGACT TTGCATCAGT CACACCATCT TTTGTTACTT TGGACTTCCC CAGCTATGTT CAATAATTAC TGTTCTTCCC TTGGGCCCCA TTGTAATGGC TACAGCCTCG ACAAAAAGTC TACACTTTGA AGCATTAAGG CTCGGACATC AGCACCAAAT TTTACATCTT TACCATCACT TCAAGTGAGG TGAGGAGCCA GTAGCCTGGA CACTGGTCTC ATCTGGTGAA AGACTGTGGG TAATGGAAGC ATTTCTGTGG GGTGCTGGCA GGACATGTGC ATGGCGAGGC AGGTCATCAG CAGCAAGTGA GAGCTGCCTC TTACTTTCTA AAGGTGACAT AGCAAATATA CAAAAAAAAA TAAATAAATT ATTAATTTAG GTAGAGCACA TAAAGGCTTT ATTTCATATT CCATTTCTCT GTATGCTTTC TTCACCAGGA AGAAATAGTT TTAGTGTCAG GAATGAATGA GTCTGCCCCT CAATTCCAGC CTGCTCAACA CACAAGGAAA CAAAGCCCTG ACAATCAGAG TGACTCCCTG GTGACTAAGC TCCCAGTCCT GGATGCATAT TTGTTTAGCA GTTCTGACAG CATTTGACCC AGCCCTCTCT CTGCATATCC CATCAGAACC TTCTTTTTTT TTTTTTTCTT TGAGACTGAG TCTTGCTCTG TCGGAAGCGA CTCCTGTGCC TCAGCCTCCC AAATACCTGG AATTATAGGC GTAAGCCATC ATGCCTGGCT AATTTTTGTA TTTTTCATGG AGATGGGGTT TTGCCATGTT GGTCAAATTG GTCTCACACT CCTGACCTCA TGTGATCCAC CTGCCTCAGC CTCCCAAACT GCTGGGATGA CAGGTGTAAG CCACCATGCT AGGCTCAGAA ATTTCCTTTT ATAAAAATGT CATTAAGGAT CTTGGCTGCA CAATATCGTT ACCAGCTTCC TTTAAATCCA CTTCTGGCCT GCCAGGAATC AGGTTCTTCA GAACCTGACA TTTTAAATGA AGAGGTCAGG CAGTTCATGA GGAAAGCCTC ATTGTCCCCA TGTCTCTGTC ACTGCTGCAC CCCTGAGACA TCACAGACAT GGACACTGGG GCCTGCTTGT TTCTCAAACT GCCCTTAGAT CGAAAGAGGG AGGAACCAGG ATGAATGCCA CTCATTTTCC CAAGAAAGGC CCTCTCCTGA GTGCCCGGGA TGGGGCTCTG TCCATTGCCT GGGGCCGCCA ATTGCTACTC TGGGTTACGG AGGAAGGACA GGGTCCTGAG AGACACCAGA GACCTCACAC AGCCCTGAAA ACATGGGGCT CCTTCATAAG TGTTTCCCAT CACCAACAGG GAGACCACGT GGAGGCCTTG CAGCCCCACT CGGTGCTTCT CCACCAAATC CCAAGGGCAG TGACGCTGAC GTCTGTGGAA AGCAGAGAAA GCCCTGGCTC CCAAAGCCCT GAAGTCCCTG TGGAGCTGAC ATTCCCTGAG TGACGGTGTG AATGGAAGGA ACTCAAGTGC GGGTGGTAGG CCACCTCCTG GCCCAGGCCT GGGTGAACTC TGAGGGGACA CATGTAGTCA CAATCCCATC CTCCCATTCT CCTTCTCAGA GGAAGGAAGT GGGCATCCAT CTGCCTCATC TCTCTCCCGT GGGGAAGATG GGGAGTTTCA GGGGAACTTT CACATAAATT TCACCAGCTC AGATCTCCTG TGAGGATGGG GCCCACCATG CTCCCGGTGC TGCCAGAGGC CCTGAGCCCC TCCCAGGGTC CCTGGGTTTG AGCCAGCCCT GTATCATCCC CAGGAGCTGA ATGTCAGAGC AATGGATAGA ATTAGATGGA AAGAGCTCTC AATTTGACCT GAGACTGTCC CCAGATACTC AGGAAAAACA GGACGTCGCA CAGAGTGGGC AGCAGGTGAG TGGCAGGTTA TAGGTCCTGA GTTTGAGTTT GTTCTCACGT GAGACAGACC CAGCCCCTCA CTCCATTCAC ACACTGGGTT TTAAATGGTG CAAGATAGGA GCAATTTTCT GGTCCCAAGA GCAGGAGGAA GGGATTTTCT GGGGTTTCCT GAGTCCAGAT TTGCATAAGA TCTCCTGAGT GTGCATTGTT CTTTGAGGAC CATTCTCTGA CTCACCAGGT AAGTGGCTGA ATTCTAACCT CTGTAATGAG CATTGCACCC AATACCAGTT CTGAACTCTA CCTGGTGACC AGGGACCAGG ACCTTTATAA GGTGGAAGGC TTGATGTCCT CCCCAGACTC AGCTCCTGGT GAAGCTCCCA GCCATCAGCC ATGAGGGTCT TGTATCTCCT CTTCTCGTTC CTCTTCATAT TCCTGATGCC TCTTCCAGGT GAGATGGGCC AGGGAAATAG GAGGGTTGGC CAAATGGAAG AATGGCGTAG AAGTTCTCTG TCTCCTCTCA TTCCCCTCCA CCTATCTCTC CCTCATCCCT CTCTCTCCTT CCTCTCTCTG TGTGTCCCCT CCATCCTTTT CTCCTGCTTC TCTCTCTTCT TCCCTCTCTC TCTTTTTTCT GTCTTTCTTT TTCCTCTCTC CCTAGAGCAT GTCTTTCTTT CTTTCTCTTT CCTTTCTTCT ACCCACACTT TTAGACTGAA TGCCCTATTT AATTGAACAA AGCATTGCTT CCTTCAATAG AAAAGGAGTT TGAGAACCCA ATGGACACCT CACTCGTTCT TCTAAGCCAA TATGAAGGAG CCCAGTAGCT TGTAAATATC ATCTCTTCAC TGCTTTCCAT GCTACAACTG CTGAGACTAT GGTTGAAACC TGTTAGGTGA CTTTTTAAAT AAAAGGCAGA AATTTTGATT TTATCTAAAG AAAGTAGTAT AGAATGTCAT TTTCTAAATT TTTATATTTA AAGGGTAGAT ACTGCAACCT AGAGAATTCC AGATAATCTT AAGGCCCAGC CTATACTGTG AGAACTACTG CAGCAAGACA CTCTGCCTCC AGGACTTTTC TGATCAGAGG CCCTGAGAAC AGTCCCTGCC ACTAGGCCAC TGCAGGTTCA CAGGACAGGG TACAGCCCAT TGAAACCTAC TTTTAAACCT GGATGCCTAA CCTTCATTTT CTCCTTGATA TTATGAAAAT AAAATAAAAA CCATGAAAGG ATAAAAGAGG GAGAGTGGAA GGGAAGGATG GAGAAAGGGA AAAAGAAAAT TTGAGAGTAA ATCCTAAAAC AATTAATCTA ATAGATATCA TCTTGTGAAA TCCTCATTTT ACCAATCTTA TTTATGAGTC CTGGGTTTTG TGAGAACAAT GGGGTTCTGA GAGGCACCAG AGACCTCATG TTTTCCAAAA CCTAGAACAG TATAATGAAG GAAGGCGGGG AGGCAGGGAG GCAGGGAGGC AGGGAGGCAG GGAGGCGGGC AGGTGGGGAG GGAGGGACGG AAGGAGGGAG GGAGGGAGGG AGGGAGGGAG GGAGGGATAA AAAAAGAAGA ATGAGGTTGA AACCAGGACT TAGATATTAG AAACAAGCCA TTACAAAATT TATTTCTATG GTTAATTGTG GTTTTCAACT GTAAGTTACT TGGTGTTAAT TTCCTATTAA ACAATTTCAG TAAGTTGCAT CTTTTTATCC CATCTCAGGT CAAATACTTA ACAGACTAAA TGATTTGAAA AAGCAAAAGT TTACTGGCTT GTGTGTGTTA AAATGGAGGT ATGGTGGCTT TGATATTATC TTCTTGTGGT GGAGCTGAAT TCACAAGAGA TCGTTGCTGA GCTCCTACCA GACCCCACCT GGAGGCCCCA GTCACTCAGG AGAGATCAGG GTCTTTCACA ATCAGGTTCT ACAAAAATAA ACATCCCCCC AACCACAGCA GTGCCAGTTT CCATGTCAGA AACTTAGATC CAAATGACTG ACTCGCGTCT CATTATCATG ATGGAAAAGC CCAGGCTTGA GAAAGAAGCC CGCTGCGGAT TTACTCAAGG CGATACTGAC ACAGGGTTTG TGTTTTTCCA ACATGAGTTT TGAGTTCTTA CACGCTGTTT GCTCTTTTTG TGTGTTTTTT CCCTGTTAGG TGTTTTTGGT GGTATAGGCG ATCCTGTTAC CTGCCTTAAG AGTGGAGCCA TATGTCATCC AGTCTTTTGC CCTAGAAGGT ATAAACAAAT TGGCACCTGT GGTCTCCCTG GAACAAAATG CTGCAAAAAG CCATGAGGAG GCCAAGAAGC TGCTGTGGCT GATGCGGATT CAGAAAGGGC TCCCTCATCA GAGACGTGCG ACATGTAAAC CAAATTAAAC TATGGTGTCC AAAGATACGC AATCTTTATC CTAGTAATTG TGGTCATTGG GTGATGTTGG TTTGGGCAGG CCATCTCTAA TATCCTTGAA ACACCTTTTT CTGCTCTCCA GGAAGGGGTC AGGGCTGCCA CAGCGGGGCT TGGAGTGCTT

TCCAGGGTCA CAGGCATCTG TATTCTTTGG ATTCCTTGAC CTTCCCCATT TATTCCCGGC ATTTTCCTAA AACGTGTGCT
TTGCTCCTCC TGCATCCTCC CCTTGCATGC CCTCACCTAC CCCACATCTT CCCTAAAAAA AGCAAGCCCA ACTCAAAGAC
CAGTTCCCTC ATGGAATCAT AGTGGATCTG CCAAGGGAGG GGATGCCCAG TCCTCTGTTC TTCACAAGAC TCCCTTCTTC
TGGCTAAGGT TTCTTATGCA ATTAT GAATTCACAT TTCTCACCTT TTGATGTATT AAGAAAGTAT GGAGAAATAT
ATCCTCTATC AAATTTTCAT GCCTTCAATA ATTTCTAATT CATCAGTCAG TGTTTTTCCA TCCTTTACTG TGATGATGCC
CTTTCTTCCA AACTTTTTCA TTGCATCAGA GATGATGTTA CCAATTTCTT TGTCTCCATT TGCAGAAATT GTAGCAACCT
GTGCAATTTC TTCAGGTTTG GTCACAGGTT TAGACTGCTT TTTAAGTTCA GCAATTACAG CATCAACAGC TAACATCACA
CCTCTCTTGA TTTCCACTGG ATTAGCACCT TTGCTAACCT TCTGGAAGGC TTATTTGGAA ATAGAGCATA CCAGTACAGC
AGCAGTGATA GTGCCATCCC CCAGTCTCTC CATTTGTGTT ATTGGCAACA TCTTGGACAA GTTTAGCTCC AATGCTTTTA
TATTTATCCT TTAAGTCAAT TGACTTTGCA TCAGTCACAC CATCTTTTGT TACTTTGGGA CTTCCCCAGC TATGTTCAAT
AATTACTGTT CTTCCCTTTG GCCCCATTGT AATGGCTACA GCATCGACAA AAAGTCTACA CTTTGAAGCA TTAAGGCTCA
GACATCAGCA CCAAATTTTA CATCTTTACC ATCACTTCAA GTGAGGTGAG GAGCCAGTAG CCTGGACACT GGTCTCATCT
GGTGAAAGAC TGTGGGTAAT GGAAGCATTT CTGTGGGGTG GTGGCAGGAC ATGTGCATGG TGAGGCAGGT CATCAGCAGC
AAGTGAGAGC TGCCTCTTAC TTTCTAAAGG TGACATAGCA AGTATACAAA AAAAAATAAA ATATTAATTT AGGCAGAGCA
CATAAAGGCT TTATTTCATA TTCCATTTCT CTGTATGCTT TCTTCACCAG GAAGAAATAG TTTTAGTGTC AGGAATGAAT
GAGTCTGCCC CTCAATTCCA GCCTGCTCAG CACACAAGGA AACAAAGCCC TGACAATCAG AGTGACTCCC TGGTGACTAA
GCTCCAGTCC TGGATGCATA TTTGTTTAGC AGTTCTGACA GCATCTGACC CAGCCCTCTC TTTGCATACC CCACCAGAAC
CTTCTTTTTT TTTTTTTTTC TTTGAGACTG AGTCTTGCTC TGTCGGAAGC GATTCCCGTG CCTCAGCCTC CCAAATACCT
GGAATTATAG GCGTAAGCCA TCATGCCTGG CTAATTTTTG TATTTTTCAT GGAGATGGGG TTTTGCCATG TTGGTCAAAT
TGGTCTCACA CTCCTGACCT CATGTGATCC ACCTGCCTCA GCCTCCCAAA GTGCTGGGAT GACAGGTGTA AGCCACCATG
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CTCATTGTCC CCATGTCTCT GTCACTGCTG CACCCCTGAG ACATCACAGA CATGGACACT GGGGCCTGCT TGTTTCTCAA
ACTGCCCTTA GATCGAAAGA GGGAGGAACC AGGATGAATG CCACTCATTT TCCCAAGAAA GGCCCTCTCC TGAGTGCCCG
GGATGGGGCT CTGTCCATTG CCTGGGGCCG CCAATTGCTA CTCTGGGTTA CGGAAGAAGG ACAGGGTCCT GAGAGACACC
AGAGACCTCA CACAGCCCTG AAAACATGGG GCTCCTTCAT AAGTGTTTCC CATCACCAAC AGGGAGACCA CGTGGAGGCC
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CTCCCAAAGC CCTGAAGTCC TGTGGAGCTG ACATTCCCTG AGTGACGGTG TGAATGGAAG GAACTCAAGT GCGGGTGGTA
GGCCACCTCC TGGCCCAGGC CTGGGTGAAC TCTGAGGGGA CACATGTAGT CACAATCCCA TCCTCCCATT CTCCTTCTCA
GAGGAAGGAA GTGGGCATCC ATCTGCCTCA TCTCTCTCCC GTGGGGAAGA TGGGGAGTTT CAGGGGAACT TTCACATAAA
TTTCACCAGC TCAGATCTCC TGTGAGGATG GGGCCCACCA TGCTCCCGGT GCTGCCAGAG GCCCTGAGCC CCTCCAGGGT
CCCTGGGTTT GAGCCAGCCC TGTATCATCC CCAGGAGCTG AATGTCCGAA CAATGGATAG AATTAGATGG AAAGAGCTCT
CAATTTGGCC TGAGACTGTC CCCAGATACT CAGGAAAAAC AGGACGTCGC ACAGAGTGGG CAGCAGGTGA GTGGCAGGTT
ATAGGTCCTG AGTTTGAGTT TGTTCTCACG TGAGACAGAC CCAGCCCCTC ACTCCATTCA CACACTGGGT TTTAAATGGT
GCAAGATAGG AGGAATTTTC TGGTCCCAAG AGCAGGAGGA AGGGATTTTC TGGGGTTTCC TGAGTCCAGA TTTGCATAAG
ATCTCCTGAG TGTGCATTGT TCTTTGAGGA CCATTCTCTG ACTCACCAGG TAAGTGGCTG AATTCTAACC TCTGTAATGA
GCATTGCACC CAATACCAGT TCTGAACTCT ACCTGGTGAC CAGGGACCAG GACCTTTATA AGGTGGAAGG CTTGATGTCC
TCCCCAGACT CAGCTCCTGG TGAAGCTCCC AGCCATCAGC CATGAGGGTC TTGTATCTCC TCTTCTCGTT CCTCTTCATA
TTCCTGATGC CTCTTCCAGG TGAGATGGGC CAGGGAAATA GGAGGGTTGG CCAAATGGAA GAATGGCGTA GAAGTTCTCT
GTCTCCTCTC ATTCCCCTCC ACCTATCTCT CCCTCATCCC TCTCTCTCCT TCCTCTCTCT GTGTGTCCCC TCCATCCTTT
TCTCCTGCTT CTCTCTCTTC TTCCCTCTCT CTCTTTTTTT CTGTCTTTCT TTTTCCTCTC TCCCTAGAGC ATGTCTTTCT
TTCTTTCTCT TTCCTTTCTT CTACCCACAC TTTTAGACTG AGTAGACTGA ATGCCCTATT TAATTGAACC AAGCATTGCT
TCCTTCAATA GAAAAGGAGT TTGAGAACCC AATGGACAAC TCACTCGTTC TTCTAAGCCA ATATGAAGGA GCCCAGTAGT
TTGTAAATAT CATCTCTTCA CTGCTTTCCA TGCTACAACT GCTGAGACTA TGGTTGAAAC CTGTTAGGTG ACTTTTTAAA
TAAAAGGCAG AAATTTTGAT TTTATCTAAA GAAAGTAGTA TAGAATGTCA TTTTCTAAAT TTTTATATTT AAAGAGTAGA
TACTGCAACC TAGAGAATTC CAGATAATCT TAAGGCCCAG CCTATACTGT GAGAACTACT GCAGCAGACA CTCTGCCCCC
AGGACTTTTC TGATCAGAGG CCCTGAGAAC AGTCCCTGCC ACTAGGCCAC TGCAGGTTCA CAGGACAGGG ACAGCCCATT
GAAACCAACT TTTAAACCTG GATGCCTAAC CTTCATTTTC TCCTTGATAT TATGAAAATA AAATAAAAAC CATGAAAGGA
TAAAAGAGGG AGAGTGGAAG GGAAGGATGG AGAAAGGGAA AAAGAAAATT TGAGAGTAAA TCCTAAAACA
ATTAATCTAA TAGATATCAT CTTGTGAAAT CCTCATTTTA CCAATCTTAT TTATGAGTCC TGGGTTTTGT GAGAACAATG
GGGTTCTGAG AGGCACCAGA GACCTCATAT TTTCCAAAAC CTAGAACAGT ATAATGAAGG AAGGAGGGAA GGAGGGAGGG
AGGGAGGGAA GGAGGGAAGG AGGGAGGGAG GGAGGGAAAC AAAAAGAAGA ATGAGGTTGA AACCAGGACT
TAGATATTAG AAACAAGCCA TTACAAAATT TATTTCTATG GTTAATTGTG GTTTTCAACT GTAAGTTACT TGGTGTTAAT
TTCCTATTAA ACAATTTCAG TAAGTTGCAT CTTTTTTATC CCATCTCAGA TCAAATACTT AACAGACTAA ATGATTTGAA
AAAGCAAAAG TTTACTGGCT TGTGTGTGTT AAAATGGAGG TATGGTGGCT TTGATATTAT CTTCTTGTGG TGGAGCTGAA
TTCACAAGAG ATCGTTGCTG AGCTCCTGCC AGACCCCACC TGGAGGCCCC AGTCACTCAG GAGAGATCAG GGTCTTTCAC
AATCAGGTTC TACAAAAATA AACATCCCCC AAACCACAGC AGTGCCAGTT TCCATGTCAG AAACTTAGAT CCAAATGACT
GACTCGCGTC TCATTATCAT GATGGAAAAG CCCAGGCTTG AGAAAGAAGC CCGCTGCGGA TTTACTCAAG GCGATACTGA
CACAGGGTTT GTGTTTTTCC AACATGAGTT TTGAGTTCTT ACACGCTGTT TGCTCTTTTT GTGTGTTTTT TCCCTGTTAG
GTGTTTTTGG TGGTATAGGC GATCCTGTTA CCTGCCTTAA GAGTGGAGCC ATATGTCATC CAGTCTTTTG CCCTAGAAGG
TATAAACAAA TTGGCACCTG TGGTCTCCCT GGAACAAAAT GCTGCAAAAA GCCATGAGGA GGCCAAGAAG CTGCTGTGGC
TGATGCGGAT TCAGAAAGGG CTCCCTCATC AGAGACGTGC GACATGTAAA CCAAATTAAA CTATGGTGTC CAAAGATACG
CAATCTTTAT CCTAGTAATT GTGGTCATTG GGTGATGTTG GTTTGGGCAG GCCATCTCTA ATATCCTTGA AACACCTTTT
TCTGCTCTCC AGGAAGGGGT CAGGGCTGCC ACAGCGGGGC TTGGAGTGC-3' **(FRAG. NO:___) (SEQ. ID NO:2473)**
5'-GAATTCACAT TTCTCACCTT TTGATGTATT AAGAAAGTAT GGAGAAATAT ATCCTCTATC AAATTTTCAT GCCTTCAATA
ATTTCTAATT CATCAGTCAG TGTTTTTCCA TCCTTTACTG TGATGATGCC CTTTCTTCCA AACTTTTTCA TTGCATCAGA
GATGATGTTA CCAATTTCTT TGTCTCCATT TGCAGAAATT GTAGCAACCT GTGCAATTTC TTCAGGTTTG GTCACAGGTT
TAGACTGCTT TTTAAGTTCA GCAATTACAG CATCAACAGC TAACATCACA CCTCTCTTGA TTTCCACTGG ATTAGCACCT
TTGCTAACCT TCTGGAAGGC TTATTTGGAA ATAGAGCATA CCAGTACAGC AGCAGTGATA GTGCCATCCC CCAGTCTCTC

CATTTGTGTT ATTGGCAACA TCTTGGACAA GTTTAGCTCC AATGCTTTTA TATTTATCCT TTAAGTCAAT TGACTTTGCA
TCAGTCACAC CATCTTTTGT TACTTTGGGA CTTCCCCAGC TATGTTCAAT AATTACTGTT CTTCCCTTTG GCCCCATTGT
AATGGCTACA GCATCGACAA AAAGTCTACA CTTTGAAGCA TTAAGGCTCA GACATCAGCA CCAAATTTTA CATCTTTACC
ATCACTTCAA GTGAGGTGAG GAGCCAGTAG CCTGGACACT GGTCTCATCT GGTGAAAGAC TGTGGGTAAT GGAAGCATTT
CTGTGGGGTG GTGGCAGGAC ATGTGCATGG TGAGGCAGGT CATCAGCAGC AAGTGAGAGC TGCCTCTTAC TTTCTAAAGG
TGACATAGCA AGTATACAAA AAAAAATAAA ATATTAATTT AGGCAGAGCA CATAAAGGCT TTATTTCATA TTCCATTTCT
CTGTATGCTT TCTTCACCAG GAAGAAATAG TTTTAGTGTC AGGAATGAAT GAGTCTGCCC CTCAATTCCA GCCTGCTCAG
CACACAAGGA AACAAAGCCC TGACAATCAG AGTGACTCCC TGGTGACTAA GCTCCAGTCC TGGATGCATA TTTGTTTAGC
AGTTCTGACA GCATCTGACC CAGCCCTCTC TTTGCATACC CCACCAGAAC CTTCTTTTTT TTTTTTTTTC TTTGAGACTG
AGTCTTGCTC TGTCGGAAGC GATTCCCGTG CCTCAGCCTC CCAAATACCT GGAATTATAG GCGTAAGCCA TCATGCCTGG
CTAATTTTTG TATTTTTCAT GGAGATGGGG TTTTGCCATG TTGGTCAAAT TGGTCTCACA CTCCTGACCT CATGTGATCC
ACCTGCCTCA GCCTCCCAAA GTGCTGGGAT GACAGGTGTA AGCCACCATG CTAGGCTCAG AAATTTCCTT TTATAAAAAT
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TTGGAGTGC-3' **(FRAG. NO:___) (SEQ. ID NO:2476)**

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Human Defensin 3 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CGCTGCBBTC TGCTCCGGGG CTGCBGCBBC CTCBTCBGCTC TTGCCTGGBGTG GCTCBGCCTGG GCCTGCBGGG CCBCCBGGBGB BTGGCBGCBBG GBTGGCGBGGG TCCTCBTGGC TGGGGTCBCCT GGBGGBGGGB GBGCBGGGGG TCCTCBTGGC TGGGGTCCCT CTCTCCCGTC CT CCTACCTTGC TATAGAAGAC CTGGGACAGA GGACTGCTGT CTGCCCTCTC TGGTCACCCT GCCTAGCTAG AGGATCTGTG ACCCCAGCCA TGAGGACCCT CGCCATCCTT GCTGCCATTC TCCTGGTGGC CCTGCAGGCC CAGGCTGAGC CACTCCAGGC AAGAGCTGAT GAGGTTGCTG CAGCCCCGGA GCAGATTGCA GCGGACATCC CAGAAGTGGT TGTTTCCCTT GCATGGGACG AAAGCTTGGC TCCAAAGCAT CCAGGCTCAA GGAAAAACAT GGACTGCTAT TGCAGAATAC CAGCGTGCAT TGCAGGAGAA CGTCGCTATG GAACCTGCAT CTACCAGGGA AGACTCTGGG CATTCTGCTG CTGAGCTTGC AGAAAAAGAA AAATGAGCTC AAAATTTGCT TTGAGAGCTA CAGGGAATTG CTATTACTCC TGTACCTTCT GCTCAATTTC CTTT-3' **(FRAG. NO:1804) (SEQ. ID NO:1815)**

5'-CCTACCTTGC TATAGAAGAC CTGGGACAGA GGACTGCTGT CTGCCCTCTC TGGTCACCCT GCCTAGCTAG AGGATCTGTG ACCCCAGCCA TGAGGACCCT CGCCATCCTT GCTGCCATTC TCCTGGTGGC CCTGCAGGCC CAGGCTGAGC CACTCCAGGC AAGAGCTGAT GAGGTTGCTG CAGCCCCGGA GCAGATTGCA GCGGACATCC CAGAAGTGGT TGTTTCCCTT GCATGGGACG AAAGCTTGGC TCCAAAGCAT CCAGGCTCAA GGAAAAACAT GGACTGCTAT TGCAGAATAC CAGCGTGCAT TGCAGGAGAA CGTCGCTATG GAACCTGCAT CTACCAGGGA AGACTCTGGG CATTCTGCTG CTGAGCTTGC AGAAAAAGAA AAATGAGCTC AAAATTTGCT TTGAGAGCTA CAGGGAATTG CTATTACTCC TGTACCTTCT GCTCAATTTC CTTT-3' **(FRAG. NO:___) (SEQ. ID NO:2478)**

5'-GAATTCCCTG TAAGCCCTGT TACAGGGGCT GCACCCCAGA TACAACCTGA CCTGTGTCCA AGGCGGGCAA CTCAACCCTT AGATATTGAA TGGGTCCCAT GGCACCAATG CTTAAACACC AGCAGCCCTC ACAACCACAG ATCGTGTTTT AAGGATGAGG AGGTAGTTCT CTGGATGCAC AGGCTTCAAT CCAAATGGGC TCATGACGCC GCAGCACACA CCCAGTCTGC AGCCTGAAGA GTTGGAGCAT TGCATTCACA GAAAGCATCC AGACATGATC ATGGGCTCAG GGATACACCT GTTCTCCGAT GTGTACCAGT GAAGGATGGA AACTCCTATG CCTCCCAGAA AGCACCACTC AAGCTTTTGC TGAATGCTTC TCTGAAGGCC CACAAGGCTG AGAGGCTGTG CAACACCAGC AGTAAAGTGA ATGCCCAGAC TCCCACCTCC TTTCTTGGGT GGCCATCTGG AAAGGCCACT CCCACCCTGA TGGCTAATGC CTCAGACCAG TTCTTGGCCC AGATGATCCT AGACAATTGT TTAAGCTTAA ACTGTTCATT GGCCAAGCAA ACAGGTGATA GTACCTCTGG GGAACCACAT GCCGCGTGTA CATCCAGATC TCAGGAGAAC CCAAAAATGT CTGTTCCACA TAGCAACAGA AGCCCAGGTA GCACTCAGTC TCACCTGGGT GTTCTCCAAC ATCCCAGCTC AGCCAAATGG CTTTCATTAG TTTTTATGGT TAGACCCCAG GTCCTCGGGA CACTGCTTTA GAAACACATT CCAAATCCTC CTCTGTGTGC AGGTGGCATT CCTATCCCAA TCTCTTTGCA GGGCGTATAC TGTGATACGC AGCCAGGCTG TCCCAGAGGC CTTAAATATT CCCTTGGTGC AGGTAGTTCA GCTTAGCCAC AGCCAATGCA TCACAGGGTC AACTGTGTTA GGAGCCATTG AGAATCCATA GTTGGTTGCT GCCTGGGCCT GGCCAGGGCT GACCAAGGTA GATGAGAGGT TCCTCTGTGG AGTTCTACTT TAACCTCACC TTCCCACCAA ATTTCTCAAC TGTCCTTGCC ACCACAATTA TTTAATGGAC CCAACAGAAA GTAACCCCGG AAATTAGGAC ACCTCATCCC AAAAGACCTT TAAATAGGGG AAGTCCACTT GTGCACGGCT GCTCCTTGCT ATAGAAGACC TGGGACAGAG GACTGCTGTC TGCCCTCTCT GGTCACCCTG CCTAGCTAGA GGATCTGTAA GTACTACAAA ACTTAAACTT TACACTGAGT TTTCATCATT GAAGCTATGC CTCCAATCTG ACCTCTGACT GTGGGGCCGC CCCAGAGGGA CCCAGCGGGT GAATCCCTGC TAGGAACGTC TGTCCGGACC TCTGGTGACT GCTGGGGACG ATGGCTTCCA GCTAACTTAA TAGAGAAACT CAAGCAGTTT CCTTCTAAAT ACACATGTCA CATGTCCTGG TTGACATGTC CAGTAAGAAG ACTATCACAG GTCTTTGGAA CATTCTTTTG AGAGAAACCT ATTTAGGTCC TTGGTCTGTT TTTCAATCAG GTTGTTTGAT TTTTGCTATT GAGTTGTTGG AATTCCTTAT GTATTCAGAT ATTTGCCCCT TCTGCCATGT AGGTTTTGCA AATATTTTCT CTCATTTTCT GGGTTATCTT TTCACTCGGT TGATTGTTTC CTTTGCTGTG CAGATGCTTT AGCGTTAAAT GAAGCCACAC TTGTCTATTT TCCCTTTTAT TGCCTGTGCC TTTGGTGTCA TAGCCAAGAA ATCATTACCT ACATCAATGT CAAAAGCTTT ATCCTTCTAT ACACTTCTAG TAGTTTATGG TTTCAGTTGT TACATTTAGG TTTTCAATTC ATTCTGAGTT GATGTTCCTA CATGGTGTGA GATAAAGATT TAAATACATA CATATATAAA ATCATGAGGT AGTGTACACT ATAAATATAC AATTGTTAAT TGTTACTCAA GTCTAAGTAG AGGTGGAAAT AATAAACTTT CTTTTTTTTA CTTAAACCAC TCTGTGTCAC TGAGCTGATT TCACCTTTAG CCTGATAAAA TCATTGTCCT CTCCACCCTG ATTCCTACAG GAGACTACTC ACCCCATAAC CTCAAAAACC TCTTCATGAG GATGGTAAGT CACCTGAATC CTGAAGTGAA TTACTCGCTA TTCCATTGGA ACTCATATAG GACACCAGAA TCTAGACCTC CAGAGAACAG CAGGACCCAT

CTTCAGAAAA TAAGAAGCAT TTGTTCCCTG AGCCTGTTGA ATCAAAGTGC AATTTCTATT CTTTTTGGAA TGTTAAAAAG TGAATCATAA TATTTAAGCA GGTGAACCCA CGAGTAACAT AGCAGGGTCT TTCTTGTCAT TATTAGCTCC AACCTAGCAC AGACATTAAA GGTACAGATG TATACTAGCA TGAAACTGGG AGAACAGGAG CATTCGAGCA ACCTTGAGAC CAATGGGCCT CTCTTATAAA ATGCACACCT CCTCTCACTG AGATTGAGGA AGGTTTCTTG TCTCCGAGCC TTCTCCCAGT AGAGCTATAA ATCCAGGCTG GCTCCTCCCT CCCCACACAG CTGCTCCTGC TCTCCCTCCT CCAGGTGACC CCAGCCATGA GGACCCTCGC CATCCTTGCT GCCATTCTCC TGGTGGCCCT GCAGGCCCAG GCTGAGCCAC TCCAGGCAAG AGCTGATGAG GTTGCTGCAG CCCCGGAGCA GATTGCAGCG GACATCCCAG AAGTGGTTGT TTCCCTTGCA TGGGACGAAA GCTTGGCTCC AAAGCATCCA GGTGAGAGAG GCAGGCATGC AGAGCTGCTA AGTCTAGAGG GAAGGACGGG AGAGAGGTTC CAGAGTTGGG TCTCAGCAGT CTATGTCACT GAGGTGGCTT CACTTAGAAT CTCTGGGCAT TGATTTTCTC ATCTAGAAAT TGAACAGAGA GCCAAATAAA CCTGAGAAAC TTTATTTCTC CAAAGACTTG ATTCCAAGAA ACATCTGTGA AATTCACTAA GTTTAAGATA TGAAGAGACA GACTAGTTAT TTCTGGATCT AAACAAGTAG ACTTAGTTGT AAAGAGAACA TTTTACTCTA TCTACAGAAG AGCTTTTAAA AACTGCAGCC AAGCCTGAGG GTAAGTTCAG GTGTGTGTGT GATGGGGCAG GAATGCAAAA ATGAGAGCAA AGGAGAATGA GTCTCAAATT CTGTGTGACA AGCACTGCTC TGCGTGTTTA TTCCTATCGA CTGAGGTTGT TCGTGCTACC GGCTGCAATG CAGCCAGCAT CACCTGTCAG CTAGCATGTG ACTTCCCCGA GATTCTTTTT CTTACCCACT GCTAACTCCA TACTCAATTT CTCATGCTCT CCCTGTCCCA GGCTCAAGGA AAAACATGGA CTGCTATTGC AGAATACCAG CGTGCATTGC AGGAGAACGT CGCTATGGAA CCTGCATCTA CCAGGGAAGA CTCTGGGCAT TCTGCTGCTG AGCTTGCAGA AAAAGAAAAA TGAGCTCAAA ATTTGCTTTG AGAGCTACAG GGAATTGCTA TTACTCCTGT ACCTTCTGCT CAATTTCCTT TCCTCATCTC AAATAAATGC CTTGTTACAA GATTTCTGTG TTTCCACCTC TTTAATGTGT GATATGTGTC TGTGTCAAGA CACTTGGGAT ACACGTACCA AAACGCAAAA TCAAATTTTT GAACAATATA-3' **(FRAG. NO:___) (SEQ. ID NO:2477)**

5'-GGCBGCBBGG-3' **(FRAG. NO:1805) (SEQ. ID NO:1816)**

5'-GG CTG GGG-3' **(FRAG. NO:1806) (SEQ. ID NO:1817)**

5'-GGGGTCBCC-3' **(FRAG. NO:1807) (SEQ. ID NO:1818)**

5'-GGG TCC TCB TGG CTG GGG TC-3' **(FRAG. NO:1216) (SEQ. ID NO:1226)**

5'-CCT CTC TCC CGT CCT-3' **(FRAG. NO:1217) (SEQ. ID NO:1227)**

5'-CGCTGCBBTC TGCTCCGGGG CTGCBGCBBC CTCBTCBGCTC TTGCCTGGBGTG GCTCBGCCTGG GCCTGCBGGG CCBCCBGGBGB BTGGCBGCBBG GBTGGCGBGGG TCCTCBTGGC TGGGGTCBCCT GGBGGBGGGB GBGCBGG-3' **(FRAG. NO:1808) (SEQ. ID NO:1819)**

Human Macrophage Inflammatory Protein-1-alpha/RANTES Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GTCTTTGTTT CTGGGCTCGT GCCCCBTCCC GGCTTCTCTC TGGTTCCGTC CTCTGTGGTG TTTGGCCCTG CTTCCTTTTG CCTGTTGAGG GGGCAGCAGT TGGGCCCCAA AGGCCCTCTC GTTCACCTTC TGGCACGGAGTT GCATCCCCATA GTCAAACTCT GTGGTCGTGT CATAGTCCTC TGTGGTGTTT GGAGTTTCCA TCCCGGCTTC TCTCTGGTTC CAAGGGAGB GGGGGCBGCB GTTGGGCCCC BBBGGCCCTC TCGTTCBCCT TCTGGCBCGG BGTTGCBTCC CCBTBGTCBB BCTCTGTGGT CGTGTCBTBG TCCTCTGTGG TGTTTGGBGT TTCCBTCCCG GCTTCTCTCT GGTTCCBBGG GB-3' **(FRAG. NO:1809) (SEQ. ID NO:1820)**

5'-GGGCC CC-3' **(FRAG. NO:1810) (SEQ. ID NO:1821)**

5'-GGGGGCBGC-3' **(FRAG. NO:1811) (SEQ. ID NO:1822)**

5'-CCCGGCTTC-3' **(FRAG. NO:1812) (SEQ. ID NO:1823)**

5'-GTC TTT GTT TCT GGG CTC GTG CC-3' **(FRAG. NO:1218) (SEQ. ID NO:1228)**

5'-CCB TCC CGG CTT CTC TCT GGT TCC-3' **(FRAG. NO:1219) (SEQ. ID NO:1229)**

5'-GTC CTCTGT GGT GTT TGG-3' **(FRAG. NO:1220) (SEQ. ID NO:1230)**

5'-CCC TGC TTC CTT TTG CCT GTT-3' **(FRAG. NO:1221) (SEQ. ID NO:1231)**

5'-GAGGGGGCAG CAGTTGGGCC CCAAAGGCCC TCTCGTTCAC CTTCTGGCAC GGAGTTGCAT CCCCATAGTC AAACTCTGTG GTCGT-3' **(FRAG. NO:1222) (SEQ. ID NO:1232)**

5'-GTCATAGTCCTCTGTGGTGTTTGGAGTTTCCATCCCGGCTTCTCTCTGGTTCCAAGGGA-3'**(FRAG. NO:1223)(SEQ.ID NO:1233)**

5'-GBGGGGGCBG CBGTTGGGCC CCBBBGGCCC TCTCGTTCBC CTTCTGGCBC GGBGTTGCBT CCCCBTBGTC BBBCTCTGTG GTCGTG-3' **(FRAG. NO:1224) (SEQ. ID NO:1234)**

5'-TCBTBGTCCTCTGTGGTGTTTGGBGTTTCCBTCCCGGCTTCTCTCTGGTTCCBBGGGB-3' **(FRAG. NO:1225) (SEQ. ID NO:1235)**

RANTES Antisense Oligonucleotide Fragments

5'-GGGCBCGGGG CBGTGGGCGG GCBBTGTBGG CBBBGCBGCB GGGTGTGGTG TCCGBGGBBT BTGGGGBGGC BGBTGCBGGB GCGCBGBGGG CBGTBGCBBT GBGGBTGBCB GCGBGGCGTG CCGCGGBGBC CTTCBTGGTB CCTGTGGBGB GGCTGTCGGB GGGGGTGTGG TGTCCGCTTG GCGGTTCTTT CGGGTGTTTC TTCTCTGGGT TGGCCTGCTG CTCGTCGTGGT CGCTCCGCTC CCGGGTTCGT CTCGCTCTGT CGCCCCTTCC TTCCTTGTCG TGTTCCTCCC TTCCTTGCCT CT-3' **(FRAG. NO: 1813) (SEQ. ID NO: 1824)**

5'-GGGTTGGC-3' **(FRAG. NO: 1814) (SEQ. ID NO: 1825)**

5'-CGGGG CBG-3' **(FRAG. NO: 1815) (SEQ. ID NO: 1826)**

5'-CCCGGGTTCG-3' **(FRAG. NO: 1816) (SEQ. ID NO: 1827)**

5'-GGGTGTGGTG-3' **(FRAG. NO: 1817) (SEQ. ID NO: 1828)**

5'-GGGCBCGGGG CBGTGGGCGG GCBBTGTBGG CBBBGCBGCB GGGTGTGGTG TCCGBGGBBT BTGGGGBGGC BGBTGCBGGB GCGC-3' **(FRAG. NO:1226) (SEQ. ID NO:1236)**

5'-BGBGGGCBGTBGCBBTGBGGBTGBCBGCGBGGCGTGCCGCGGBGBCCTTCBTGGTBCCTGTGGBGBGGCTGTCGGBGG-3' **(FRAG. NO:1227) (SEQ. ID NO:1237)**

5'-GGGTGTGGTGTCCGCTTGGCGGTTCTTTCGGGTGTTTCTTCTCTGGGTTGGCCTGCTGCTCGTCGTGGTC-3' **(FRAG. NO:1228) (SEQ. ID NO:1238)**

5'-GCTCCGCTCCCGGGTTCGTCTCGCTCTGTCGCCCCTTCCTTCCTTGTCGTGTTCCTCCCTTCCTTGCCTCT-3' **(FRAG. NO:1229) (SEQ. ID NO:1239)**

5'-GGGTGTGGTGTCCG-3' **(FRAG. NO:1230) (SEQ. ID NO:1240)**

5'-CTTGGCGGTTCTTTCGGGTG-3' (FRAG. NO:1231) (SEQ. ID NO:1241)
5'-TTTCTTCTCTGGGTTGGC-3' (FRAG. NO:1232) (SEQ. ID NO:1242)
5'-CTGCTGCTCGTCGTGGTC-3' (FRAG. NO:1233) (SEQ. ID NO:1243)
5'-GCTCCGCTCCCGGGTTC-3' (FRAG. NO:1234) (SEQ. ID NO:1244)
5'-GTCTCGCTCTGTCGCCC-3' (FRAG. NO:1235) (SEQ. ID NO:1245)
5'-CTTCCTTCCTTGTC-3' (FRAG. NO:1236) (SEQ. ID NO:1246)
5'-GTGTTCCTCCCTTCCTTGCCTCT-3' (FRAG. NO:1237) (SEQ. ID NO:1247)
5'-GGGCBCGGGG CBGTGGGCGG GCBBTGTBGG CBBBGCBGCB GGGTGTGGTG TCCGBGGBBT BTGGGGBGGC BGBTGCBGGB GCGCBGBGGG CBGTBGCBBT GBGGBTGBCB GCGBGGCGTG CCGCGGBGBC CTTCBTGGTB CCTGTGGBGB GGCTGTCGGB GG-3' (FRAG. NO:1818) (SEQ. ID NO:1829)

<u>Human Muscarinic Acetylcholine Receptor HM1* Nucleic Acid and Antisense Oligonucleotide Fragments</u>

5'-GCTGCCCGGC GGGGTGTGCG CTTGGCGCTC CCGTGCTCGG TTCTCTGTCT CCCGGTCCCC CTTGCCTGGC GTCTCGGGCC TTCGTCCTCT TCCTCTTCTT CCTTCCGCTC CGTGGGGGCT GCTTGGTGGG GGCCTGTGCCT CGGGGTCCCG GGGCTTCTGG CCCTTGCCGT TCATGGTGGC TAGGTGGGGC GTTCBTGGTG GCTBGGTGGG GC-3' (FRAG. NO:1819) (SEQ. ID NO: 1830)
5'-GGTGGGGC-3' (FRAG. NO:1820) (SEQ. ID NO: 1831)
5'-GCCCGGCGGGG-3' (FRAG. NO:1821) (SEQ. ID NO: 1832)
5'-CGG GGC TTC TGG CCC-3' (FRAG. NO:1822) (SEQ. ID NO: 1833)
5'-GTT CBT GGT GGC TBG GTG GGG C-3' (FRAG. NO:1238) (SEQ. ID NO:1248)
5'-GCT GCC CGG CGG GGT GTG CGC TTG GC-3' (FRAG. NO:1239) (SEQ. ID NO:1249)
5'-GCT CCC GTG CTC GGT TCT CTG TCT CCC GGT-3' (FRAG. NO:1240) (SEQ. ID NO:1250)
5'-CCC CCT TTG CCT GGC GTC TCG G-3' (FRAG. NO:1241) (SEQ. ID NO:1251)
5'-GCC TTC GTC CTC TTC CTC TTC TTC CTT CC-3' (FRAG. NO:1242) (SEQ. ID NO:1252)
5'-GCT CCG TGG GGG CTG CTT GGT GGG GGC CTG TGC CTC GGG GTC C-3' (FRAG. NO:1243) (SEQ. ID NO:1253)
5'-CGG GGC TTC TGG CCC TTG CC-3' (FRAG. NO:1244) (SEQ. ID NO:1254)
5'-GTT CAT GGT GGC TAG GTG GGG C-3' (FRAG. NO: 1245) (SEQ. ID NO:1255)

<u>Human Muscarinic Acetylcholine Receptor HM3* Nucleic Acid and Antisense Oligonucleotide Fragments</u>

5'-GGG GTG GGT BGG CCG TGT CTG GGGGTT GGC CBT GTT GGT TGC CTCT TGG TGG TGC GCC GGG CGCG TCT TGG CTT TCT TCT CCT TCG GGC CCT CGG GCC GGT GCT TGT GGGCT CCT CCC GGG CGG CCT CCC CGG GCG GGG GCT TCT TGGCG CTG GCG GGG GGG CCT CCTGCT CTG TGG CTG GGC GTT CCT TGG TGT TCT GGG TGGTGG CGG GCG TGG TGG CCT CTG TGGGGG CCC GCG GCT GCB GGG GTTG CCT GTC TGC TTC GTCCTT TGC GCT CCC GGG CCG CCGGG GTG GGT AGG CCG TGT CTG GGGGTT GGC CAT GTT GGT TGC CGGG CCC GCG GCT GCA GGG G-3' (FRAG. NO:1823) (SEQ. ID NO:1934)
5'-CCC GGG CGG-3' (FRAG. NO:1824) (SEQ. ID NO:1835)
5'-G GCG GGG GGG CC-3' (FRAG. NO:1825) (SEQ. ID NO:1836)
5'-CCC GGG CCG CC-3' (FRAG. NO: 1826) (SEQ. ID NO: 1837)
5'-GG CCG TGT-3' (FRAG. NO:1827) (SEQ. ID NO:1838)
5'-GGG GTG GGT BGG CCG TGT CTG GGG-3' (FRAG. NO:1246) (SEQ. ID NO:1256)
5'-GTT GGC CBT GTT GGT TGC C-3' (FRAG. NO:1247) (SEQ. ID NO:1257)
5'-TCT TGG TGG TGC GCC GGG C-3' (FRAG. NO:1248) (SEQ. ID NO:1258)
5'-GCG TCT TGG CTT TCT TCT CCT TCG GGC CCT CGG GCC GGT GCT TGT GG-3' (FRAG. NO:1249) (SEQ. ID NO:1259)
5'-GCT CCT CCC GGG CGG CCT CCC CGG GCG GGG GCT TCT TG-3' (FRAG. NO:1250) (SEQ. ID NO:1260)
5'-GCG CTG GCG GGG GGG CCT CCT CC-3' (FRAG. NO:1251) (SEQ. ID NO:1261)
5'-GCT CTG TGG CTG GGC GTT CCT TGG TGT TCT GGG TGG C-3' (FRAG. NO:1252) (SEQ. ID NO:1262)
5'-TGG CGG GCG TGG TGG CCT CTG TGG TGG-3' (FRAG. NO:1253) (SEQ. ID NO:1263)
5'-GGG CCC GCG GCT GCB GGG G-3' (FRAG. NO:1254) (SEQ. ID NO:1264)
5'-TTG CCT GTC TGC TTC GTC-3' (FRAG. NO:1255) (SEQ. ID NO:1265)
5'-CTT TGC GCT CCC GGG CCG CC-3' (FRAG. NO:1256) (SEQ. ID NO:1266)
5'-GGG GTG GGT AGG CCG TGT CTG GGG-3' (FRAG. NO:1257) (SEQ. ID NO:1267)
5'-GTT GGC CAT GTT GGT TGC C-3' (FRAG. NO:1258) (SEQ. ID NO:1268)
5'-GGG CCC GCG GCT GCA GGG G-3' (FRAG. NO:1259) (SEQ. ID NO:1269)

<u>Human Fibronectin* Antisense Oligonucleotide Fragments</u>

5'-CGG TTT CCT TTG CGG TC TTG GCC CGG GCT CCG GGT G CCC GCC CGC CCG CCG GCC GCC GC CCC GCC GGG CTG TCC CCG CCC CGC CCC GGC CCG GGG CGC GGG GG CGG CCC TCC CGC CCC TCT GG GCC GGC GCG GGC GTC GG CCG CTC GCG CCT GGG GTT CCC TCT CCT CCC CCT GTG C GCC TGC CTC TTG CTC TTCTGC GTC CGC TGC CTT CTC CC CTC TCC TCG GCC GTT GCC TGT GC TGT CCG TCC TGT CGC CCT TCC GTG GTG C TGT TGT CTC TTC TGC CCT C GGT GTG CTG GTG CTG GTG GTG GTG CCT CTG CCC GTG CTC GCCCTG CCT GGG CTG GCC TCT TCG GGT GTG GCT TTG GGG CTC TCT TGG TTG CCC TTT CTT CTC GTG GTG CCT CTC CTC CCT GGC TTG GTC GT TGT CTG GGG TGG TGC TCC TCT CCC TTT CCC TGC TGG CCG TTT GT
CCT GTT TTC TGT CTT CCT CT TTC CTC CTG TTT CTC CGT TTG GCT TGC TGC TTG CGG GGC TGT CTC C CTT GCC CCT GTG GGC TTT CCC TGG TCC GGT CTT CTC CTT GGG GGT C GCC CTT CTT GGT GGG CTGGCT CGT CTG TCT TTT TCC TTC C TGG GGG TGG CCG TTG TGG GCG GTG TGG TCC GCC T TGC CTC TGC TGG TCT TTC-3' (FRAG. NO:1828) (SEQ. ID NO: 1839)
5'-GGCCCGGGC-3' (FRAG. NO:1829) (SEQ. ID NO: 1840)
5'-GCCGGCGCGGGCG-3' (FRAG. NO:1830) (SEQ. ID NO:1841)
5'-GCCTGGGCTGGCC-3' (FRAG. NO:1831) (SEQ. ID NO: 1842)
5'-GGGGG TGGCCG-3' (FRAG. NO:1832) (SEQ. ID NO: 1843)
5'-GG GGG TGG CCG TTG TGG GCG G-3' (FRAG. NO:1833) (SEQ. ID NO: 1844)
5'-CGG TTT CCT TTG CGG TC-3' (FRAG. NO:1260)(SEQ. ID NO:1270)

5'-TTG GCC CGG GCT CCG GGT G-3' (FRAG. NO:1261)(SEQ. ID NO:1271)
5'-CCC GCC CGC CCG CCG GCC GCC GC-3' (FRAG. NO:1262)(SEQ. ID NO:1272)
5'-CCC GCC GGG CTG TCC CCG CCC CGC CCC-3' (FRAG. NO:1263)(SEQ. ID NO:1273)
5'-GGC CCG GGG CGC GGG GG-3' (FRAG. NO:1264)(SEQ. ID NO:1274)
5'-CGG CCC TCC CGC CCC TCT GG-3' (FRAG. NO:1265)(SEQ. ID NO:1275)
5'-GCC GGC GCG GGC GTC GG-3' (FRAG. NO:1266)(SEQ. ID NO:1276)
5'-CCG CTC GCG CCT GGG GTT CCC TCT CCT CCC CCT GTG C-3' (FRAG. NO:1267)(SEQ. ID NO:1277)
5'-GCC TGC CTC TTG CTC TTC-3' (FRAG. NO:1268)(SEQ. ID NO:1278)
5'-TGC GTC CGC TGC CTT CTC CC-3' (FRAG. NO:1269)(SEQ. ID NO:1279)
5'CTC TCC TCG GCC GTT GCC TGT GC-3' (FRAG. NO:1270)(SEQ. ID NO:1280)
5'-TGT CCG TCC TGT CGC CCT TCC GTG GTG C-3' (FRAG. NO:1271)(SEQ. ID NO:1281)
5'-TGT TGT CTC TTC TGC CCT C-3' (FRAG. NO:1272)(SEQ. ID NO:1282)
5'-GGT GTG CTG GTG CTG GTG GTG GTG-3' (FRAG. NO:1273)(SEQ. ID NO:1283)
5'-CCT CTG CCC GTG CTC GCC-3' (FRAG. NO:1274)(SEQ. ID NO:1284)
5'-CTG CCT GGG CTG GCC TCT TCG GGT-3' (FRAG. NO:1275)(SEQ. ID NO:1285)
5'-GTG GCT TTG GGG CTC TCT TGG TTG CCC TTT-3' (FRAG. NO:1276)(SEQ. ID NO:1286)
5'-CTT CTC GTG GTG CCT CTC CTC CCT GGC TTG GTC GT-3' (FRAG. NO:1277)(SEQ. ID NO:1287)
5'- TGT CTG GGG TGG TGC TCC TCT CCC-3' (FRAG. NO:1278)(SEQ. ID NO:1288)
5'-TTT CCC TGC TGG CCG TTT GT-3' (FRAG. NO:1279)(SEQ. ID NO:1289)
5'-CCT GTT TTC TGT CTT CCT CT-3' (FRAG. NO:1280)(SEQ. ID NO:1290)
5'-TTC CTC CTG TTT CTC CGT-3' (FRAG. NO:1281)(SEQ. ID NO:1291)
5'-TTG GCT TGC TGC TTG CGG GGC TGT CTC C-3' (FRAG. NO:1282)(SEQ. ID NO:1292)
5'-CTT GCC CCT GTG GGC TTT CCC-3' (FRAG. NO:1283)(SEQ. ID NO:1293)
5'-TGG TCC GGT CTT CTC CTT GGG GGT C-3' (FRAG. NO:1284)(SEQ. ID NO:1294)
5'-GCC CTT CTT GGT GGG CTG-3' (FRAG. NO:1285)(SEQ. ID NO:1295)
5'-GCT CGT CTG TCT TTT TCC TTC C-3' (FRAG. NO:1286)(SEQ. ID NO:1296)
5'-TGG GGG TGG CCG TTG TGG GCG GTG TGG TCC GCC T-3' (FRAG. NO:1287)(SEQ. ID NO:1297)
5'-TGC CTC TGC TGG TCT TTC-3' (FRAG. NO:1288)(SEQ. ID NO:1298)

Human Interleukin-1 (IL-1) Nucleic Acid and antisense Oligocnucleotide Fragments

5'-AAGCTTCTAC CCTAGTCTGG TGCTACACTT ACATTGCTTA CATCCAAGTG TGGTTATTTC TGTGGCTCCT GTTATAACTA
TTATAGCACC AGGTCTATGA CCAGGAGAAT TAGACTGGCA TTAAATCAGA ATAAGAGATT TTGCACCTGC AATAGACCTT
ATGACACCTA ACCAACCCCA TTATTTACAA TTAAACAGGA ACAGAGGGAA TACTTTATCC AACTCACACA AGCTGTTTTC
CTCCCAGATC CATGCTTTTT TGCGTTTATT ATTTTTTAGA GATGGGGGCT TCACTATGTT GCCCACACTG GACTAAAACT
CTGGGCCTCA AGTGATTGTC CTGCCTCAGC CTCCTGAATA GCTGGGACTA CAGGGGCATG CCATCACACC TAGTTCATTT
CCTCTATTTA AAATATACAT GGCTTAAACT CCAACTGGGA ACCCAAAACA TTCATTTGCT AAGAGTCTGG TGTTCTACCA
CCTGAACTAG GCTGGCCACA GGAATTATAA AAGCTGAGAA ATTCTTTAAT AATAGTAACC AGGCAACATC ATTGAAGGCT
CATATGTAAA AATCCATGCC TTCCTTTCTC CCAATCTCCA TTCCCAAACT TAGCCACTGG TTCTGGCTGA GGCCTTACGC
ATACCTCCCG GGGCTTGCAC ACACCTTCTT CTACAGAAGA CACACCTTGG GCATATCCTA CAGAAGACCA GGCTTCTCTC
TGGTCCTTGG TAGAGGGCTA CTTTACTGTA ACAGGGCCAG GGTGGAGAGT TCTCTCCTGA AGCTCCATCC CCTCTATAGG
AAATGTGTTG ACAATATTCA GAAGAGTAAG AGGATCAAGA CTTCTTTGTG CTCAAATACC ACTGTTCTCT TCTCTACCCT
GCCCTAACCA GGAGCTTGTC ACCCCAAACT CTGAGGTGAT TTATGCCTTA ATCAAGCAAA CTTCCCTCTT CAGAAAAGAT
GGCTCATTTT CCCTCAAAAG TTGCCAGGAG CTGCCAAGTA TTCTGCCAAT TCACCCTGGA GCACAATCAA CAAATTCAGC
CAGAACACAA CTACAGCTAC TATTAGAACT ATTATTATTA ATAAATTCCT CTCCAAATCT AGCCCCTTGA CTTCGGATTT
CACGATTTCT CCCTTCCTCC TAGAAACTTG ATAAGTTTCC CGCGCTTCCC TTTTTCTAAG ACTACATGTT TGTCATCTTA
TAAAGCAAAG GGGTGAATAA ATGAACCAAA TCAATAACTT CTGGAATATC TGCAAACAAC AATAATATCA GCTATGCCAT
CTTTCACTAT TTTAGCCAGT ATCGAGTTGA ATGAACATAG AAAAATACAA AACTGAATTC TTCCCTGTAA ATTCCCCGTT
TTGACGACGC ACTTGTAGCC ACGTAGCCAC GCCTACTTAA GACAATTACA AAAGGCGAAG AAGACTGACT CAGGCTTAAG
CTGCCAGCCA GAGAGGGAGT CATTTCATTG GCGTTTGAGT CAGCAAAGGT ATTGTCCTCA CATCTCTGGC TATTAAAGTA
TTTTCTGTTG TTGTTTTTCT CTTTGGCTGT TTTCTCTCAC ATTGCCTTCT CTAAAGCTAC AGTCTCTCCT TTCTTTTCTT
GTCCCTCCCT GGTTTGGTAT GTGACCTAGA ATTACAGTCA GATTTCAGAA AATGATTCTC TCATTTTGCT GATAAGGACT
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TGCGGTGAAC CCATCATTAG CTGTGGTGAT CTGCCTGGCA TCGTGCCACA GTAGCCAAAG CCTCTGCACA GGAGTGTGGG
CAACTAAGGC TGCTGACTTT GAAGGACAGC CTCACTCAGG GGGAAGCTAT TTGCTCTCAG CCAGGCCAAG AAAATCCTGT
TTCTTTGGAA TCGGGTAGTA AGAGTGATCC CAGGGCCTCC AATTGACACT GCTGTGACTG AGGAAGATCA AAATGAGTGT
CTCTCTTTGG AGCCACTTTC CCAGCTCAGC CTCTCCTCTC CCAGTTTCTT CCCATGGGCT ACTCTCTGTT CCTGAAACAG
TTCTGGTGCC TGATTTCTGG CAGAAGTACA GCTTCACCTC TTTCCTTTCC TTCCACATTG ATCAAGTTGT TCCGCTCCTG
TGGATGGGCA CATTGCCAGC CAGTGACACA ATGGCTTCCT TCCTTCCTTC CTTCAGCATT TAAAATGTAG ACCCTCTTTC
ATTCTCCGTT CCTACTGCTA TGAGGCTCTG AGAAACCCTC AGGCCTTTGA GGGGAAACCC TAAATCAACA AAATGACCCT
GCTATTGTCT GTGAGAAGTC AAGTTATCCT GTGTCTTAGG CCAAGGAACC TCACTGTGGG TTCCCACAGA GGCTACCAAT
TACATGTATC CTACTCTCGG GGCTAGGGGT TGGGGTGACC CTGCATGCTG TGTCCCTAAC CACAAGACCC CCTTCTTTCT
TCAGTGGTGT TCTCCATGTC CTTTGTACAA GGAGAAGAAA GTAATGACAA AATACCTGTG GCCTTGGGCC TCAAGGAAAA
GAATCTGTAC CTGTCCTGCG TGTTGAAAGA TGATAAGCCC ACTCTACAGC TGGAGGTAAG TGAATGCTAT GGAATGAAGC
CCTTCTCAGC CTCCTGCTAC CACTTATTCC CAGACAATTC ACCTTCTCCC CGCCCCCATC CCTAGGAAAA GCTGGGAACA
GGTCTATTTG ACAAGTTTTG CATTAATGTA AATAAATTTA ACATAATTTT TAACTGCGTG CAACCTTCAA TCCTGCTGCA
GAAAATTAAA TCATTTTGCC GATGTTATTA TGTCCTACCA TAGTTACAAC CCCAACAGAT TATATATTGT TAGGGCTGCT
CTCATTTGAT AGACACCTTG GGAAATAGAT GACTTAAAGG GTCCCATTAT CACGTCCACT CCACTCCCAA AATCACCACC
ACTATCACCT CCAGCTTTCT CAGCAAAAGC TTCATTTCCA AGTTGATGTC ATTCTAGGAC CATAAGGAAA AATACAATAA
AAAGCCCCTG GAAACTAGGT ACTTCAAGAA GCTCTAGCTT AATTTTCACC CCCCCAAAAA AAAAAAATTC TCACCTACAT
TATGCTCCTC AGCATTTGGC ACTAAGTTTT AGAAAAGAAG AAGGGCTCTT TTAATAATCA CACAGAAAGT TGGGGGCCCA
GTTACAACTC AGGAGTCTGG CTCCTGATCA TGTGACCTGC TCGTCAGTTT CCTTTCTGGC CAACCCAAAG AACATCTTTC
CCATAGGCAT CTTTGTCCCT TGCCCCACAA AAATTCTTCT TTCTCTTTCG CTGCAGAGTG TAGATCCCAA AAATTACCCA
AAGAAGAAGA TGGAAAAGCG ATTTGTCTTC AACAAGATAG AAATCAATAA CAAGCTGGAA TTTGAGTCTG CCCAGTTCCC
CAACTGGTAC ATCAGCACCT CTCAAGCAGA AAACATGCCC GTCTTCCTGG GAGGGACCAA AGGCGGCCAG GATATAACTG
ACTTCACCAT GCAATTTGTG TCTTCCTAAA GAGAGCTGTA CCCAGAGAGT CCTGTGCTGA ATGTGGACTC AATCCCTAGG
GCTGGCAGAA AGGGAACAGA AAGGTTTTTG AGTACGGCTA TAGCCTGGAC TTTCCTGTTG TCTACACCAA TGCCCAACTG
CCTGCCTTAG GGTAGTGCTA AGAGGATCTC CTGTCCATCA GCCAGGACAG TCAGCTCTCT CCTTTCAGGG CCAATCCCCA
GCCCTTTTGT TGAGCCAGGC CTCTCTCACC TCTCCTACTC ACTTAAAGCC CGCCTGACAG AAACCACGGC CACATTTGGT
TCTAAGAAAC CCTCTGTCAT TCGCTCCCAC ATTCTGATGA GCAACCGCTT CCCTATTTAT TTATTTATTT GTTTGTTTGT
TTTGATTCAT TGGTCTAATT TATTCAAAGG GGGCAAGAAG TAGCAGTGTC TGTAAAAGAG CCTAGTTTTT AATAGCTATG
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TTTAAATGGG AATATTTATA AATGAGCAAA TATCATACTG TTCAATGGTT CTGAAATAAA CTTCACTGAA GAAAAAAAAA
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CCCACTCCTC ATTGCTGAGT GCTGCAAGTA CCTAGAAATA TCCTTGGCCA CCGAAGACTA TCCTCCTCAC CCATCCCCTT
TATTTCGTTG TTCAACAGAA GGATATTCAG TGCACATCTG GAACAGGATC AGCTGAAGCA CTGCAGGGAG TCAGGACTGG
TAGTAACAGC TACCATGATT TATCTATCAA TGCACCAAAC ATCTGTTGAG CAAGCGCTAT GTACTAGGAG CTGGGAGTAC
AGAGATGAGA ACAGTCACAA GTCCCTCCTC AGATAGGAGA GGCAGCTAGT TATAAGCAGA ACAAGGTAAC ATGACAAGTA
GAGTAAGATA GAAGAACGAA GAGGAGTAGC CAGGAAGGAG GGAGGAGAAC GACATAAGAA TCAAGCCTAA
AGGGATAAAC AGAAGATTTC CACACATGGG CTGGGCCAAT TGGGTGTCGG TTACGCCTGT AATCCCAGCA CTTTGGGTGG
CAGGGGCAGA AAGATCGCTT GAGCCCAGGA GTTCAAGACC AGCCTGGGCA ACATAGTGAG ACTCCCATCT CTACAAAAAA
TAAATAAATA AATAAAACAA TCAGCCAGGC ATGCTGGCAT GCACCTGTAG TCCTAGCTAC TTGGGAAGCT GACACTGGAG

GATTGCTTGA GCCCAGAAGT TCAAGACTGC AGTGAGCTTA TCCGTTGACC TGCAGGTCGA C-3' (FRAG. NO:_)(SEQ. ID NO:2512)

5'-ACAAACCTTT TCGAGGCAAA AGGCAAAAAA GGCTGCTCTG GGATTCTCTT CAGCCAATCT TCAATGCTCA AGTGTCTGAA GCAGCCATGG CAGAAGTACC TAAGCTCGCC AGTGAAATGA TGGCTTATTA CAGTGGCAAT GAGGATGACT TGTTCTTTGA AGCTGATGGC CCTAAACAGA TGAAGTGCTC CTTCCAGGAC CTGGACCTCT GCCCTCTGGA TGGCGGCATC CAGCTACGAA TCTCCGACCA CCACTACAGC AAGGGCTTCA GGCAGGCCGC GTCAGTTGTT GTGGCCATGG ACAAGCTGAG GAAGATGCTG GTTCCCTGCC CACAGACCTT CCAGGAGAAT GACCTGAGCA CCTTCTTTCC CTTCATCTTT GAAGAAGAAC CTATCTTCTT CGACACATGG GATAACGAGG CTTATGTGCA CGATGCACCT GTACGATCAC TGAACTGCAC GCTCCGGGAC TCACAGCAAA AAAGCTTGGT GATGTCTGGT CCATATGAAC TGAAAGCTCT CCACCTCCAG GGACAGGATA TGGAGCAACA AGTGGTGTTC TCCATGTCCT TTGTACAAGG AGAAGAAAGT AATGACAAAA TACCTGTGGC CTTGGGCCTC AAGGAAAAGA ATCTGTACCT GTCCTGCGTG TTGAAAGATG ATAAGCCCAC TCTACAGCTG GAGAGTGTAG ATCCCAAAAA TTACCCAAAG AAGAAGATGG AAAAGCGATT TGTCTTCAAC AAGATAGAAA TCAATAACAA GCTGGAATTT GAGTCTGCCC AGTTCCCCAA CTGGTACATC AGCACCTCTC AAGCAGAAAA CATGCCCGTC TTCCTGGGAG GGACCAAAGG CGGCCAGGAT ATAACTGACT TCACCATGCA ATTTGTGTCT TCCTAAAGAG AGCTGTACCC AGAGAGTCCT GTGCTGAATG TGGACTCAAT CCCTAGGGCT GGCAGAAAGG GAACAGAAAG GTTTTTGAGT ACGGCTATAG CCTGGACTTT CCTGTTGTCT ACACCAATGC CCAACTGCCT GCCTTAGGGT AGTGCTAAGA GGATCTCCTG TCCATCAGCC AGGACAGTCA GCTCTCTCCT TTCAGGGCCA ATCCCAGCCC TTTTGTTGAG CCAGGCCTCT CTCACCTCTC CTACTCACTT AAAGCCCGCC TGACAGAAAC CAGGCCACAT TTTGGTTCTA AGAAACCCTC CTCTGTCATT CGCTCCCACA TTCTGATGAG CAACCGCTTC CCTATTTATT TATTTATTTG TTTGTTTGTT TTGATTCATT GGTCTAATTT ATTCAAAGGG GGCAAGAAGT AGCAGTGTCT GTAAAAGAGC CTAGTTTTTA ATAGCTATGG AATCAATTCA ATTTGGACTG GTGTGCTCTC TTTAAATCAA GTCCTTTAAT TAAGACTGAA AATATATAAG CTCAGATTAT TTAAATGGGA ATATTTATAA ATGAGCAAAT ATCATACTGT TCAATGGTTC TCAAATAAAC TTCACT-3' (FRAG. NO:_)(SEQ. ID NO:2513)

5'-CTGGCAGGAG TAGCAGCTGC CCCTTGGCGC GACTGCTGGA GCCGCGAACT AGAGAAACAC AGACACGCCT CATAGAGCAA CGGCGTCTCT CGGAGCGTGG AGCCCGCCAA GCTCGAGCTG AGCTTTCGCT TGCCGTCCAC CACTGCCCAC ACTGTCGTTT GCTGCCATCG CAGACCTGCT GCTGACTTCC ATCCCTCTGG ATCCGGCAAG GGCCTGCGAT TTTGACAATG TCAAGATTTA CCGTATATCC CTGTTTGTTT GGATACACCA GTGACGTCCA CTTCTAGAAG ACAAAGTTAT ATTACTTAAA CAACCAAAGA TATGAAACTA TCCATGAAGA ACAATATTAT CAATACACAG CAGTCTTTTG TAACCATGCC CAATGTGATT GTACCAGATA TTGAAAAGGA AATACGAAGG ATGGAAAATG GAGCATGCAG CTCCTTTTCT GAGGATGATG ACAGTGCCTC TACATCTGAA GAATCAGAGA ATGAAAACCC TCATGCAAGG GGTTCCTTTA GTTATAAGTC ACTCAGAAAG GGAGGACCAT CACAGAGGGA GCAGTACCTG CCTGGTGCCA TTGCCATTTT TAATGTGAAC AACAGCGACA ATAAGGACCA GGAACCAGAA GAAAAAAAGA AAAAGAAAAA AGAAAAGAAG AGCAAGTCAG ATGATAAAAA CGAAAATAAA AACGACCCAA AGAAGAAGAT GGAAAAGCGA-3' (FRAG. NO:_)(SEQ. ID NO:2514)

5'-ATGGCCAAAG TTCCAGACAT GTTTGAAGAC CTGAAGAACT GTTACAGTGA AAATGAAGAA GACAGTTCCT CCATTGATCA TCTGTCTCTG AATCAGAAAT CCTTCTATCA TGTAAGCTAT GGCCCACTCC ATGAAGGCTG CATGGATCAA TCTGTGTCTC TGAGTATCTC TGAAACCTCT AAAACATCCA AGCTTACCTT CAAGGAGAGC ATGGTGGTAG TAGCAACCAA CGGGAAGGTT CTGAAGAAGA GACGGTTGAG TTTAAGCCAA TCCATCACTG ATGATGACCT GGAGGCCATC GCCAATGACT CAGAGGAAGA AATCATCAAG CCTAGGTCAG CACCTTTTAG CTTCCTGAGC AATGTGAAAT ACAACTTTAT GAGGATCATC AAATACGAAT TCATCCTGAA TGACGCCCTC AATCAAAGTA TAATTCGAGC CAATGATCAG TACCTCACGG CTGCTGCATT ACATAATCTG GATGAAGCAG TGAAATTTGA CATGGGTGCT TATAAGTCAT CAAAGGATGA TGCTAAAATT ACCGTGATTC TAAGAATCTC AAAAACTCAA TTGTATGTGA CTGCCCAAGA TGAAGACCAA CCAGTGCTGC TGAAGGAGAT GCCTGAGATA CCCAAAACCA TCACAGGTAG TGAGACCAAC CTCCTCTTCT TCTGGGAAAC TCACGGCACT AAGAACTATT TCACATCAGT TGCCCATCCA AACTTGTTTA TTGCCACAAA GCAAGACTAC TGGGTGTGCT TGGCAGGGGG GCCACCCTCT ATCACTGACT TTCAGATACT GGAAAACCAG GCGTAGGTCT GGAGTCTCAC TTGTCTCACT TGTGCAGTGT TGACAGTTCA TATGTACCAT GTACATGAAG AAGCTAAATC CTTTACTGTT AGTCATTTGC TGAGCATGTA CTGAGCCTTG TAATTCTAAA TGAATGTTTA CACTCTTTGT AAGAGTGGAA CCAACACTAA CATATAATGT TGTTATTTAA AGAACACCCT ATATTTTGCA TAGTACCAAT CATTTTAATT ATTATTCTTC ATAACAATTT TAGGAGGACC AGAGCTACTG ACTATGGCTA CCAAAAAGAC TCTACCCATA TTACAGATGG GCAAATTAAG GCATAAGAAA ACTAAGAAAT ATGCACAATA GCAGTTGAAA CAAGAAGCCA CAGACCTAGG ATTTCATGAT TTCATTTCAA CTGTTTGCCT TCTGCTTTTA AGTTGCTGAT GAACTCTTAA TCAAATAGCA TAAGTTTCTG GGACCTCAGT TTTATCATTT TCAAAATGGA GGGAATAATA CCTAAGCCTT CCTGCCGCAA CAGTTTTTTA TGCTAATCAG GGAGGTCATT TTGGTAAAAT ACTTCTCGAA GCCGAGCCTC AAGATGAAGG CAAAGCACGA AATGTTATTT TTTAATTATT ATTTATATAT GTATTTATAA ATATATTTAA GATAATTATA ATATACTATA TTTATGGGAA CCCCTTCATC CTCTGAGTGT GACCAGGCAT CCTCCACAAT AGCAGACAGT GTTTTCTGGG ATAAGTAAGT TTGATTTCAT TAATACAGGG CATTTTGGTC CAAGTTGTGC TTATCCCATA GCCAGGAAAC TCTGCATTCT AGTACTTGGG AGACCTGTAA TCATATAATA AATGTACATT AATTACCTTG AGCCAGTAAT TGGTCCGATC TTTGACTCTT TTGCCATTAA ACTTACCTGG GCATTCTTGT TTCATTCAAT TCCACCTGCA ATCAAGTCCT ACAAGCTAAA ATTAGATGAA CTCAACTTTG ACAACCATAG ACCACTGTTA TCAAAACTTT CTTTTCTGGA ATGTAATCAA TGTTTCTTCT AGGTTCTAAA AATTGTGATC AGACCATAAT GTTACATTAT TATCAACAAT AGTGATTGAT AGAGTGTTAT CAGTCATAAC TAAATAAAGC TTGCAAGTGA GGGAGTCATT TCATTGGCGT TTGAGTCAGC AAAGAAGTCA AG-3' (FRAG. NO:_)(SEQ. ID NO:2515)

5'-AGCTGCCAGC CAGAGAGGGA GTCATTTCAT TGGCGTTTGA GTCAGCAAAG AAGTCAAGAT GGCCAAAGTT CCAGACATGT TTGAAGACCT GAAGAACTGT TACAGTGAAA ATGAAGAAGA CAGTTCCTCC ATTGATCATC TGTCTCTGAA TCAGAAATCC TTCTATCATG TAAGCTATGG CCCACTCCAT GAAGGCTGCA TGGATCAATC TGTGTCTCTG AGTATCTCTG AAACCTCTAA AACATCCAAG CTTACCTTCA AGGAGAGCAT GGTGGTAGTA GCAACCAACG GGAAGGTTCT GAAGAAGAGA CGGTTGAGTT TAAGCCAATC CATCACTGAT GATGACCTGG AGGCCATCGC CAATGACTCA GAGGAAGAAA TCATCAAGCC TAGGTCATCA CCTTTTAGCT TCCTGAGCAA TGTGAAATAC AACTTTATGA GGATCATCAA ATACGAATTC ATCCTGAATG

ACGCCCTCAA TCAAAGTATA ATTCGAGCCA ATGATCAGTA CCTCACGGCT GCTGCATTAC ATAATCTGGA TGAAGCAGTG
AAATTTGACA TGGGTGCTTA TAAGTCATCA AAGGATGATG CTAAAATTAC CGTGATTCTA AGAATCTCAA AAACTCAATT
GTATGTGACT GCCCAAGATG AAGACCAACC AGTGCTGCTG AAGGAGATGC CTGAGATACC CAAAACCATC ACAGGTAGTG
AGACCAACCT CCTCTTCTTC TGGGAAACTC ACGGCACTAA GAACTATTTC ACATCAGTTG CCCATCCAAA CTTGTTTATT
GCCACAAAGC AAGACTACTG GGTGTGCTTG GCAGGGGGGC CACCCTCTAT CACTGACTTT CAGATACTGG AAAACCAGGC
GTAGGTCTGG AGTCTCACTT GTCTCACTTG TGCAGTGTTG ACAGTTCATA TGTACCATGT ACATGAAGAA GCTAAATCCT
TTACTGTTAG TCATTTGCTG AGCATGTACT GAGCCTTGTA ATTCTAAATG AATGTTTACA CTCTTTGTAA GAGTGGAACC
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AACAATTTTA GGAGGACCAG AGCTACTGAC TATGGCTACC AAAAAGACTC TACCCATATT ACAGATGGGC AAATTAAGGC
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GTTTGCCTTC TGCTTTTAAG TTGCTGATGA ACTCTTAATC AAATAGCATA AGTTTCTGGG ACCTCAGTTT TATCATTTTC
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TTCTCGAAGC CGAGCCTCAA GATGAAGGCA AAGCACGAAA TGTTATTTTT TAATTATTAT TTATATATGT ATTTATAAAT
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CAGACAGTGT TTTCTGGGAT AAGTAAGTTT GATTTCATTA ATACAGGGCA TTTTGGTCCA AGTTGTGCTT ATCCCATAGC
CAGGAAACTC TGCATTCTAG TACTTGGGAG ACCTGTAATC ATATAATAAA TGTACATTAA TTACCTTGAG CCAGTAATTG
GTCCGATCTT TGACTCTTTT GCCATTAAAC TTACCTGGGC ATTCTTGTTT CATTCAATTC CACCTGCAAT CAAGTCCTAC
AAGCTAAAAT TAGATGAACT CAACTTTGAC AACCATGAGA CCACTGTTAT CAAAACTTTC TTTTCTGGAA TGTAATCAAT
GTTTCTTCTA GGTTCTAAAA ATTGTGATCA GACCATAATG TTACATTATT ATCAACAATA GTGATTGATA GAGTGTTATC
AGTCATAACT AAATAAAGCT TGCAACAAAA TTCTCTG-3' (FRAG. NO:_)(SEQ. ID NO:2516)

Human Interleukin-1 Receptor (IL-1 R) Nucleic Acids and Anti-sense Oligonucleotide Fragments

5'-GCCACGTGCT GCTGGGTCTC AGTCCTCCAC TTCCCGTGTC CTCTGGAAGT TGTCAGGAGC AATGTTGCGC TTGTACGTGT
TGGTAATGGG AGTTTCTGCC TTCACCCTTC AGCCTGCGGC ACACACAGGG GCTGCCAGAA GCTGCCGGTT TCGTGGGAGG
CATTACAAGC GGGAGTTCAG GCTGGAAGGG GAGCCTGTAG CCCTGAGGTG CCCCCAGGTG CCCTACTGGT TGTGGGCCTC
TGTCAGCCCC CGCATCAACC TGACATGGCA TAAAAATGAC TCTGCTAGGA CGGTCCCAGG AGAAGAAGAG ACACGGATGT
GGGCCCAGGA CGGTGCTCTG TGGCTTCTGC CAGCCTTGCA GGAGGACTCT GGCACCTACG TCTGCACTAC TAGAAATGCT
TCTTACTGTG ACAAAATGTC CATTGAGCTC AGAGTTTTTG AGAATACAGA TGCTTTCCTG CCGTTCATCT CATACCCGCA
AATTTTAACC TTGTCAACCT CTGGGGTATT AGTATGCCCT GACCTGAGTG AATTCACCCG TGACAAAACT GACGTGAAGA
TTCAATGGTA CAAGGATTCT CTTCTTTTGG ATAAAGACAA TGAGAAATTT CTAAGTGTGA GGGGGACCAC TCACTTACTC
GTACACGATG TGGCCCTGGA AGATGCTGGC TATTACCGCT GTGTCCTGAC ATTTGCCCAT GAAGGCCAGC AATACAACAT
CACTAGGAGT ATTGAGCTAC GCATCAAGAA AAAAAAAGAA GAGACCATTC CTGTGATCAT TTCCCCCCTC AAGACCATAT
CAGCTTCTCT GGGGTCAAGA CTGACAATCC CGTGTAAGGT GTTTCTGGGA ACCGGCACAC CCTTAACCAC CATGCTGTGG
TGGACGGCCA ATGACACCCA CATAGAGAGC GCCTACCCGG GAGGCCGCGT GACCGAGGGG CCACGCCAGG AATATTCAGA
AAATAATGAG AACTACATTG AAGTGCCATT GATTTTTGAT CCTGTCACAA GAGAGGATTT GCACATGGAT TTTAAATGTG
TTGTCCATAA TACCCTGAGT TTTCAGACAC TACGCACCAC AGTCAAGGAA GCCTCCTCCA CGTTCTCCTG GGGCATTGTG
CTGGCCCCAC TTTCACTGGC CTTCTTGGTT TTGGGGGGAA TATGGATGCA CAGACGGTGC AAACACAGAA CTGGAAAAGC
AGATGGTCTG ACTGTGCTAT GGCCTCATCA TCAAGACTTT CAATCCTATC CCAAGTGAAA TAAATGGAAT GAAATAATTC
AAACACAAAA AAAAAAAAAA AAAAAAAA GCCGGAGCCG ACTCGGAGCG CGCGGCGCGG CCGGGAGGAG CCGAGCGCGC
CGGGCGCGGC GTGGGGGCGC CGGCTGCCCC GCGCGCCCAG GGAGCGGCAG GAATGTGACA ATCGCGCGCC CGCACCGTAG
CACTCCTCGC TCGGCTCCTA GGGCTCTCGC CCTCTGAGCT GAGCCGGGTT CCGCCCGGGC TGGGATCCCA TCACCCTCCA
CGGCCGTCCG TCCAGGTAGA CGCACCCTCT GAAGATGGTG ACTCCCTCCT GAGAAGCTGG ACCCCTTGGT AAAAGACAAG
GCCTTCTCCA AGAAGAATAT GAAAGTGTTA CTCAGACTTA TTTGTTTCAT AGCTCTACTG ATTTCTTCTC TGGAGGCTGA
TAAATGCAAG GAACGTGAAG AAAAAATAAT TTTAGTGTCA TCTGCAAATG AAATTGATGT TCGTCCCTGT CCTCTTAACC
CAAATGAACA CAAAGGCACT ATAACTTGGT ATAAAGATGA CAGCAAGACA CCTGTATCTA CAGAACAAGC CTCCAGGATT
CATCAACACA AAGAGAAACT TTGGTTTGTT CCTGCTAAGG TGGAGGATTC AGGACATTAC TATTGCGTGG TAAGAAATTC
ATCTTACTGC CTCAGAATTA AAATAAGTGC AAAATTTGTG GAGAATGAGC CTAACTTATG TTATAATGCA CAAGCCATAT
TTAAGCAGAA ACTACCCGTT GCAGGAGACG GAGGACTTGT GTGCCCTTAT ATGGAGTTTT TTAAAAATGA AAATAATGAG
TTACCTAAAT TACAGTGGTA TAAGGATTGC AAACCTCTAC TTCTTGACAA TATACACTTT AGTGGAGTCA AAGATAGGCT
CATCGTGATG AATGTGGCTG AAAAGCATAG AGGGAACTAT ACTTGTCATG CATCCTACAC ATACTTGGGC AAGCAATATC
CTATTACCCG GGTAATAGAA TTTATTACTC TAGAGGAAAA CAAACCCACA AGGCCTGTGA TTGTGAGCCC AGCTAATGAG
ACAATGGAAG TAGACTTGGG ATCCCAGATA CAATTGATCT GTAATGTCAC CGGCCAGTTG AGTGACATTG CTTACTGGAA
GTGGAATGGG TCAGTAATTG ATGAAGATGA CCCAGTGCTA GGGGAAGACT ATTACAGTGT GGAAAATCCT GCAAACAAAA
GAAGGAGTAC CCTCATCACA GTGCTTAATA TATCGGAAAT TGAAAGTAGA TTTTATAAAC ATCCATTTAC CTGTTTTGCC
AAGAATACAC ATGGTATAGA TGCAGCATAT ATCCAGTTAA TATATCCAGT CACTAATTTC CAGAAGCACA TGATTGGTAT
ATGTGTCACG TTGACAGTCA TAATTGTGTG TTCTGTTTTC ATCTATAAAA TCTTCAAGAT TGACATTGTG CTTTGGTACA
GGGATTCCTG CTATGATTTT CTCCCAATAA AAGCTTCAGA TGGAAAGACC TATGACGCAT ATATACTGTA TCCAAAGACT
GTTGGGGAAG GGTCTACCTC TGACTGTGAT ATTTTTGTGT TTAAAGTCTT GCCTGAGGTC TTGGAAAAAC AGTGTGGATA
TAAGCTGTTC ATTTATGGAA GGGATGACTA CGTTGGGGAA GACATTGTTG AGGTCATTAA TGAAAACGTA AAGAAAAGCA
GAAGACTGAT TATCATTTTA GTCAGAGAAA CATCAGGCTT CAGCTGGCTG GGTGGTTCAT CTGAAGAGCA AATAGCCATG
TATAATGCTC TTGTTCAGGA TGGAATTAAA GTTGTCCTGC TTGAGCTGGA GAAAATCCAA GACTATGAGA AAATGCCAGA
ATCGATTAAA TTCATTAAGC AGAAACATGG GGCTATCCGC TGGTCAGGGG ACTTTACACA GGGACCACAG TCTGCAAAGA
CAAGGTTCTG GAAGAATGTC AGGTACCACA TGCCAGTCCA GCGACGGTCA CCTTCATCTA AACACCAGTT ACTGTCACCA
GCCACTAAGG AGAAACTGCA AAGAGAGGCT CACGTGCCTC TCGGGTAGCA TGGAGAAGTT GCCAAGAGTT CTTTAGGTGC
CTCCTGTCTT ATGGCGTTGC AGGCCAGGTT ATGCCTCATG CTGACTTGCA GAGTTCATGG AATGTAACTA TATCATCCTT
TATCCCTGAG GTCACCAGGA ATCAGG-3' (FRAG. NO:_)(SEQ. ID NO:2521)

5'-GCCACGTGCT GCTGGGTCTC AGTCCTCCAC TTCCCGTGTC CTCTGGAAGT TGTCAGGAGC AATGTTGCGC TTGTACGTGT TGGTAATGGG AGTTTCTGCC TTCACCCTTC AGCCTGCGGC ACACACAGGG GCTGCCAGAA GCTGCCGGTT TCGTGGGAGG CATTACAAGC GGGAGTTCAG GCTGGAAGGG GAGCCTGTAG CCCTGAGGTG CCCCCAGGTG CCCTACTGGT TGTGGGCCTC TGTCAGCCCC CGCATCAACC TGACATGGCA TAAAAATGAC TCTGCTAGGA CGGTCCCAGG AGAAGAAGAG ACACGGATGT GGGCCCAGGA CGGTGCTCTG TGGCTTCTGC CAGCCTTGCA GGAGGACTCT GGCACCTACG TCTGCACTAC TAGAAATGCT TCTTACTGTG ACAAAATGTC CATTGAGCTC AGAGTTTTTG AGAATACAGA TGCTTTCCTG CCGTTCATCT CATACCCGCA AATTTTAACC TTGTCAACCT CTGGGGTATT AGTATGCCCT GACCTGAGTG AATTCACCCG TGACAAAACT GACGTGAAGA TTCAATGGTA CAAGGATTCT CTTCTTTTGG ATAAAGACAA TGAGAAATTT CTAAGTGTGA GGGGGACCAC TCACTTACTC GTACACGATG TGGCCCTGGA AGATGCTGGC TATTACCGCT GTGTCCTGAC ATTTGCCCAT GAAGGCCAGC AATACAACAT CACTAGGAGT ATTGAGCTAC GCATCAAGAA AAAAAAAGAA GAGACCATTC CTGTGATCAT TTCCCCCCTC AAGACCATAT CAGCTTCTCT GGGGTCAAGA CTGACAATCC CGTGTAAGGT GTTTCTGGGA ACCGGCACAC CCTTAACCAC CATGCTGTGG TGGACGGCCA ATGACACCCA CATAGAGAGC GCCTACCCGG GAGGCCGCGT GACCGAGGGG CCACGCCAGG AATATTCAGA AAATAATGAG AACTACATTG AAGTGCCATT GATTTTTGAT CCTGTCACAA GAGAGGATTT GCACATGGAT TTTAAATGTG TTGTCCATAA TACCCTGAGT TTTCAGACAC TACGCACCAC AGTCAAGGAA GCCTCCTCCA CGTTCTCCTG GGGCATTGTG CTGGCCCCAC TTTCACTGGC CTTCTTGGTT TTGGGGGGAA TATGGATGCA CAGACGGTGC AAACACAGAA CTGGAAAAGC AGATGGTCTG ACTGTGCTAT GGCCTCATCA TCAAGACTTT CAATCCTATC CCAAGTGAAA TAAATGGAAT GAAATAATTC AAACACAAAA AAAAAAAAAA AAAAAAAA-3' (FRAG. NO:_)(SEQ. ID NO:2518)

5'-GCCGGAGCCG ACTCGGAGCG CGCGGCGCGG CCGGGAGGAG CCGAGCGCGC CGGGCGCGGC GTGGGGGCGC CGGCTGCCCC GCGCGCCCAG GGAGCGGCAG GAATGTGACA ATCGCGCGCC CGCACCGTAG CACTCCTCGC TCGGCTCCTA GGGCTCTCGC CCTCTGAGCT GAGCCGGGTT CCGCCCGGGC TGGGATCCCA TCACCCTCCA CGGCCGTCCG TCCAGGTAGA CGCACCCTCT GAAGATGGTG ACTCCCTCCT GAGAAGCTGG ACCCCTTGGT AAAAGACAAG GCCTTCTCCA AGAAGAATAT GAAAGTGTTA CTCAGACTTA TTTGTTTCAT AGCTCTACTG ATTTCTTCTC TGGAGGCTGA TAAATGCAAG GAACGTGAAG AAAAAATAAT TTTAGTGTCA TCTGCAAATG AAATTGATGT TCGTCCCTGT CCTCTTAACC CAAATGAACA CAAAGGCACT ATAACTTGGT ATAAAGATGA CAGCAAGACA CCTGTATCTA CAGAACAAGC CTCCAGGATT CATCAACACA AAGAGAAACT TTGGTTTGTT CCTGCTAAGG TGGAGGATTC AGGACATTAC TATTGCGTGG TAAGAAATTC ATCTTACTGC CTCAGAATTA AAATAAGTGC AAAATTTGTG GAGAATGAGC CTAACTTATG TTATAATGCA CAAGCCATAT TTAAGCAGAA ACTACCCGTT GCAGGAGACG GAGGACTTGT GTGCCCTTAT ATGGAGTTTT TTAAAAATGA AAATAATGAG TTACCTAAAT TACAGTGGTA TAAGGATTGC AAACCTCTAC TTCTTGACAA TATACAGTTT AGTGGAGTCA AAGATAGGCT CATCGTGATG AATGTGGCTG AAAAGCATAG AGGGAACTAT ACTTGTCATG CATCCTACAC ATACTTGGGC AAGCAATATC CTATTACCCG GGTAATAGAA TTTATTACTC TAGAGGAAAA CAAACCCACA AGGCCTGTGA TTGTGAGCCC AGCTAATGAG ACAATGGAAG TAGACTTGGG ATCCCAGATA CAATTGATCT GTAATGTCAC CGGCCAGTTG AGTGACATTG CTTACTGGAA GTGGAATGGG TCAGTAATTG ATGAAGATGA CCCAGTGCTA GGGGAAGACT ATTACAGTGT GGAAAATCCT GCAAACAAAA GAAGGAGTAC CCTCATCACA GTGCTTAATA TATCGGAAAT TGAAAGTAGA TTTTATAAAC ATCCATTTAC CTGTTTTGCC AAGAATACAC ATGGTATAGA TGCAGCATAT ATCCAGTTAA TATATCCAGT CACTAATTTC CAGAAGCACA TGATTGGTAT ATGTGTCACG TTGACAGTCA TAATTGTGTG TTCTGTTTTC ATCTATAAAA TCTTCAAGAT TGACATTGTG CTTTGGTACA GGGATTCCTG CTATGATTTT CTCCCAATAA AAGCTTCAGA TGGAAAGACC TATGACGCAT ATATACTGTA TCCAAAGACT GTTGGGGAAG GGTCTACCTC TGACTGTGAT ATTTTTGTGT TTAAAGTCTT GCCTGAGGTC TTGGAAAAAC AGTGTGGATA TAAGCTGTTC ATTTATGGAA GGGATGACTA CGTTGGGGAA GACATTGTTG AGGTCATTAA TGAAAACGTA AAGAAAAGCA GAAGACTGAT TATCATTTTA GTCAGAGAAA CATCAGGCTT CAGCTGGCTG GGTGGTTCAT CTGAAGAGCA AATAGCCATG TATAATGCTC TTGTTCAGGA TGGAATTAAA GTTGTCCTGC TTGAGCTGGA GAAAATCCAA GACTATGAGA AAATGCCAGA ATCGATTAAA TTCATTAAGC AGAAACATGG GGCTATCCGC TGGTCAGGGG ACTTTACACA GGGACCACAG TCTGCAAAGA CAAGGTTCTG GAAGAATGTC AGGTACCACA TGCCAGTCCA GCGACGGTCA CCTTCATCTA AACACCAGTT ACTGTCACCA GCCACTAAGG AGAAACTGCA AAGAGAGGCT CACGTGCCTC TCGGGTAGCA TGGAGAAGTT GCCAAGAGTT CTTTAGGTGC CTCCTGTCTT ATGGCGTTGC AGGCCAGGTT ATGCCTCATG CTGACTTGCA GAGTTCATGG AATGTAACTA TATCATCCTT TATCCCTGAG GTCACCAGGA ATCAGG-3' (FRAG. NO:_)(SEQ. ID NO:2519)

Human Interleukin-8* Fragments Antisense Oligonucleotide Fragments

5'-GBTGTTTGTT BCCBBBGCBT CBBGBBTBGC TTTGCTBTCT BBGGBTCBCB TTTBGBCBTB GGBBBBCGCT GTBGGTCBGBB BGBTGTGCTT BCCTTCBCBC BGBGCTGCBG BBBTCBGGBBGG CTGCCBBGBGBG CCBCGGCCBGC TTGGBGTCBT GTTTBCBCBC BGTGBGGTGC TCCGGTGGCT TTTTGCTTGT GTGCTCTGCT GTCTCTG TTC CTTCCGGTGG TTTCTTCCTG GCTCTTGTCC TTTCTCTTGG CCCTTGGCCC-3' **(FRAG. NO:1834) (SEQ. ID NO:1845)**

5'-G CTC CGG-3' **(FRAG. NO:1835) (SEQ. ID NO:1846)**

5'-CBBGBBTBGC-3' **(FRAG. NO:1836) (SEQ. ID NO:1847)**

5'-CBCBC BGTGBGGTGC-3' **(FRAG. NO:1837) (SEQ. ID NO:1848)**

5'-BCCBBBGCBT CBBGBBTBGC-3' **(FRAG. NO:1838) (SEQ. ID NO:1849)**

5'-GCCBBGBGBG CCBCGGCCBGC-3' **(FRAG. NO:1839) (SEQ. ID NO:1850)**

5'-GTG CTC CGG TGG CTT TTT-3' **(FRAG. NO:1289)(SEQ. ID NO:1299)**

5'-GCT TGT GTG CTC TGC TGT CTC TG-3' **(FRAG. NO:1290)(SEQ. ID NO:1300)**

5'-TTC CTT CCG GTG GTT TCT TCC TGG CTC TTG TCC T-3' **(FRAG. NO:1291)(SEQ. ID NO:1301)**

5'-TTC TCT TGG CCC TTG GCC C-3' **(FRAG. NO:1292)(SEQ. ID NO:1302)**

5'-GBTGTTTGTT BCCBBBGCBT CBBGBBTBGC TTTGCTBTCT BBGGBTCBCB TTTBGBCBTB GGBBBBCGCT GTBGGTCBGBB BGBTGTGCTT BCCTTCBCBC BGBGCTGCBG BBBTCBGGBBGG CTGCCBBGBGBG CCBCGGCCBGC TTGGBGTCBT GTTTBCBCBC BGTGBGGTGC TCCGGTGGCT TTTTGCTTGT-3' **(FRAG. NO:1840) (SEQ. ID NO:1851)**

Human IL-8 Receptor Alpha Antisense Oligonucleotide Fragments

5'-ACAGGGGCTG TAATCTTCATC TGCAGGTGGC ATGCCAGTGA AATTTAGATC ATCAAAATCC CACATCTGTG GATCTGTAAT ATTTGACATG TCCTCTTCAG TTTCAGCAAT GGTTTGATCT AACTGAAGCA CCGGCCAGGB CBGGGGCTGT BBTCTTCBTC TGCBGGTGGC BTGCCBGTGB BBTTTBGBTC BTCBBBBTCC CBCBTCTGTG GBTCTGTBBT BTTTGBCBTG TCCTCTTCBG TTTCBGCBB TGGTTTGBTC TBBCTGBBGC BCCGGCCBGG TGGCTCGGTG CTTCTGCCCC TGTTGTTGCG GCGCTCGGTT GGTGTGGCCC CTGTGGTGCT TCGTTTCCCC CTCTTTCTCT TTGTTCGGGG GTTCTTGTGG CGGGCTGCTT GTCTCGTTCC-3'

(FRAG. NO:1841) (SEQ. ID NO:1852)
5'-CBGGGGC-3' (FRAG. NO:1842) (SEQ. ID NO:1853)
5'-GCBGGTGGC-3' (FRAG. NO:1843) (SEQ. ID NO:1854)
5'-GCGGCGCTC-3' (FRAG. NO:1844) (SEQ. ID NO:1855)
5'-TGGCTCGGTGCTTCTGCCCC (FRAG. NO:1293)(SEQ. ID NO:1303)
5'-TGTTGTTGCGGCGCTC (FRAG. NO:1294)(SEQ. ID NO:1304)
5'-GGTTGGTGTGGCCCCTG (FRAG. NO:1295)(SEQ. ID NO:1305)
5'-TGGTGCTTCGTTTCC (FRAG. NO:1296)(SEQ. ID NO:1306)
5'-CCCTCTTTCTCTTTGTTC (FRAG. NO:1297)(SEQ. ID NO:1307)
5'-GGGGGTTCTTGTGGC (FRAG. NO:1298)(SEQ. ID NO:1308)
5'-GGGCTGCTTGTCTCGTTCC (FRAG. NO:1299)(SEQ. ID NO:1309)
5'-ACAGGGGCTG TAATCTTCATC TGCAGGTGGC ATGCCAGTGA AATTTAGATC ATCAAAATCC CACATCTGTG GATCTGTAAT ATTTGACATG TCCTCTTCAG TTTCAGCAAT GGTTTGATCT AACTGAAGCA CCGGCCAGG-3' (FRAG. NO:1845) (SEQ. ID NO:1856)
5'-B CBGGGGCTGT BBTCTTCBTC TGCBGGTGGC BTGCCBGTGB BBTTTBGBTC BTCBBBBTCC CBCBTCTGTG GBTCTGTBBT BTTTGBCBTG TCCTCTTCBG TTTCBGCBB TGGTTTGBTC TBBCTGBBGC BCCGGCCBGG-3' (FRAG. NO:1846) (SEQ. ID NO:1857)

Interleukin-11 (IL-11) Nucleic Acid and Antisnese Oligonucleotide Fragments

5'-GCTCAGGGCA CATGCCTCCC CTCCCCAGGC CGCGGCCCAG CTGACCCTCG GGGCTCCCCC GGCAGCGGAC AGGGAAGGGT TAAAGGCCCC CGGCTCCCTG CCCCCTGCCC TGGGGAACCC CTGGCCCTGT GGGGACATGA ACTGTGTTTG CCGCCTGGTC CTGGTCGTGC TGAGCCTGTG GCCAGATACA GCTGTCGCCC CTGGGCCACC ACCTGGCCCC CCTCGAGTTT CCCCAGACCC TCGGGCCGAG CTGGACAGCA CCGTGCTCCT GACCCGCTCT CTCCTGGCGG ACACGCGGCA GCTGGCTGCA CAGCTGAGGG ACAAATTCCC AGCTGACGGG GACCACAACC TGGATTCCCT GCCCACCCTG GCCATGAGTG CGGGGGCACT GGGAGCTCTA CAGCTCCCAG GTGTGCTGAC AAGGCTGCGA GCGGACCTAC TGTCCTACCT GCGGCACGTG CAGTGGCTGC GCCGGGCAGG TGGCTCTTCC CTGAAGACCC TGGAGCCCGA GCTGGGCACC CTGCAGGCCC GACTGGACCG GCTGCTGCGC CGGCTGCAGC TCCTGATGTC CCGCCTGGCC CTGCCCCAGC CACCCCCGGA CCCGCCGGCG CCCCCGCTGG CGCCCCCCTC CTCAGCCTGG GGGGGCATCA GGGCCGCCCA CGCCATCCTG GGGGGGCTGC ACCTGACACT TGACTGGGCC GTGAGGGGAC TGCTGCTGCT GAAGACTCGG CTGTGACCCG GGGCCCAAAG CCACCACCGT CCTTCCAAAG CCAGATCTTA TTTATTTATT TATTTCAGTA CTGGGGGCGA AACAGCCAGG TGATCCCCCC GCCATTATCT CCCCCTAGTT AGAGACAGTC CTTCCGTGAG GCCTGGGGGA CATCTGTGCC TTATTTATAC TTATTTATTT CAGGAGCAGG GGTGGGAGGC AGGTGGACTC CTGGGTCCCC GAGGAGGAGG GGACTGGGGT CCCGGATTCT TGGGTCTCCA AGAAGTCTGT CCACAGACTT CTGCCCTGGC TCTTCCCCAT CTAGGCCTGG GCAGGAACAT ATATTATTTA TTTAAGCAAT TACTTTTCAT GTTGGGGTGG GGACGGAGGG GAAAGGGAAG CCTGGGTTTT TGTACAAAAA TGTGAGAAAC CTTTGTGAGA CAGAGAACAG GGAATTAAAT GTGTCATACA TATCC
CAGCTGCGGC ATCCTCTGTC TCAGAGTCTT GGTGTCTCTG TTCCTTTCCC CTCGGGGTCT CCCTGGGTCT CCCCAAGTCC CTCCTGCTGT CTTCCTCCCG CTCTCTGATC TCTGACTCCC AGAACCTCTC CCTCTGTCTC CAGGGCTGCC CCTCTGATCC TCTTTGCTTC TCTGGTGTGT CTCTCTGGCT GCCTCCATCT CTGTGGATCT CCGTCTCCCT GTCTCTGTCT CAGTCTGTCC TTCACTCTGT GTGTGTGTGT GTCTCTCTCT CTCTCTCTCC TTCCCTTCCA CTCCCTCTTC CTCCTGCCTC CACCTCTCCA GGCCCCTGTC TTGTCCCTCC GTCCGGCCTT TCTCTGCCTT TCCGTCCTCC TGCCTCCCCA TCTCTCTCTG CTAGTCCTGT CCAGCCGGAC CCCCACCCAC AGTCGGGCCC CAGCGCTTGA GCCTGAGTGT CTGCTCCGGC CCGTGGAGGT GGAGGGAGGG GACGCCAATG ACCTCACCAG CCCCTCTCCG ACCACCCCCC CCTTTCCCTT TTCAACTTTT CCAACTTTTC CTTCCGTGCC CTCCTCCGAG CGCGGCGGCG TGAGCCCTGC AAGGCAGCCG CTCCGTCTGA ATGGAAAAGG CAGGCAGGGA GGGTGAGTCA GGATGTGTCA GGCCGGCCCT CCCCTGCCGC CTGCCCCCCG CCCGCCCGCC CCAGGCCCCC TATATAACCC CCCAGGCGTC CACACTCCCT CACTGCCGCG GGCCCTGCTG CTCAGGGCAC ATGCCTCCCC TCCCCAGCCG CGGGCCCAGC TGACCCTCGG GGCTCCCCCG GCAGCGGACA GGGAAGGGTT AAAGGCCCCC GGCTCCCTGC CCCCTGCCCT GGGGAACCCC TGGCCCTGTG GGGACATGAA CTGTAAGTTG GTTCATGGGG AGGGTGGAGG GGACAGGGAG GCAGGGAGGA GAGGGACCCA CGGCGGGGGT GGGAGCAGAC CCCGCTGAGT CGCACAGAGA GGGACCCGGA GACAGGCAGC CGGGGAGGAG AGCAGCTTCG GAGACAGGAG GCGGCGGAGG AGATGGGCAG AGAGAGACAC AGACAGGAGC GGATGGAGGC AGCCAATCAG AGGCGCCGCA GGAGGGACGG GCCAGACAGG GCCCGAGAGG AGCGAGACGC GAGACCGAGC AGGGGCAGGG ACGCAGGGAC TGGTGCCGGG AGGGAGGTGA CCCCCATCGA CCCAGGCCCC AGGGAGCCCG CGGGGACCGG GAGACTCCCT GGGATTCCGG CAGAGAGGCT CCGGAGGGAA ACTGAGGCAG GGTCCGCGGA GAGCGGAGCA AGCCAGGGAG TAGCGACCCC AGCCGGGGGG AGGAGAGAGA CTGGGCGCCG GGGGAAAGCG GGAGAGCCCG GGCAGATGCG GCCGACGGAG GCGCGGACAG ACCGACGGCT GGCGGGCCCG GGGGGCGGGC TGGGGGTGTG CGAGGCGCGG GCGGCCGGGG AGCGCTGATT GGCTGGCGGG TGGCCGGGTG GGCGGGGCGG CCGGGGTGGG CTGCGGGGAG CGAGCTCCGG ACCCCCGCGC CCCCGGCGCC CCCCGCGCCC CCCGCCGCCA GCTCTCCCGC TCCCGGCGCC CGGCCGGGCC ATGGCTCTGC CCCTCTCCGC CCAGGTGCGC TGCGGCCCGG GCTTCTGCCG CCCACCCGGC GGGCTCCTGG GAGGGCGTCT AAGGGGTCTC CCGTGGGAGA GGTCCGTGTC TCCCGGACTC CGTCCTGGGC TTTTGGCTCC TTCCCCTGCT CCCAGCCAGC TCGGGCTCCC GCGGCCCGGG GAGGGGGCAG GTTCTGGCCT GTGCCTCCCC CACCATCCGC GCCCCGGGGC CCAGATTCCG GCGTCCGGGG GCGGACGGGA GACGCCCGGG CCGCGTCTGC TCCGACGGGC GGGGCAGCCA GAGCCAGGGA GGGAGAGGGA AGCCCGCCTG GCCCTGCGAC CTGCCCGCGG GCGTTCCACC CTGGGACTTA AGACCTCCAG CTCCATCCTC CCTAAGGCCG GGAGTCCAGG CCCCAGACCC TCCTCCCCGA GACCCAGGAG TCCAGACCCC AGGCCTTCCT CCCTCAGACC TAGGAGTCCA GGCCCCCAGC

CTCTCCTCCC TCAGACCCAG GAGGAGTCCA GACCCCAGTT CCTCCTCCCT CAGACCCGGG AGTCCAGCCC AGGCCCTCCT
CTCTCAGACC CGGAGTCCAG CCTGAGCTCT CTGCCTTATC CTGCCCCCAG GTGTTTGCCG CCTGGTCCTG GTCGTGCTGA
GCCTGTGGCC AGATACAGCT GTCGCCCCTG GGCCACCACC TGGCCCCCCT CGAGTTTCCC CAGACCCTCG GGCCGAGCTG
GACAGCACCG TGCTCCTGAC CCGCTCTCTC CTGGCGGACA CGCGGCAGCT GGCTGCACAG CTGGTAGGAG AGACTGGGCT
GGGGCCAGCA CAGGAGTGAG AGGCAGAGAG GAACGGAGAG GAGTCTGCGG GCAGCCACTT GGAGGGGTTC TGGGCTCTCA
GGTGGCAGAG TGAGGGAGGG GAAGAGTTGG GGGCCTGGCG TGGGGGATGG AGGGAGCCCC GAGGCTGGGC
AGGGGCCACC TCACAGCTTT TTTCCCTGCC AGAGGGACAA ATTCCCAGCT GACGGGGACC ACAACCTGGA TTCCCTGCCC
ACCCTGGCCA TGAGTGCAGG GGCACTGGGA GCTCTACAGG TAAGGGCAAG GGAGTGGGCT GGGGACAAGG TGGGAGGCAG
GCAGTGAAGG GGGCGGGGAG GATGAGGGGC ACTGGTCGGG TGTTCTCTGA TGTCCCGGCT CTATCCCCAG CTCCCAGGTG
TGCTGACAAG GCTGCGAGCG GACCTACTGT CCTACCTGCG GCACGTGCAG TGGCTGCGCC GGGCAGGTGG CTCTTCCCTG
AAGACCCTGG AGCCCGAGCT GGGCACCCTG CAGGCCCGAC TGGACCGGCT GCTGCGCCGG CTGCAGCTCC TGGTATGTCC
TGGCCCCAAG ACCTGACACC CCAGACCCCC ACCCCTGGCC CCAAAATCCT GTGGCCTGAG TCCTTGAAGC CTGAGACCCC
AGACCCGAGT GCAACAGCCC CGCTCTGAGA CCCTGACACC CTAACAGCCC GCTCTGAGAC CCTGACACCG TAACAGCCCC
GCTCTGAGAC CCTGACCCTA ACAGTCCTGC TCTGAGACCC TGACCCTGCA GTCCCAAGAT CCTGTGGCCC TGAGACCCTG
AGGCCCTAGA CCCCCAAATC CTGCCCAGAA ACTTCAAATT CTCACCCAAG ACCCTGAGAC TCCATCATCC ATGACCTCAA
AGTCCCCAGA TCCCAGCCCC TAAGACCCAA GACCCCATCC TGAAGCCCAA AGCCTTGAGA ATTCAAATCC TCACCTCAAG
ACTTGGAGAC CCTGGCCCCA TGACATTGAA AACCATGGAC CTGGCCAGGC GTGGTGGCTC ACGCCTGTAA TCCCAGCACT
TTGGGAGGCC GAGGCAAGTG GATCACCTGA GGTCGGGAGT TCAAGACCAG CCAGACCAAC ATGGTGAAAC CCTGTCTCTA
CTAAAAATAC AAAATTAGCC AGGCGTGGTG GTGCATGCCT GTAATCCCAG CTACTTGGGA GGCTGAGGCA GGAGAATCGC
TTGAACCTGG GAGGCGGAGG TTGCAGTGAG CCGAGATCGC ACCATTACAC TCCAGCCTGG GCAACAAGAG CAAAACTCCC
TCTCTCTCAA AAAAAAAAAA AAAAAAAAAA AAGAAGGAAA AGAAAACCAT GGACCTCCAG ACCCTGAGAC CCCAGGCCCC
AGCCCTGAGA TCCTGACATC TTAAAGATCC CAGGCCCTAA GATACAAGAC CTTGACCCAA AGCCAGCCTT GGGACCCTGG
CTGTACAAAC CCAAGACCTC CAGGACCTAG ACCCCGAGCC CTGAGGCCCT ATGTCTCACT CCCAACATCG AAAACCCTGA
CACCTCAGAT CCTGAGCCTG CGCCTGTACG ACTCCAAGAC CCTCACTTCC AAAGCCAGGC CCAAAGCCCT GAGACCAGAA
GACTTCAAAC CCTGGTTCTT GGGCCTAACT CCAAAGACCC TGGATCTCAA ATTCCAACTT CTAGCTCTGA GACTCCAGCC
CTCACCCATG AGTTCCTGAA CTTGAACCCA GAGACCCCAT CTCTAAGACT TCAGCCTTGA GATCCAGGGC CTGACCCTAG
ACTCGAGCCC ACAGACCTCA GATACTGTCT GTAAAACCCC AGCTCTGGTG GGGAGCAGTG GCTCACTCCT GTAATCCCAA
GGCAGGGGAG GCCAAGGCAG AAGGACCTCT TGAGGCCATG AGTTTGAGAC AGCCTGGGCA GCATAGCAAG ACTCTGTTTC
TTAATTATTA TTATTATTAT TATTTTTTGG AGACAGAGTC TCGCGCTCTG TTGCCCAGGC TAGAGTGCAA TGGTGCCATT
TCGGCTTGCT GGAACCTCCG CCTCCTGGGC TCAAGCGATT CTCCTGCCTC AGCCTCCTGA GTAGCTGGGA CTTCAGGTGC
ACACTGCCAC ACCCGGATAA TTTTTTTGTA TTTTAGTAGA CACAGGGTTT CACCGTGTTG CCCAGGCTGG TCACAAACTC
CTGAGCTCAG GCCATCCGCC CGCCTCGGCC TCCCAAAGCG CTGGGATAAC AGGCGTGACG CCGCGCCTGG CTTCTTAATT
GTTCTAACAG CAGCGACAAC AACAAAAACC CAGCTCTGAG ATTCCAGCCC CGGCGACTCT AACAGTCCCA GGCCCGATCC
CTCACCTAGA ACCGAGATGC CAGCCCTGAC TCCACAGACT TCACCCCCAA CCCCCACACT CAGCTCTGGA AGCCCGTCCT
GACTCCAGCC TCCATTTTCG GAACCCCACA GCCTGAAGAG CTCCCGGCCT AAACACTTCA CCCCACGCGC CACAGTCCCC
CTGTGAATAT GCAGCCCCGA TTCAGCTGCA GCTCCACAGC ACCCCTGCCC TGCACCCCCG CTGCACCCCC TACCTGTGAC
TCACCTCTCT CCTCTCCCCA CAGATGTCCC GCCTGGCCCT GCCCCAGCCA CCCCCGGACC CGCCGGCGCC CCCGCTGGCG
CCCCCCTCCT CAGCCTGGGG GGGCATCAGG GCCGCCCACG CCATCCTGGG GGGGCTGCAC CTGACACTTG ACTGGGCCGT
GAGGGGACTG CTGCTGCTGA AGACTCGGCT GTGACCCGGG GCCCAAAGCC ACCACCGTCC TTCCAAAGCC AGATCTTATT
TATTTATTTA TTTCAGTACT GGGGGCGAAA CAGCCAGGTG ATCCCCCCGC CATTATCTCC CCCTAGTTAG AGACAGTCCT
TCCGTGAGGC CTGGGGGGCA TCTGTGCCTT ATTTATACTT ATTTATTTCA GGAGCAGGGG TGGGAGGCAG GTGGACTCCT
GGGTCCCCGA GGAGGAGGGG ACTGGGGTCC CGGATTCTTG GGTCTCCAAG AAGTCTGTCC ACAGACTTCT GCCCTGGCTC
TTCCCCATCT AGGCCTGGGC AGGAACATAT ATTATTTATT TAAGCAATTA CTTTTCATGT TGGGGTGGGG ACGGAGGGGA
AAGGGAAGCC TGGGTTTTTG TACAAAAATG TGAGAAACCT TTGTGAGACA GAGAACAGGG AATTAAATGT GTCATACATA
TCCACTTGAG GGCGATTTGT CTGAGAGCTG GGGCTGGATG CTTGGGTAAC TGGGGCAGGG CAGGTGGAGG GGAGACCTCC
ATTCAGGTGG AGGTCCCGAG TGGGCGGGGC AGCGACTGGG AGATGGGTCG GTCACCCAGA CAGCTCTGTG GAGGCAGGGT
CTGAGCCTTG CCTGGGGCCC CGCACTGCAT AGGGCCGTTT GTTTGTTTTT TGAGATGGAG TCTCGCTCTG TTGCCTAGGC
TGGAGTGCAG TGAGGCAATC TAAGGTCACT GCAACCTCCA CCTCCCGGGT TCAAGCAATT CTCCTGCCTC AGCCTCCCGA
TTAGCTGGGA TCACAGGTGT GCACCACCAT GCCCAGCTAA TTATTTATTT CTTTTGTATT TTTAGTAGAG ACAGGGTTTC
ACCATGTTGG CCAGGCTGGT TTCGAACTCC TGACCTCAGG TGATCCTCCT GCCTCGGCCT CCCAAAGTGC TGGGATTACA
GGTGTGAGCC ACCACACCTG ACCCATAGGT CTTCAATAAA TATTTAATGG AAGGTTCCAC AAGTCACCCT GTGATCAACA
GTACCCGTAT GGGACAAAGC TGCAAGGTCA AGATGGTTCA TTATGGCTGT GTTCACCATA GCAAACTGGA AACAATCTAG
ATATCCAACA GTGAGGGTTA AGCAACATGG TGCATCTGTG GATAGAACGC CACCCAGCCG CCCGGAGCAG GGACTGTCAT
TCAGGGAGGC TAAGGAGAGA GGCTTGCTTG GGATATAGAA AGATATCCTG ACATTGGCCA GGCATGGTGG CTCACGCCTG
TAATCCTGGC ACTTTGGGAG GACGAAGCGA GTGGATCACT GAAGTCCAAG AGTTTGAGAC CGGCCTGCGA GACATGGCAA
AACCCTGTCT CAAAAAAGAA AGAATGATGT CCTGACATGA AACAGCAGGC TACAAAACCA CTGCATGCTG TGATCCCAAT
TTTGTGTTTT TCTTTCTATA TATGGATTAA AACAAAAATC CTAAAGGGAA ATACGCCAAA ATGTTGACAA TGACTGTCTC
CAGGTCAAAG GAGAGAGGTG GGATTGTGGG TGACTTTTAA TGTGTATGAT TGTCTGTATT TTACAGAATT TCTGCCATGA
CTGTGTATTT TGCATGACAC ATTTTAAAAA TAATAAACAC TATTTTTAGA ATAACAGAAT ATCAGCCTCC TCCTCTCCAA

AAATAAGCCC TCAGGAGGGG ACAAAGTTGA CCGCTGATTG AGCCTGTCAG GGCTGTGCAC-3' (FRAG. NO:_)(SEQ. ID NO:2523)

5'-GCTCAGGGCA CATGCCTCCC CTCCCCAGGC CGCGGCCCAG CTGACCCTCG GGGCTCCCCC GGCAGCGGAC AGGGAAGGGT TAAAGGCCCC CGGCTCCCTG CCCCCTGCCC TGGGGAACCC CTGGCCCTGT GGGGACATGA ACTGTGTTTG CCGCCTGGTC CTGGTCGTGC TGAGCCTGTG GCCAGATACA GCTGTCGCCC CTGGGCCACC ACCTGGCCCC CCTCGAGTTT CCCCAGACCC TCGGGCCGAG CTGGACAGCA CCGTGCTCCT GACCCGCTCT CTCCTGGCGG ACACGCGGCA GCTGGCTGCA CAGCTGAGGG ACAAATTCCC AGCTGACGGG GACCACAACC TGGATTCCCT GCCCACCCTG GCCATGAGTG CGGGGGCACT GGGAGCTCTA CAGCTCCCAG GTGTGCTGAC AAGGCTGCGA GCGGACCTAC TGTCCTACCT GCGGCACGTG CAGTGGCTGC GCCGGGCAGG TGGCTCTTCC CTGAAGACCC TGGAGCCCGA GCTGGGCACC CTGCAGGCCC GACTGGACCG GCTGCTGCGC CGGCTGCAGC TCCTGATGTC CCGCCTGGCC CTGCCCCAGC CACCCCCGGA CCCGCCGGCG CCCCCGCTGG CGCCCCCCTC CTCAGCCTGG GGGGGCATCA GGGCCGCCCA CGCCATCCTG GGGGGGCTGC ACCTGACACT TGACTGGGCC GTGAGGGGAC TGCTGCTGCT GAAGACTCGG CTGTGACCCG GGGCCCAAAG CCACCACCGT CCTTCCAAAG CCAGATCTTA TTTATTTATT TATTTCAGTA CTGGGGGCGA AACAGCCAGG TGATCCCCCC GCCATTATCT CCCCCTAGTT AGAGACAGTC CTTCCGTGAG GCCTGGGGGA CATCTGTGCC TTATTTATAC TTATTTATTT CAGGAGCAGG GGTGGGAGGC AGGTGGACTC CTGGGTCCCC GAGGAGGAGG GGACTGGGGT CCCGGATTCT TGGGTCTCCA AGAAGTCTGT CCACAGACTT CTGCCCTGGC TCTTCCCCAT CTAGGCCTGG GCAGGAACAT ATATTATTTA TTTAAGCAAT TACTTTTCAT GTTGGGGTGG GGACGGAGGG GAAAGGGAAG CCTGGGTTTT TGTACAAAAA TGTGAGAAAC CTTTGTGAGA CAGAGAACAG GGAATTAAAT GTGTCATACA TATCC-3' (FRAG. NO:_)(SEQ. ID NO:2521)

5'-CAGCTGCGGC ATCCTCTGTC TCAGAGTCTT GGTGTCTCTG TTCCTTTCCC CTCGGGGTCT CCCTGGGTCT CCCCAAGTCC CTCCTGCTGT CTTCCTCCCG CTCTCTGATC TCTGACTCCC AGAACCTCTC CCTCTGTCTC CAGGGCTGCC CCTCTGATCC TCTTTGCTTC TCTGGTGTGT CTCTCTGGCT GCCTCCATCT CTGTGGATCT CCGTCTCCCT GTCTCTGTCT CAGTCTGTCC TTCACTCTGT GTGTGTGTGT GTCTCTCTCT CTCTCTCTCC TTCCCTTCCA CTCCCTCTTC CTCCTGCCTC CACCTCTCCA GGCCCCTGTC TTGTCCCTCC GTCCGGCCTT TCTCTGCCTT TCCGTCCTCC TGCCTCCCCA TCTCTCTCTG CTAGTCCTGT CCAGCCGGAC CCCCACCCAC AGTCGGGCCC CAGCGCTTGA GCCTGAGTGT CTGCTCCGGC CCGTGGAGGT GGAGGGAGGG GACGCCAATG ACCTCACCAG CCCCTCTCCG ACCACCCCCC CCTTTCCCTT TTCAACTTTT CCAACTTTTC CTTCCGTGCC CTCCTCCGAG CGCGGCGGCG TGAGCCCTGC AAGGCAGCCG CTCCGTCTGA ATGGAAAAGG CAGGCAGGGA GGGTGAGTCA GGATGTGTCA GGCCGGCCCT CCCCTGCCGC CTGCCCCCCG CCCGCCCGCC CCAGGCCCCC TATATAACCC CCCAGGCGTC CACACTCCCT CACTGCCGCG GGCCCTGCTG CTCAGGGCAC ATGCCTCCCC TCCCCAGCCG CGGGCCCAGC TGACCCTCGG GGCTCCCCCG GCAGCGGACA GGGAAGGGTT AAAGGCCCCC GGCTCCCTGC CCCCTGCCCT GGGGAACCCC TGGCCCTGTG GGGACATGAA CTGTAAGTTG GTTCATGGGG AGGGTGGAGG GGACAGGGAG GCAGGGAGGA GAGGGACCCA CGGCGGGGGT GGGAGCAGAC CCCGCTGAGT CGCACAGAGA GGGACCCGGA GACAGGCAGC CGGGGAGGAG AGCAGCTTCG GAGACAGGAG GCGGCGGAGG AGATGGGCAG AGAGAGACAC AGACAGGAGC GGATGGAGGC AGCCAATCAG AGGCGCCGCA GGAGGGACGG GCCAGACAGG GCCCGAGAGG AGCGAGACGC GAGACCGAGC AGGGGCAGGG ACGCAGGGAC TGGTGCCGGG AGGGAGGTGA CCCCCATCGA CCCAGGCCCC AGGGAGCCCG CGGGGACCGG GAGACTCCCT GGGATTCCGG CAGAGAGGCT CCGGAGGGAA ACTGAGGCAG GGTCCGCGGA GAGCGGAGCA AGCCAGGGAG TAGCGACCCC AGCCGGGGGG AGGAGAGAGA CTGGGCGCCG GGGGAAAGCG GGGAGAGCCG GGCAGATGCG GCCGACGGAG GCGCGGACAG ACCGACGGCT GGCGGGCCCG GGGGGCGGGC TGGGGGTGTG CGAGGCGCGG GCGGCCGGGG AGCGCTGATT GGCTGGCGGG TGGCCGGGTG GGCGGGGCGG CCGGGGTGGG CTGCGGGGAG CGAGCTCCGG ACCCCCGCGC CCCCGGCGCC CCCCGCGCCC CCCGCCGCCA GCTCTCCCGC TCCCGGCGCC CGGCCGGGCC ATGGCTCTGC CCCTCTCCGC CCAGGTGCGC TGCGGCCCGG GCTTCTGCCG CCCACCCGGC GGGCTCCTGG GAGGGCGTCT AAGGGGTCTC CCGTGGGAGA GGTCCGTGTC TCCCGGACTC CGTCCTGGGC TTTTGGCTCC TTCCCCTGCT CCCAGCCAGC TCGGGCTCCC GCGGCCCGGG GAGGGGGCAG GTTCTGGCCT GTGCCTCCCC CACCATCCGC GCCCCGGGGC CCAGATTCCG GCGTCCGGGG GCGGACGGGA GACGCCCGGG CCGCGTCTGC TCCGACGGGC GGGGCAGCCA GAGCCAGGGA GGGAGAGGGA AGCCCGCCTG GCCCTGCGAC CTGCCCGCGG GCGTTCCACC CTGGGACTTA AGACCTCCAG CTCCATCCTC CCTAAGGCCG GGAGTCCAGG CCCCAGACCC TCCTCCCCGA GACCCAGGAG TCCAGACCCC AGGCCTTCCT CCCTCAGACC TAGGAGTCCA GGCCCCCAGC CTCTCCTCCC TCAGACCCAG GAGGAGTCCA GACCCCAGTT CCTCCTCCCT CAGACCCGGG AGTCCAGCCC AGGCCCTCCT CTCTCAGACC CGGAGTCCAG CCTGAGCTCT CTGCCTTATC CTGCCCCCAG GTGTTTGCCG CCTGGTCCTG GTCGTGCTGA GCCTGTGGCC AGATACAGCT GTCGCCCCTG GGCCACCACC TGGCCCCCCT CGAGTTTCCC CAGACCCTCG GGCCGAGCTG GACAGCACCG TGCTCCTGAC CCGCTCTCTC CTGGCGGACA CGCGGCAGCT GGCTGCACAG CTGGTAGGAG AGACTGGGCT GGGGCCAGCA CAGGAGTGAG AGGCAGAGAG GAACGGAGAG GAGTCTGCGG GCAGCCACTT GGAGGGGTTC TGGGCTCTCA GGTGGCAGAG TGAGGGAGGG GAAGAGTTGG GGGCCTGGCG TGGGGGATGG AGGGAGCCCC GAGGCTGGGC AGGGGCCACC TCACAGCTTT TTTCCCTGCC AGAGGGACAA ATTCCCAGCT GACGGGGACC ACAACCTGGA TTCCCTGCCC ACCCTGGCCA TGAGTGCAGG GGCACTGGGA GCTCTACAGG TAAGGGCAAG GGAGTGGGCT GGGGACAAGG TGGGAGGCAG GCAGTGAAGG GGGCGGGGAG GATGAGGGGC ACTGGTCGGG TGTTCTCTGA TGTCCCGGCT CTATCCCCAG CTCCCAGGTG TGCTGACAAG GCTGCGAGCG GACCTACTGT CCTACCTGCG GCACGTGCAG TGGCTGCGCC GGGCAGGTGG CTCTTCCCTG AAGACCCTGG AGCCCGAGCT GGGCACCCTG CAGGCCCGAC TGGACCGGCT GCTGCGCCGG CTGCAGCTCC TGGTATGTCC TGGCCCCAAG ACCTGACACC CCAGACCCCC ACCCCTGGCC CCAAAATCCT GTGGCCTGAG TCCTTGAAGC CTGAGACCCC AGACCCGAGT GCAACAGCCC CGCTCTGAGA CCCTGACACC CTAACAGCCC GCTCTGAGAC CCTGACACCG TAACAGCCCC GCTCTGAGAC CCTGACCCTA ACAGTCCTGC TCTGAGACCC TGACCCTGCA GTCCCAAGAT CCTGTGGCCC TGAGACCCTG AGGCCCTAGA CCCCCAAATC CTGCCCAGAA ACTTCAAATT CTCACCCAAG ACCCTGAGAC TCCATCATCC ATGACCTCAA AGTCCCCAGA TCCCAGCCCC TAAGACCCAA GACCCCATCC TGAAGCCCAA AGCCTTGAGA ATTCAAATCC TCACCTCAAG ACTTGGAGAC CCTGGCCCCA TGACATTGAA AACCATGGAC CTGGCCAGGC GTGGTGGCTC ACGCCTGTAA TCCCAGCACT TTGGGAGGCC GAGGCAAGTG GATCACCTGA GGTCGGGAGT TCAAGACCAG CCAGACCAAC ATGGTGAAAC CCTGTCTCTA CTAAAAATAC AAAATTAGCC AGGCGTGGTG GTGCATGCCT GTAATCCCAG CTACTTGGGA GGCTGAGGCA GGAGAATCGC TTGAACCTGG GAGGCGGAGG TTGCAGTGAG CCGAGATCGC ACCATTACAC TCCAGCCTGG GCAACAAGAG CAAAACTCCC TCTCTCTCAA AAAAAAAAAA AAAAAAAAAA AAGAAGGAAA AGAAAACCAT GGACCTCCAG ACCCTGAGAC CCCAGGCCCC AGCCCTGAGA TCCTGACATC TTAAAGATCC CAGGCCCTAA GATACAAGAC CTTGACCCAA AGCCAGCCTT GGGACCCTGG CTGTACAAAC CCAAGACCTC CAGGACCTAG ACCCCGAGCC CTGAGGCCCT ATGTCTCACT CCCAACATCG AAAACCCTGA

CACCTCAGAT CCTGAGCCTG CGCCTGTACG ACTCCAAGAC CCTCACTTCC AAAGCCAGGC CCAAAGCCCT GAGACCAGAA GACTTCAAAC CCTGGTTCTT GGGCCTAACT CCAAAGACCC TGGATCTCAA ATTCCAACTT CTAGCTCTGA GACTCCAGCC CTCACCCATG AGTTCCTGAA CTTGAACCCA GAGACCCCAT CTCTAAGACT TCAGCCTTGA GATCCAGGGC CTGACCCTAG ACTCGAGCCC ACAGACCTCA GATACTGTCT GTAAAACCCC AGCTCTGGTG GGAGCAGTG GCTCACTCCT GTAATCCCAA GGCAGGGGAG GCCAAGGCAG AAGGACCTCT TGAGGCCATG AGTTTGAGAC AGCCTGGGCA GCATAGCAAG ACTCTGTTTC TTAATTATTA TTATTATTAT TATTTTTTGG AGACAGAGTC TCGCGCTCTG TTGCCCAGGC TAGAGTGCAA TGGTGCCATT TCGGCTTGCT GGAACCTCCG CCTCCTGGGC TCAAGCGATT CTCCTGCCTC AGCCTCCTGA GTAGCTGGGA CTTCAGGTGC ACACTGCCAC ACCCGGATAA TTTTTTTGTA TTTTAGTAGA CACAGGGTTT CACCGTGTTG CCCAGGCTGG TCACAAACTC CTGAGCTCAG GCCATCCGCC CGCCTCGGCC TCCCAAAGCG CTGGGATAAC AGGCGTGACG CCGCGCCTGG CTTCTTAATT GTTCTAACAG CAGCGACAAC AACAAAAACC CAGCTCTGAG ATTCCAGCCC CGGCGACTCT AACAGTCCCA GGCCCGATCC CTCACCTAGA ACCGAGATGC CAGCCCTGAC TCCACAGACT TCACCCCCAA CCCCCACACT CAGCTCTGGA AGCCCGTCCT GACTCCAGCC TCCATTTTCG GAACCCCACA GCCTGAAGAG CTCCCGGCCT AAACACTTCA CCCCACGCGC CACAGTCCCC CTGTGAATAT GCAGCCCCGA TTCAGCTGCA GCTCCACAGC ACCCCTGCCC TGCACCCCCG CTGCACCCCC TACCTGTGAC TCACCTCTCT CCTCTCCCCA CAGATGTCCC GCCTGGCCCT GCCCCAGCCA CCCCCGGACC CGCCGGCGCC CCCGCTGGCG CCCCCCTCCT CAGCCTGGGG GGGCATCAGG GCCGCCCACG CCATCCTGGG GGGGCTGCAC CTGACACTTG ACTGGGCCGT GAGGGGACTG CTGCTGCTGA AGACTCGGCT GTGACCCGGG GCCCAAAGCC ACCACCGTCC TTCCAAAGCC AGATCTTATT TATTTATTTA TTTCAGTACT GGGGGCGAAA CAGCCAGGTG ATCCCCCCGC CATTATCTCC CCCTAGTTAG AGACAGTCCT TCCGTGAGGC CTGGGGGGCA TCTGTGCCTT ATTTATACTT ATTTATTTCA GGAGCAGGGG TGGGAGGCAG GTGGACTCCT GGGTCCCCGA GGAGGAGGGG ACTGGGGTCC CGGATTCTTG GGTCTCCAAG AAGTCTGTCC ACAGACTTCT GCCCTGGCTC TTCCCCATCT AGGCCTGGGC AGGAACATAT ATTATTTATT TAAGCAATTA CTTTTCATGT TGGGGTGGGG ACGGAGGGGA AAGGGAAGCC TGGGTTTTTG TACAAAAATG TGAGAAACCT TTGTGAGACA GAGAACAGGG AATTAAATGT GTCATACATA TCCACTTGAG GGCGATTTGT CTGAGAGCTG GGGCTGGATG CTTGGGTAAC TGGGGCAGGG CAGGTGGAGG GGAGACCTCC ATTCAGGTGG AGGTCCCGAG TGGGCGGGGC AGCGACTGGG AGATGGGTCG GTCACCCAGA CAGCTCTGTG GAGGCAGGGT CTGAGCCTTG CCTGGGGCCC CGCACTGCAT AGGGCCGTTT GTTTGTTTTT TGAGATGGAG TCTCGCTCTG TTGCCTAGGC TGGAGTGCAG TGAGGCAATC TAAGGTCACT GCAACCTCCA CCTCCCGGGT TCAAGCAATT CTCCTGCCTC AGCCTCCCGA TTAGCTGGGA TCACAGGTGT GCACCACCAT GCCCAGCTAA TTATTTATTT CTTTTGTATT TTTAGTAGAG ACAGGGTTTC ACCATGTTGG CCAGGCTGGT TTCGAACTCC TGACCTCAGG TGATCCTCCT GCCTCGGCCT CCCAAAGTGC TGGGATTACA GGTGTGAGCC ACCACACCTG ACCCATAGGT CTTCAATAAA TATTTAATGG AAGGTTCCAC AAGTCACCCT GTGATCAACA GTACCCGTAT GGGACAAAGC TGCAAGGTCA AGATGGTTCA TTATGGCTGT GTTCACCATA GCAAACTGGA AACAATCTAG ATATCCAACA GTGAGGGTTA AGCAACATGG TGCATCTGTG GATAGAACGC CACCCAGCCG CCCGGAGCAG GGACTGTCAT TCAGGGAGGC TAAGGAGAGA GGCTTGCTTG GGATATAGAA AGATATCCTG ACATTGGCCA GGCATGGTGG CTCACGCCTG TAATCCTGGC ACTTTGGGAG GACGAAGCGA GTGGATCACT GAAGTCCAAG AGTTTGAGAC CGGCCTGCGA GACATGGCAA AACCCTGTCT CAAAAAAGAA AGAATGATGT CCTGACATGA AACAGCAGGC TACAAAACCA CTGCATGCTG TGATCCCAAT TTTGTGTTTT TCTTTCTATA TATGGATTAA AACAAAAATC CTAAAGGGAA ATACGCCAAA ATGTTGACAA TGACTGTCTC CAGGTCAAAG GAGAGAGGTG GGATTGTGGG TGACTTTTAA TGTGTATGAT TGTCTGTATT TTACAGAATT TCTGCCATGA CTGTGTATTT TGCATGACAC ATTTTAAAAA TAATAAACAC TATTTTTAGA ATAACAGAAT ATCAGCCTCC TCCTCTCCAA AAATAAGCCC TCAGGAGGGG ACAAAGTTGA CCGCTGATTG AGCCTGTCAG GGCTGTGCAC-3' (FRAG. NO:_) (SEQ. ID NO:2522)

Human GM-CSF Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTTGBGCBGG BBGCTCTGGG GCBGGGBGCT GGCBGGGCCC BGGGGGGTGG CTTCCTGCBC TGTCCBGBGT GCBCTGTGCC BCBGCBGCBG CTGCBGGGCC BTCBGCTTCB TGGGGCTCTG GGTGGCBGGT CCBGCCBTGG GTCTGGGTGG GGCTGGGCTG CBGGCTCCGG GCGGTCCBGCCBTGGGTCTG GGGGCTGGG CTGCBGGCTC CGGGCGGGCG GGTGCGGGCT GCGTGCTGGG GGCTGCCCCG CAGGCCCTGC GGTCCBGCCB TGGGTCTGGG GGCTGGGCTG CBGGCTCCGG GCGGGCGGGT GCGGGCTGCG TGCTGGGGGC TGCCCCGCAG GCCCTGC-3' **(FRAG. NO:1847) (SEQ. ID NO: 1858)**

5'-GBGCBGG BBG-3' **(FRAG. NO:1848) (SEQ. ID NO: 1859)**

5'-GCCBCBGCBGCBGC-3' **(FRAG. NO:1849) (SEQ. ID NO: 1860)**

5'-GGG TGC GGG C-3' **(FRAG. NO:1850) (SEQ. ID NO: 1861)**

5'-GGT CCB GCC BTG GGT CTG GG-3' **(FRAG. NO:1300)(SEQ. ID NO:1310)**

5'-GGC TGG GCT GCB GGC TCC GG-3' **(FRAG. NO:1301)(SEQ. ID NO:1311)**

5'-GCG GGC GGG TGC GGG CTG CGT GCT GGG-3' **(FRAG. NO:1302)(SEQ. ID NO:1312)**

5'-GGC TGC CCC GCA GGC CCT GC-3' **(FRAG. NO:1303)(SEQ. ID NO:1313)**

5'-CTTGBGCBGG BBGCTCTGGG GCBGGGBGCT GGCBGGGCCC BGGGGGGTGG CTTCCTGCBC TGTCCBGBGT GCBCTGTGCC BCBGCBGCBG CTGCBGGGCC BTCBGCTTCB TGGGGCTCTG GGTGGCBGGT CCBGCCBTGG GTCTGGGTGG GGCTGGGCTG CBGGCTCCGG GC-3' **(FRAG. NO:1851) (SEQ. ID NO: 1862)**

Human Tumor Necrosis Factor " Antisense Oligonucleotide Fragments

5'-GCBCCGCCTG GBGCCCTGGG GCCCCCCTGT CTTCTTGGGG BGCGCCTCCT CGGCCBGCTC CBCGTCCCGG BTCBTGCTTT CBGTGCTCBT GGTGTCCTTT CCBGGGGBGB GBGGGGCTGG TCCTCTGCTG TCCTTGCTGG TGCTCBTGGT GTCCTTTCCG CCCTGGGGCC CCCCTGTCTT CTTGGGGCCT CTTCCCTCTG GGGGCCGTCT CTCTCCCTCT CTTGCGTCTC TCTCTTTCTC TCTCTCTCTT CCCCTTTCCC GCTCTTTCTG TCTCGGTGTC TGGTTTTCTC TCTCCGCTGG CTGCCTGTCT GGCCTGCGCT CTTGGCCTGT GCTGTTCCTC CTCCGGTTCC TGTCCTCTCT GTCTGTCGCC CCCTCTGGGG TCTCCCTCTG GGTGGTGGTC TTGTTGCTTG GGCTGGGCTC CGTGTCTCCB GTGCTCBTGG TGTCCGCTGB GGGBGCGTCT GCTGGCGCTG GTCCTCTGCTGTC CTTGCTGGTG CTCBTGGTGT CCTTTCCGCC CTGGGGCCCC CCTGTCTTCT TGGGGCCTCT TCCCTCTGGG GGCCGTCTC TCTCCCTCTC TTGCGTCTCT CTCTTTCTCT CTCTCTCTTC CCCTTTCCCG CTCTTTCTGT CTCGGTGTCT GGTTTTCTCT CTCCGCTGGC TGCCTGTCTG GCCTGCGCTC TTGGCCTGTG CTGTTCCTCC TCCGGTTCCT GTCCTCTCTG TCTGTCGCCC CCTCTGGGGT CTCCCTCTGG CGTGGTGGTC TTGTTGCTTG GGCTGGGCTC CGTGTCTCCB GTGCTCBTGG TGTCCGCTGB GGGBGCGTCT GCTGGC-3' **(FRAG. NO:1852) (SEQ. ID NO:1863)**

5'-GGGGCCCCCC-3' **(FRAG. NO:1853) (SEQ. ID NO:1864)**

5'- GGG GGC CG TCT-3' **(FRAG. NO:1854) (SEQ. ID NO:1865)**
5'-CCBGGGGBGB GBGGGGCTGG-3' **(FRAG. NO:1855) (SEQ. ID NO:1866)**
5'-
GCBCCGCCTGGBGCCCTGGGGCCCCCCTGTCTTCTTGGGGBGCGCCTCCTCGGCCBGCTCCBCGTCCCGGBTCBTGCTTTCBGTGC TCBTGGTGTCCTTTCCBGGGGBGBGBGGG-3' **(FRAG. NO:1304) (SEQ. ID NO:1314)**
5'-GCT GGT CCT CTG CTG TCC TTG CTG GTG CTC BTG GTG TCC TTT CC GCC CTG GGG CCC CCC TGT CTT CTT GGG G CCT CTT CCC TCT GGG GGC CG TCT CTC TCC CTC TCT TGC GTC TCT C TCT TTC TCT CTC TCT CTT CCC C TTT CCC GCT CTT TCT GTC TC GGT GTC TGG TTT TCT CTC TCC GCT GGC TGC CTG TCT GGC CTG CGC TCT T GGC CTG TGC TGT TCC TCC TCC GGT TCC TGT CCT CTC TGT CTG TC GCC CCC TCT GGG GTC TCC CTC TGG C GTG GTG GTC TTG TTG CTT GGG CTG GGC TCC GTG TCT C CBG TGC TCB TGG TGT CC-3' **(FRAG. NO:1305) (SEQ. ID NO:1315)**
5'-GCT GBG GGB GCG TCT GCT GGC GCT GGT CCT CTG CTG TCC TTG CTG GTG CTC BTG GTG TCC TTT CC GCC CTG GGG CCC CCC TGT CTT CTT GGG G CCT CTT CCC TCT GGG GGC CG TCT CTC TCC CTC TCT TGC GTC TCT C TCT TTC TCT CTC TCT CTT CCC C TTT CCC GCT CTT TCT GTC TC GGT GTC TGG TTT TCT CTC TCC GCT GGC TGC CTG TCT GGC CTG CGC TCT T GGC CTG TGC TGT TCC TCC TCC GGT TCC TGT CCT CTC TGT CTG TC GCC CCC TCT GGG GTC TCC CTC TGG C GTG GTG GTC TTG TTG CTT GGG CTG GGC TCC GTG TCT C CBG TGC TCB TGG TGT CC GCT GBG GGB GCG TCT GCT GGC-3'
(FRAG. NO:1306) (SEQ. ID NO:1316)
5'-GCT GGT CCT CTG CTG TCC TTG CTG-3' **(FRAG. NO:1655) (SEQ. ID NO:1665)**
5'-GTG CTC BTG GTG TCC TTT CC-3' **(FRAG. NO:1656)(SEQ. ID NO:1666)**
5'-GCC CTG GGG CCC CCC TGT CTT CTT GGG G-3' **(FRAG. NO:1657)(SEQ. ID NO:1667)**
5'-CCT CTT CCC TCT GGG GGC CG-3' **(FRAG. NO:1658)(SEQ. ID NO:1668)**
5'-TCT CTC TCC CTC TCT TGC GTC TCT C-3' **(FRAG. NO:1659)(SEQ. ID NO:1669)**
5'-TCT TTC TCT CTC TCT CTT CCC C-3' **(FRAG. NO:1660)(SEQ. ID NO:1670)**
5'-TTT CCC GCT CTT TCT GTC TC-3' **(FRAG. NO:1661)(SEQ. ID NO:1671)**
5'-GGT GTC TGG TTT TCT CTC TCC-3' **(FRAG. NO:1662)(SEQ. ID NO:1672)**
5'-GCT GGC TGC CTG TCT GGC CTG CGC TCT T-3' **(FRAG. NO:1663)(SEQ. ID NO:1673)**
5'-GGC CTG TGC TGT TCC TCC-3' **(FRAG. NO:1664)(SEQ. ID NO:1673)**
5'-TCC GGT TCC TGT CCT CTC TGT CTG TC-3' **(FRAG. NO:1665)(SEQ. ID NO:1675)**
5'-GCC CCC TCT GGG GTC TCC CTC TGG C-3' **(FRAG. NO:1666)(SEQ. ID NO:1676)**
5'-GTG GTG GTC TTG TTG CTT-3' **(FRAG. NO:1667)(SEQ. ID NO:1677)**
5'-GGG CTG GGC TCC GTG TCT C-3' **(FRAG. NO:1668)(SEQ. ID NO:1678)**
5'-CBG TGC TCB TGG TGT CC-3' **(FRAG. NO:1669)(SEQ. ID NO:1679)**
5'-GCT GBG GGB GCG TCT GCT GGC-3' **(FRAG. NO:1670)(SEQ. ID NO:1680)**

Human Leukotriene C4 Synthase Nucleic Acids and Antisense Oligonucleotide Fragments

5'-CTCGGTBGBC GCGCTCGBBC TCGGGTGGGC CGGTGGTGBG CGGCGGCGBCB CGCGGBBGGC CCTGCGCGCC GBGBTCBCCTG CBGGGBGBBG TBGGCTTGCB GCBGGBCTCC CBGGBGGGTG BCBGCBGCCB GTBGBGCTBC CTCGTCCTTC BTGGTBCCGT CGGTGTGGTG GCBCGGGCTG TGTGTGBBGG CGBGCTGGGC CCCGTCTGCT GCTCCTCGTG CCGCCTCGTC CTTCA TGG TA CCGTCGGTGT GGTGGCCTCG GGTGGGCCGG TGGTGGGGCG CGCGCGCTCG CGTGGCTCCG GCTCTTCTTT CCCGGCTCCGT CGGCCCGGGG GCCTTGGTCT CCCTCGTCCT TCBTGGTBCC G-3' **(FRAG. NO:1856) (SEQ ID NO: 1867)**
5'-GCB GCBGGBC-3' **(FRAG. NO:1857) (SEQ ID NO: 1868)**
5'-CCCGGCTCCG-3' **(FRAG. NO:1858) (SEQ ID NO: 1869)**
5'-CGGCCCGGGG GCC-3' **(FRAG. NO:1859) (SEQ ID NO: 1870)**
5'-CB CGCGG-3' **(FRAG. NO:1860) (SEQ ID NO: 1871)**
5'-GCC CCG TCT GCT GCT CCT CGT GCC G-3' **(FRAG. NO:1307)(SEQ. ID NO:1317)**
5'-CCT CGT CCT TCA TGG TAC CGT CGG TGT GGT GGC-3' **(FRAG. NO:1308)(SEQ. ID NO:1318)**
5'-CTC GGG TGG GCC GGT GGT G-3' **(FRAG. NO:1309)(SEQ. ID NO:1319)**
5'-GGG CGC GCG CGC TCG CGT-3' **(FRAG. NO:1310)(SEQ. ID NO:1320)**
5'-GGC TCC GGC TCT TCT TTC CCG GCT CCG TCG GCC CGG GGG CCT TGG TCT C-3' **(FRAG. NO:1311) (SEQ. ID NO:1321)**
5'-CCT CGT CCT TCB TGG TBC CG-3' **(FRAG. NO:1312)(SEQ. ID NO:1322)**
5'-CTCGGTBGBC GCGCTCGBBC TCGGGTGGGC CGGTGGTGBG CGGCGGCGBCB CGCGGBBGGC CCTGCGCGCC GBGBTCBCCTG CBGGGBGBBG TBGGCTTGCB GCBGGBCTCC CBGGBGGGTG BCBGCBGCCB GTBGBGCTBC CTCGTCCTTC BTGGTBCCGT CGGTGTGGTG GCBCGGGCTG TGTGTGBBGG CGBGCTGG-3' **(FRAG. NO:1861) (SEQ ID NO: 1872)**

Human Endothelin-1 Nucleic Acids and Antisense Oligonucleotide Fragments

5'-BCCGGCGGBG CCGCCBGGGT GGBCTGGGBG TGGGTTTCTC CCCGCCGTTC TCBCCCBCCG CGCTGBGCTC BGCGCCTBBG BCTGCTGTTT CTGGBGCTCC TTGGCBBGCC BCBBBCBGCB GBGBGBBBBT CBTGBGCBBB TBBTCCBTTC TGBBBBBBBG GGBTCBBBBB CCTCCCGTTC CCCGTTCGCC TGGCGCGCGC TGCGGGTTCC TCGTGGGTTT CTCCCCGCCG TTCTCCGGTC TGTTGCCTTT GTGGGCTTCT TGTCTTTTTG GCTGTTCTTT TCCTGCTTGG CGTCTTTTCC TTTCTTTGTG CTCGGTTGTG GGTCCGCTGG TCCTTTGCCC TGTGTGTTTC TGCTGCCCGT TCGCCTGGCG CGCGCTGCGG GTTCCTCGTG GGTTTCTCCC CGCCGTTCTC CGGTCTGTTG CCTTTGTGGG CTTCTTGTCT TTTTGGCTGT TCTTTTCCTG CTTGGCGTCT TTTCCTTTCT TTGTGCTCGG TTGTGGGTCC GCTGGTCCTT TGCCCTGTGT GTTTCTGCTG-3' **(FRAG. NO:1862) (SEQ. ID NO:1873)**
5'-CCGGCGGBG CCGCCBGGGT GGBC-3' **(FRAG. NO:1863) (SEQ. ID NO:1874)**
5'-CCGCCBGGG-3' **(FRAG. NO:1864) (SEQ. ID NO:1875)**
5'-GGCGCGCGC-3' **(FRAG. NO:1865) (SEQ. ID NO:1876)**
5'-GTGGGTCCGC-3' **(FRAG. NO:1866) (SEQ. ID NO:1877)**
5'-CCCGTTCGCCTGGCGC-3' **(FRAG. NO:1313)(SEQ. ID NO:1323)**
5'-GCGCTGCGGGTTCCTC-3' **(FRAG. NO:1314)(SEQ. ID NO:1324)**
5'-GTGGGTTTCTCCCCGCCGTTCTC-3' **(FRAG. NO:1315)(SEQ. ID NO:1325)**
5'-CGGTCTGTTGCCTTTGTGGG -3' **(FRAG. NO:1316)(SEQ. ID NO:1326)**

5'-CTTCTTGTCTTTTTGGCT-3' (FRAG. NO:1317)(SEQ. ID NO:1327)
5'-GTTCTTTTCCTGCTTGGC-3' (FRAG. NO:1318)(SEQ. ID NO:1328)
5'-GTCTTTTCCTTTCTT-3' (FRAG. NO:1319)(SEQ. ID NO:1329)
5'-TGTGCTCGGTTGTGGGTC-3' (FRAG. NO:1320)(SEQ. ID NO:1330)
5'-CGCTGGTCCTTTGCC-3' (FRAG. NO:1321)(SEQ. ID NO:1331)
5'-CTGTGTGTTTCTGCTG-3' (FRAG. NO:1322)(SEQ. ID NO:1332)
5'-CCCGTTCGCCTGGCGC-3' (FRAG. NO:1323)(SEQ. ID NO:1333)
5'-GCGCTGCGGGTTCCTC-3' (FRAG. NO:1324)(SEQ. ID NO:1334)
5'-GTGGGTTTCTCCCCGCCGTTCTC-3' (FRAG. NO:1325(SEQ. ID NO:1335)
5'-CGGTCTGTTGCCTTTGTGGG-3' (FRAG. NO:1326)(SEQ. ID NO:1336)
5'-CTTCTTGTCTTTTTGGCT-3' (FRAG. NO:1327)(SEQ. ID NO:1337)
5'-GTTCTTTTCCTGCTTGGC-3' (FRAG. NO:1328)(SEQ. ID NO:1338)
5'-GTCTTTTCCTTTCTT-3' (FRAG. NO:1329)(SEQ. ID NO:1339)
5'-TGTGCTCGGTTGTGGGTC-3' (FRAG. NO:1330)(SEQ. ID NO:1340)
5'-CGCTGGTCCTTTGCC-3' (FRAG. NO:1331)(SEQ. ID NO:1341)
5'-CTGTGTGTTTCTGCTG-3' (FRAG. NO:1332)(SEQ. ID NO:1342)

Endothelin Receptor ET-B Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GCCCTGTCGG GCGGGAAGCC TCTCTCCTCT CCCCAGATC CGCGACAGGC CGCAGGCAAG AACCAGCGCA ACCAGGGCGC GTCCGCACAG ACTTGGAGGC GGCTGCATGC TGCTACCTGC TCCAGAAGCG TCCGGTGGCC GCCGCGCC CTGTCGGGCG GGBBGCCTCT CTCCTCTCCC CBGBTCCGCG BCBGGCCGCB GGCBBGBBCC BGCGCBBCCB GGGCGCGTCC GCBCBGBCTT GGBGGCGGCT GCBTGCTGCT BCCTGCTCGGGCG GGBBGCCTCCG GTGGCCGCCG CGCGTCCGGT GGCCGCCGCG CCTCTCTCCT CTCCCCGTGG CCCTGTCGGG CGGGTCCTGC CGTCCTGTCT CCTTTTCTTT TGCTGTCTTG TCTTCCCGTC TCTGCTTT-3' (FRAG. NO: 1867) (SEQ. ID NO: 1878)
5'-CGGGCG GGBBGCC-3' (FRAG. NO: 1868) (SEQ. ID NO: 1879)
5'-CGGGCGGG-3' (FRAG. NO: 1869) (SEQ. ID NO: 1880)
5'-CCGCBCBGBC-3' (FRAG. NO: 1870) (SEQ. ID NO: 1881)
5'-GCGTCCGGTGGCCGCCGC-3' (FRAG. NO:1333)(SEQ. ID NO:1343)
5'-GCCTCTCTCCTCTCCCC-3' (FRAG. NO:1334)(SEQ. ID NO:1344)
5'-GTGGCCCTGTCGGGCGGG-3' (FRAG. NO:1335)(SEQ. ID NO:1345)
5'-TCCTGCCGTCCTGTCTCCTTT-3' (FRAG. NO:1336)(SEQ. ID NO:1346)
5'-TCTTTTGCTGTCTTGT-3' (FRAG. NO:1337)(SEQ. ID NO:1347)
5'-CTTCCCGTCTCTGCTTT-3' (FRAG. NO:1338)(SEQ. ID NO:1348)
5'-GCCCTGTCGG GCGGGAAGCC TCTCTCCTCT CCCCAGATC CGCGACAGGC CGCAGGCAAG AACCAGCGCA ACCAGGGCGC GTCCGCACAG ACTTGGAGGC GGCTGCATGC TGCTACCTGC TCCAGAAGCG TCCGGTGGCC GCCGC-3' (FRAG. NO: 1871) (SEQ. ID NO: 1882)
5'-GCCCTGTCGG GCGGGBBGCC TCTCTCCTCT CCCCBGBTCC GCGBCBGGCC GCBGGCBBGB BCCBGCGCB BCCBGGGCGC GTCCGCBCBG BCTTGGBGGC GGCTGCBTGC TGCTBCCTGC TCCBGBBGCG TCCGGTGGCC GCCGC-3' (FRAG. NO: 1872) (SEQ. ID NO: 1883)

Endothelin ETA Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GTCTGTCCTC CCCGTCTCCT CCCACTGCTT CTCCCGGGGG CTTCCCCGGC TTCGGGTGGC CGGTGTCCCG GGCTCCGGCG CGGCGGCGGC TTCGGCTGCG GGTGGGTGGC GCGGGCTGCC GGGTCCGCGC GGCGCCTGGG CCCTTGTGCT GCTTTTTGCT TGTTCCGTTC TGGCTGCTCC GGTCTGTGTT GTGGTTGTTT TGTTTCTTCT TGGGTGTGGG CCTTGCGGTT TTGGCTGTGG GCCCTTTGGG GCCTTGGCTT CTGGCTCGTC TGTCCTCCCC GTCTCCTCCC ACTGCTTCT CCCGGGGGCT TCCCCGGCTT CGGGTGGCCG GTGTCCCGGG CTCCGGCGCG GCGGCGGCTT CGGCTGCGGG TGGGTGGCGC GGGCTGCCGG GTCCGCGCGG CGCCTGGGCC CTTGTGCTGC TTTTTGCTTG TTCCGTTCTG GCTGCTCCGG TCTGTGTTGT GGTTGTTTTG TTTCTTCTTG GGTGTGGGCC TTGCGGTTTT GGCTGTGGGC CCTTTGGGGC CTTGGCTTCT GGCTCCAT CCACATGATT GCTTAGATTT GTGCTGTATC TCTCAGGATT ATCACTGATT ACACATCCAA CCAGTGCCAG CCAAAAGGAT GCCCTGAGGC AAAGGGTTTC CATCTTGAGG CAAATTTGAG GACBTCCBC BTGBTTGCTT BGBTTTGTGC TGTBTCTCTC BGGBTTBTCB CTGBTTBCBC BTCCBBCCBG TGCCBGCCBB BBGGBTGCCC TGBGGCBBBG GGTTTCCBTC TTGBGGCBBB TTTGBGGB-3' (FRAG. NO:1873) (SEQ. ID NO: 1884)
5'-GBGGCBBBGGG-3' (FRAG. NO:1874) (SEQ. ID NO: 1885)
5'-GCCBGCCBB BBGGB-3' (FRAG. NO:1875) (SEQ. ID NO: 1886)
5'-CGCCTGGGCC C-3' (FRAG. NO:1876) (SEQ. ID NO: 1887)
5'-GTCTGTCCTCCCCGTCTCCTCCC-3' (FRAG. NO:1339)(SEQ. ID NO:1349)
5'-ACTGCTTCTCCCGGGG-3' (FRAG. NO:1340)(SEQ. ID NO:1350)
5'-GCTTCCCCGGCTTC-3' (FRAG. NO:1341)(SEQ. ID NO:1351)
5'-GGGTGGCCGGTGTCCCGGGCTCCGGCGCGGCGGC-3' (FRAG. NO:1342)(SEQ. ID NO:1352)
5'-GGCTTCGGCTGC-3' (FRAG. NO:1343)(SEQ. ID NO:1353)
5'-GGGTGGGTGGCGCGG-3' (FRAG. NO:1344)(SEQ. ID NO:1354)
5'-GCTGCCGGGTCCGCGCGGCGCCTGGGCC-3' (FRAG. NO:1345)(SEQ. ID NO:1355)
5'-CTTGTGCTGCTTTTT-3' (FRAG. NO:1346(SEQ. ID NO:1356)
5'-TGCTTGTTCCGTTC-3' (FRAG. NO:1347)(SEQ. ID NO:1357)
5'-TGGCTGCTCCGGTCTGTGTTGTGGTTGTTTTG-3' (FRAG. NO:1348)(SEQ. ID NO:1358)
5'-TTTCTTCTTGGGTGTGGG-3' (FRAG. NO:1349)(SEQ. ID NO:1359)
5'-CCTTGCGGTTTTGG-3' (FRAG. NO:1350)(SEQ. ID NO:1360)
5'-CTGTGGGCCCTTTG-3' (FRAG. NO:1351)(SEQ. ID NO:1361)
5'-GGGCCTTGGCTTCTGGCTC-3' (FRAG. NO:1352)(SEQ. ID NO:1362)
5'-CATCCACATG ATTGCTTAGA TTTGTGCTGT ATCTCTCAGG ATTATCACTG ATTACACATC CAACCAGTGC CAGCCAAAAG GATGCCCTGA GGCAAAGGGT TTCCATCTTG AGGCAAATTT GAGGA-3' (FRAG. NO:1353)(SEQ. ID NO:1363)

5'-CBTCCBCBTG BTTGCTTBGB TTTGTGCTGT BTCTCTCBGG BTTBTCBCTG BTTBCBCBTC CBBCCBGTGC CBGCCBBBBG GBTGCCCTGB GGCBBBGGGT TTCCBTCTTG BGGCBBBTTT GBGGB-3' (FRAG. NO:1354)(SEQ. ID NO:1364)

Endothelin Receptor A Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCCACCATGG AAACCCTTTG CCTCAGGGCA TCCTTTTGGC TGGCACTGGT TGGATGTGTA ATCAGTGATA ATCCTGAGAG ATACAGCACA AATCTAAGCA ATCATGTGGA TGATTTCACC ACTTTTCGTG GCACAGAGCT CAGCTTCCTG GTTACCACTC ATCAACCCAC TAATTTGGTC CTACCCAGCA ATGGCTCAAT GCACAACTAT TGCCCACAGC AGACTAAAAT TACTTCAGCT TTCAAATACA TTAACACTGT GATATCTTGT ACTATTTTCA TCGTGGGAAT GGTGGGGAAT GCAACTCTGC TCAGGATCAT TTACCAGAAC AAATGTATGA GGAATGGCCC CAACGCGCTG ATAGCCAGTC TTGCCCTTGG AGACCTTATC TATGTGGTCA TTGATCTCCC TATCAATGTA TGGCTGGGCG CTGGCCTTTT GATCACAATG ACTTTGGCGT ATTTCTTTGC AAGCTGTTCC CCTTTTTGCA GAAGTCCTCG GTGGGGATCA CCGTCCTCAA CCTCTGCGCT CTTAGTGTTG ACAGGTACAG AGCAGTTGCC TCCTGGAGTC GTGTTCAGGG AATTGGGATT CCTTTGGTAA CTGCCATTGA AATTGCCTCC ATCTGGATCC TGTCCTTTAT CCTGGCCATT CCTGAAGCGA TTGGCTTCGT CATGGTACCC TTTGAATATA GGGGTGGACA GCATAAAACC TGTATGCTCA ATGCCACATC AAAATTCATG GAGTTCTACC AAGATGTAAA GGACTGGTGG CTCTTCGGGT TCTATTTCTG TATGCCCTTG GTGTGCACTG CGATCTTCTA CACCCTCATG ACTGGTGAGA TGTTGAACAG AAGGAATGGC AGCTTGAGAA TTGCCCTCAG TGAACATCTT AAGCAGCGTC GAGAAGTGGC AAAAACAGTT TTCTGCTTGG TTGTAATTTT TGCTCTTTGC TGGTTCCCTC TTCATTTAAG CCGTATATTG AAGAAAACTG TGTATAACGA GATGGACAAG AACCGATGTG AATTACTTAG TTTCTTACTG CTCATGGATT ACATCGGTAT TAACTTGGCA ACCATGAATT CATGTATAAA CCCCATAGCT CTGTATTTTG TGAGCAAGAA ATTTAAAAAT TGTTTCCAGT CATGCCTCTG CTGCTGCTGT TACCAGTCCA AAAGTCTGAT GACCTCGGTC CCCATGAACG GAACAAGCAT CCAGTGGAAG AACCACGATC AAAACAACCA CAACACAGAC CGGAGCAGCC ATAAGGACAG CATGAACTGA CCACCCTTAG AAGCACTCCT GAATTCGGGA AAAAGTGAAG GTGTAAAAGC AGCACAAGTG CAATAAGAGA TATTTCCTCA AATTTGCCTC AAGATGGAAA CCCTTTGCCT CAGGGCATCC TTTTGGCTGG CACTGGTTGG ATGTGTAATC AGTGATAATC CTGAGAGATA CAGCACAAAT CTAAGCAATC ATGTGGATGA TTTCACCACT TTTCGTGGCA CAGAGCTCAG CTTCCTGGTT ACCACTCATC AACCCACTAA TTTGGTCCTA CCCAGCAATG GCTCAATGCA CAACTATTGC CCACAGCAGA CTAAAATTAC TTCAGCTTTC AAATACATTA ACACTGTGAT ATCTTGTACT ATTTTCATCG TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTTA CCAGAACAAA TGTATGAGGA ATGGCCCCAA CGCGCTGATA GCCAGTCTTG CCCTTGGAGA CCTTATCTAT GTGGTCATTG ATCTCCCTAT CAATGTATTT AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT CACAATGACT TTGGCGTATT TCTTTGCAAG CTGTTCCCCT TTTTGCAGAA GTCCTCGGTG GGGATCACCG TCCTCAACCT CTGCGCTCTT AGTGTTGACA GGTACAGAGC AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT TGGGATTCCT TTGGTAACTG CCATTGAAAT TGTCTCCATC TGGATCCTGT CCTTTATCCT GGCCATTCCT GAAGCGATTG GCTTCGTCAT GGTACCCTTT GAATATAGGG GTGAACAGCA TAAAACCTGT ATGCTCAATG CCACATCAAA ATTCATGGAG TTCTACCAAG ATGTAAAGGA CTGGTGGCTC TTCGGGTTCT ATTTCTGTAT GCCCTTGGTG TGCACTGCGA TCTTCTACAC CCTCATGACT TGTGAGATGT TGAACAGAAG GAATGGCAGC TTGAGAATTG CCCTCAGTGA ACATCTTAAG CAGCGTCGAG AAGTGGCAAA AACAGTTTTC TGCTTGGTTG TAATTTTTGC TCTTTGCTGG TTCCCTCTTC ATTTAAGCCG TATATTGAAG AAAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT TACTTAGTTT CTTACTGCTC ATGGATTACA TCGGTATTAA CTTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTTGTGA GCAAGAAATT TAAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC CAGTCCAAAA GTCTGATGAC CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA ACAACCACAA CACAGACCGG AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTTAGAAG CACTCCTCGG TACTCCCATA ATCCTCTCGG AGAAAAAAAT CACAAGGCAA CTGTGAGTCC GGGAATCTCT TCTCTGATCC TTCTTCCTTA ATTCACTCCC ACACCCAAGA AGAAATGCTT TCCAAAACCG CAAGGGTAGA CTGGTTTATC CACCCACAAC ATCTACGAAT CGTACTTCTT TAATTGATCT AATTTACATA TTCTGCGTGT TGTATTCAGC ACTAAAAAAT GGTGGGAGCT GGGGGAGAAT GAAGACTGTT AAATGAAACC AGAAGGATAT TTACTACTTT TGCATGAAAA TAGAGCTTTC AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTCACCAT GAAACTTTAG AGATTAACGA CAAGATTTTC TACTTTTTTT AAGTGATTTT TTTGTCCTTC AGCCAAACAC AATATGGGCT CAAGTCACTT TTATTTGAAA TGTCATTTGG TGCCAGTATC CCGAATTC GAATTCGGGA AAAAGTGAAG GTGTAAAAGC AGCACAAGTG CAATAAGAGA TATTTCCTCA AATTTGCCTC AAGATGGAAA CCCTTTGCCT CAGGGCATCC TTTTGGCTGG CACTGGTTGG ATGTGTAATC AGTGATAATC CTGAGAGATA CAGCACAAAT CTAAGCAATC ATGTGGATGA TTTCACCACT TTTCGTGGCA CAGAGCTCAG CTTCCTGGTT ACCACTCATC AACCCACTAA TTTGGTCCTA CCCAGCAATG GCTCAATGCA CAACTATTGC CCACAGCAGA CTAAAATTAC TTCAGCTTTC AAATACATTA ACACTGTGAT ATCTTGTACT ATTTTCATCG TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTTA CCAGAACAAA TGTATGAGGA ATGGCCCCAA CGCGCTGATA GCCAGTCTTG CCCTTGGAGA CCTTATCTAT GTGGTCATTG ATCTCCCTAT CAATGTATTT AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT CACAATGACT TTGGCGTATT TCTTTGCAAG CTGTTCCCCT TTTTGCAGAA GTCCTCGGTG GGGATCACCG TCCTCAACCT CTGCGCTCTT AGTGTTGACA GGTACAGAGC AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT TGGGATTCCT TTGGTAACTG CCATTGAAAT TGTCTCCATC TGGATCCTGT CCTTTATCCT GGCCATTCCT GAAGCGATTG GCTTCGTCAT GGTACCCTTT GAATATAGGG GTGAACAGCA TAAAACCTGT ATGCTCAATG CCACATCAAA ATTCATGGAG TTCTACCAAG ATGTAAAGGA CTGGTGGCTC TTCGGGTTCT ATTTCTGTAT GCCCTTGGTG TGCACTGCGA TCTTCTACAC CCTCATGACT TGTGAGATGT TGAACAGAAG GAATGGCAGC TTGAGAATTG CCCTCAGTGA ACATCTTAAG CAGCGTCGAG AAGTGGCAAA AACAGTTTTC TGCTTGGTTG TAATTTTTGC TCTTTGCTGG TTCCCTCTTC ATTTAAGCCG TATATTGAAG AAAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT TACTTAGTTT CTTACTGCTC ATGGATTACA TCGGTATTAA CTTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTTGTGA GCAAGAAATT TAAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC CAGTCCAAAA GTCTGATGAC CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA ACAACCACAA CACAGACCGG AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTTAGAAG CACTCCTCGG TACTCCCATA ATCCTCTCGG AGAAAAAAAT CACAAGGCAA CTGTGAGTCC GGGAATCTCT TCTCTGATCC TTCTTCCTTA ATTCACTCCC ACACCCAAGA AGAAATGCTT TCCAAAACCG CAAGGGTAGA CTGGTTTATC CACCCACAAC ATCTACGAAT CGTACTTCTT TAATTGATCT AATTTACATA TTCTGCGTGT TGTATTCAGC ACTAAAAAAT GGTGGGAGCT GGGGGAGAAT GAAGACTGTT AAATGAAACC AGAAGGATAT TTACTACTTT TGCATGAAAA TAGAGCTTTC AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTCACCAT GAAACTTTAG AGATTAACGA CAAGATTTTC TACTTTTTTT AAGTGATTTT TTTGTCCTTC AGCCAAACAC AATATGGGCT CAAGTCACTT TTATTTGAAA TGTCATTTGG TGCCAGTATC CCGAATTC-3' (FRAG. NO:__) (SEQ ID NO: 2471)

5'-GAATTCGGGA AAAAGTGAAG GTGTAAAAGC AGCACAAGTG CAATAAGAGA TATTTCCTCA AATTTGCCTC AAGATGGAAA CCCTTTGCCT CAGGGCATCC TTTTGGCTGG CACTGGTTGG ATGTGTAATC AGTGATAATC CTGAGAGATA

CAGCACAAAT CTAAGCAATC ATGTGGATGA TTTCACCACT TTTCGTGGCA CAGAGCTCAG CTTCCTGGTT ACCACTCATC AACCCACTAA TTTGGTCCTA CCCAGCAATG GCTCAATGCA CAACTATTGC CCACAGCAGA CTAAAATTAC TTCAGCTTTC AAATACATTA ACACTGTGAT ATCTTGTACT ATTTTCATCG TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTTA CCAGAACAAA TGTATGAGGA ATGGCCCCAA CGCGCTGATA GCCAGTCTTG CCCTTGGAGA CCTTATCTAT GTGGTCATTG ATCTCCCTAT CAATGTATTT AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT CACAATGACT TTGGCGTATT TCTTTGCAAG CTGTTCCCCT TTTTGCAGAA GTCCTCGGTG GGGATCACCG TCCTCAACCT CTGCGCTCTT AGTGTTGACA GGTACAGAGC AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT TGGGATTCCT TTGGTAACTG CCATTGAAAT TGTCTCCATC TGGATCCTGT CCTTTATCCT GGCCATTCCT GAAGCGATTG GCTTCGTCAT GGTACCCTTT GAATATAGGG GTGAACAGCA TAAAACCTGT ATGCTCAATG CCACATCAAA ATTCATGGAG TTCTACCAAG ATGTAAAGGA CTGGTGGCTC TTCGGGTTCT ATTTCTGTAT GCCCTTGGTG TGCACTGCGA TCTTCTACAC CCTCATGACT TGTGAGATGT TGAACAGAAG GAATGGCAGC TTGAGAATTG CCCTCAGTGA ACATCTTAAG CAGCGTCGAG AAGTGGCAAA AACAGTTTTC TGCTTGGTTG TAATTTTTGC TCTTTGCTGG TTCCCTCTTC ATTTAAGCCG TATATTGAAG AAAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT TACTTAGTTT CTTACTGCTC ATGGATTACA TCGGTATTAA CTTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTTGTGA GCAAGAAATT TAAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC CAGTCCAAAA GTCTGATGAC CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA ACAACCACAA CACAGACCGG AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTTAGAAG CACTCCTCGG TACTCCCATA ATCCTCTCGG AGAAAAAAAT CACAAGGCAA CTGTGAGTCC GGGAATCTCT TCTCTGATCC TTCTTCCTTA ATTCACTCCC ACACCCAAGA AGAAATGCTT TCCAAAACCG CAAGGGTAGA CTGGTTTATC CACCCACAAC ATCTACGAAT CGTACTTCTT TAATTGATCT AATTTACATA TTCTGCGTGT TGTATTCAGC ACTAAAAAAT GGTGGGAGCT GGGGGAGAAT GAAGACTGTT AAATGAAACC AGAAGGATAT TTACTACTTT TGCATGAAAA TAGAGCTTTC AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTCACCAT GAAACTTTAG AGATTAACGA CAAGATTTTC TACTTTTTTT AAGTGATTTT TTTGTCCTTC AGCCAAACAC AATATGGGCT CAAGTCACTT TTATTTGAAA TGTCATTTGG TGCCAGTATC CCGAATTC-3' **(FRAG. NO:___) (SEQ ID NO: 2482)**

5'-GAATTCGGGA AAAAGTGAAG GTGTAAAAGC AGCACAAGTG CAATAAGAGA TATTTCCTCA AATTTGCCTC AAGATGGAAA CCCTTTGCCT CAGGGCATCC TTTTGGCTGG CACTGGTTGG ATGTGTAATC AGTGATAATC CTGAGAGATA CAGCACAAAT CTAAGCAATC ATGTGGATGA TTTCACCACT TTTCGTGGCA CAGAGCTCAG CTTCCTGGTT ACCACTCATC AACCCACTAA TTTGGTCCTA CCCAGCAATG GCTCAATGCA CAACTATTGC CCACAGCAGA CTAAAATTAC TTCAGCTTTC AAATACATTA ACACTGTGAT ATCTTGTACT ATTTTCATCG TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTTA CCAGAACAAA TGTATGAGGA ATGGCCCCAA CGCGCTGATA GCCAGTCTTG CCCTTGGAGA CCTTATCTAT GTGGTCATTG ATCTCCCTAT CAATGTATTT AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT CACAATGACT TTGGCGTATT TCTTTGCAAG CTGTTCCCCT TTTTGCAGAA GTCCTCGGTG GGGATCACCG TCCTCAACCT CTGCGCTCTT AGTGTTGACA GGTACAGAGC AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT TGGGATTCCT TTGGTAACTG CCATTGAAAT TGTCTCCATC TGGATCCTGT CCTTTATCCT GGCCATTCCT GAAGCGATTG GCTTCGTCAT GGTACCCTTT GAATATAGGG GTGAACAGCA TAAAACCTGT ATGCTCAATG CCACATCAAA ATTCATGGAG TTCTACCAAG ATGTAAAGGA CTGGTGGCTC TTCGGGTTCT ATTTCTGTAT GCCCTTGGTG TGCACTGCGA TCTTCTACAC CCTCATGACT TGTGAGATGT TGAACAGAAG GAATGGCAGC TTGAGAATTG CCCTCAGTGA ACATCTTAAG CAGCGTCGAG AAGTGGCAAA AACAGTTTTC TGCTTGGTTG TAATTTTTGC TCTTTGCTGG TTCCCTCTTC ATTTAAGCCG TATATTGAAG AAAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT TACTTAGTTT CTTACTGCTC ATGGATTACA TCGGTATTAA CTTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTTGTGA GCAAGAAATT TAAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC CAGTCCAAAA GTCTGATGAC CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA ACAACCACAA CACAGACCGG AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTTAGAAG CACTCCTCGG TACTCCCATA ATCCTCTCGG AGAAAAAAAT CACAAGGCAA CTGTGAGTCC GGGAATCTCT TCTCTGATCC TTCTTCCTTA ATTCACTCCC ACACCCAAGA AGAAATGCTT TCCAAAACCG CAAGGGTAGA CTGGTTTATC CACCCACAAC ATCTACGAAT CGTACTTCTT TAATTGATCT AATTTACATA TTCTGCGTGT TGTATTCAGC ACTAAAAAAT GGTGGGAGCT GGGGGAGAAT GAAGACTGTT AAATGAAACC AGAAGGATAT TTACTACTTT TGCATGAAAA TAGAGCTTTC AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTCACCAT GAAACTTTAG AGATTAACGA CAAGATTTTC TACTTTTTTT AAGTGATTTT TTTGTCCTTC AGCCAAACAC AATATGGGCT CAAGTCACTT TTATTTGAAA TGTCATTTGG TGCCAGTATC CCGAATTC-3' **(FRAG. NO:___) (SEQ ID NO: 2470)**

5'-GCCACCATGG AAACCCTTTG CCTCAGGGCA TCCTTTTGGC TGGCACTGGT TGGATGTGTA ATCAGTGATA ATCCTGAGAG ATACAGCACA AATCTAAGCA ATCATGTGGA TGATTTCACC ACTTTTCGTG GCACAGAGCT CAGCTTCCTG GTTACCACTC ATCAACCCAC TAATTTGGTC CTACCCAGCA ATGGCTCAAT GCACAACTAT TGCCCACAGC AGACTAAAAT TACTTCAGCT TTCAAATACA TTAACACTGT GATATCTTGT ACTATTTTCA TCGTGGGAAT GGTGGGGAAT GCAACTCTGC TCAGGATCAT TTACCAGAAC AAATGTATGA GGAATGGCCC CAACGCGCTG ATAGCCAGTC TTGCCCTTGG AGACCTTATC TATGTGGTCA TTGATCTCCC TATCAATGTA TGGCTGGGCG CTGGCCTTTT GATCACAATG ACTTTGGCGT ATTTCTTTGC AAGCTGTTCC CCTTTTTGCA GAAGTCCTCG GTGGGGATCA CCGTCCTCAA CCTCTGCGCT CTTAGTGTTG ACAGGTACAG AGCAGTTGCC TCCTGGAGTC GTGTTCAGGG AATTGGGATT CCTTTGGTAA CTGCCATTGA AATTGCCTCC ATCTGGATCC TGTCCTTTAT CCTGGCCATT CCTGAAGCGA TTGGCTTCGT CATGGTACCC TTTGAATATA GGGGTGGACA GCATAAAACC TGTATGCTCA ATGCCACATC AAAATTCATG GAGTTCTACC AAGATGTAAA GGACTGGTGG CTCTTCGGGT TCTATTTCTG TATGCCCTTG GTGTGCACTG CGATCTTCTA CACCCTCATG ACTGGTGAGA TGTTGAACAG AAGGAATGGC AGCTTGAGAA TTGCCCTCAG TGAACATCTT AAGCAGCGTC GAGAAGTGGC AAAAACAGTT TTCTGCTTGG TTGTAATTTT TGCTCTTTGC TGGTTCCCTC TTCATTTAAG CCGTATATTG AAGAAAACTG TGTATAACGA GATGGACAAG AACCGATGTG AATTACTTAG TTTCTTACTG CTCATGGATT ACATCGGTAT TAACTTGGCA ACCATGAATT CATGTATAAA CCCCATAGCT CTGTATTTTG TGAGCAAGAA ATTTAAAAAT TGTTTCCAGT CATGCCTCTG CTGCTGCTGT TACCAGTCCA AAAGTCTGAT GACCTCGGTC CCCATGAACG GAACAAGCAT CCAGTGGAAG AACCACGATC AAAACAACCA CAACACAGAC CGGAGCAGCC ATAAGGACAG CATGAACTGA CCACCCTTAG AAGCACTCCT-3' **(FRAG. NO:_) (SEQ ID NO: 2469)**

<u>Substance P Antisense Nucleic Acids and Oligonucleotide Antisense Oligonucleotide Fragments</u>

5'-CTGCTGBGGC TTGGGTCTCC GGGCGBTTCT CTGCBGBBGB TGCTCBBBGG GCTCCGGCBG TTCCTCCTTG BTCTGGTCGCT GTCGTBCCBG TCGGBCCBGT BBTTCBGBTC BTCBTTGGCT CCTBTTTCTT CTGCBBBCBG CTGBGTGGBG BCBBGBBBBB BGBCTGCCBB GGCCBCBGBG BTTTTCBTGT TGGBTTTTGC GBCGGBCBGT CCCGCGGGGT GCTGAGTTTC TCTGGTTCCT CCGBGCGCBC GTGGTCGCTC CGCGTTTCTC TGGTTCCTCC GGTCCCGCGG GGTGCTGTCT GGTCGCTGTC GTGGCTTGGG TCTCCGGGCG GTTTCCTTCC TTTTCCGC-3' **(FRAG. NO:1877) (SEQ ID NO: 1888)**

5'-CTCC GGGCGB-3' (FRAG. NO:1878) (SEQ ID NO: 1889)
5'-GGCCBCGBGG-3' (FRAG. NO:1879) (SEQ ID NO: 1890)
5'-GGGTCTCCGGGCG-3' (FRAG. NO:1880) (SEQ ID NO: 1891)
5'-GGG TCTCCGGGCG G-3' (FRAG. NO:1881) (SEQ ID NO:1892)
5'-CGTGGTCGCTCCGC-3' (FRAG. NO:1355)(SEQ. ID NO:1365)
5'-GTTTCTCTGGTTCCTCCG-3' (FRAG. NO:1356)(SEQ. ID NO:1366)
5'-GTCCCGCGGGGTGCTG-3' (FRAG. NO:1357)(SEQ. ID NO:1367)
5'-TCTGGTCGCTGTCGT-3' (FRAG. NO:1358)(SEQ. ID NO:1368)
5'-GGCTTGGGTCTCCGGGCG-3' (FRAG. NO:1359)(SEQ. ID NO:1369)
5'-GTTTCCTTCCTTTTCCGC-3' (FRAG. NO:1360)(SEQ. ID NO:1370)
5'-CTGCTGBGGC TTGGGTCTCC GGGCGBTTCT CTGCBGBBGB TGCTCBBBGG GCTCCGGCBG TTCCTCCTTG BTCTGGTCGCT GTCGTBCCBG TCGGBCCBGT BBTTCBGBTC BTCBTTGGCT CCTBTTTCTT CTGCBBBCBG CTGBGTGGBG BCBBGBBBBB BGBCTGCCBB GGCCBCGBGG BTTTTCBTGT TGGBTTTTGC GBCGGBCBGT CCCGCGGGGT GCTGAGTTTC TCTGGTTCCT CCGBGCGCB-3' (FRAG. NO:1882) (SEQ ID NO: 1893)

Substance P Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GGGCTBBGBT GBTCCBCBTC BCTBCCBCGT TGCCCBCCBC BGBGGTCBCC BCBBTGBCCG TGTBGGCBGC TGCCCBBBGG BCBBTTTGCC BGGCTGGTTG CBCGBBCTGB TTGGGTTCCG BGGTGTTBGT GGBGBTGTTT GGGGBGBGGT CTGBGTCCBC CGGGBGGBCG TTBTCCBTTT CGBBGCTBGG CGGTBBBGCC CTBCTBTCTG TBCBCBBCCC CCCTCTGCBG CBGBGTCCTG TCGTGGCGCC TGGGGCTCBG GGTCCGGGC TAAGATGATC CACATCACTA CCACGTTGCC CACCACAGAG GTCACCACAA TGACCGTGTA GGCAGCTGCC CAAAGGACAA TTTGCCAGGC TGGTTGCACG AACTGATTGG GTTCCGAGGT GTTAGTGGAG ATGTTTGGGG AGAGGTCTGA GTCCACCGGG AGGACGTTAT CCATTTCGAA GCTAGGCGGT AAAGCCCTAC TATCTGTACA CAACCCCCCT CTGCAGCAGA GTCCTGTCGT GGCGCCTGGG GCTCAGGGTC CGTCCTGTCG TGGCGCCTGG GGCTCTTCTT TTGTGGGCTC TTTGGTGGCT GTGGCTGTGG TCTCTGTGGT TGCTGCCCTG GGTCTGGGGG TGTGGCCTTG GGGCCGTCCT CTGGCTCCTC CTCGTGGGCC CCC-3' (FRAG. NO:1883) (SEQ. ID NO:1894)
5'-GGGBGGBCG-3' (FRAG. NO:1884) (SEQ. ID NO:1895)
5'-GGGTC CG-3' (FRAG. NO:1885) (SEQ. ID NO:1896)
5-'GGGCC CCC-3' (FRAG. NO:1886) (SEQ. ID NO:1897)
5'-GTCCTGTCGTGGCGCCTGGGGCTC-3' (FRAG. NO:1361)(SEQ. ID NO:1371)
5'-TTCTTTTGTGGGCT-3' (FRAG. NO:1362)(SEQ. ID NO:1372)
5'-CTTTGGTGGCTGTGGCTG-3' (FRAG. NO:1363)(SEQ. ID NO:1373)
5'-TGGTCTCTGTGGTTG-3' (FRAG. NO:1364)(SEQ. ID NO:1374)
5'-CTGCCCTGGGTCTGG-3' (FRAG. NO:1365)(SEQ. ID NO:1375)
5'-GGGTGTGGCCTTGGGGCCGTCCTCTGGCTCCTCCTCGTGGGCCCCC (FRAG. NO:1366)(SEQ. ID NO:1376)
5'-GGGCTAAGAT GATCCACATC ACTACCACGT TGCCCACCAC AGAGGTCACC ACAATGACCG TGTAGGCAGC TGCCCAAAGG ACAATTTGCC AGGCTGGTTG CACGAACTGA TTGGGTTCCG AGGTGTTAGT GGAGATGTTT GGGGAGAGGT CTGAGTCCAC CGGGAGGACG TTATCCATTTC GAAGCTAGGC GGTAAAGCCC TACTATCTGTA CACAACCCCC CTCTGCAGCA GAGTCCTGTC GTGGCGCCTG GGGCTCAGGGTCC-3' (FRAG. NO:1367)(SEQ. ID NO:1377)
5'-GGGCTBBGBT GBTCCBCBTC BCTBCCBCGT TGCCCBCCBC BGBGGTCBCC BCBBTGBCCG TGTBGGCBGC TGCCCBBBGG BCBBTTTGCC BGGCTGGTTG CBCGBBCTGB TTGGGTTCCG BGGTGTTBGT GGBGBTGTTT GGGGBGBGGTC TGBGTCCBCC GGGBGGBCGT TBTCCBTTTC GBBGCTBGGC GGTBBBGCCC TBCTBTCTGTB CBCBBCCCCC CTCTGCBGCB GBGTCCTGTC GTGGCGCCTG GGGCTCBGGG TCC-3' (FRAG. NO:1368) (SEQ. ID NO:1378)

Chymase Antisense Nucleic Acids and Oligonucleotides Antisense Oligonucleotide Fragments

5'-GGBGCTGBTB CTGCBGATTT CBGBGGGBBG BBCCCTGBTB CTCBCCBGCT TCBGCTCTGG BGCBCBBGBG BBBGBGCBGC BGGGGGBGBG GBBGBBGCBG CBTCTTCCCB GBGBGGCTGC CTGBGCBBBT GCTGGTTTTC CTTTCCBGTC TTGGGTTTTB TBBCTCCCBG BBGGCBBGBG BGGGGCBBGG CGTTTTCTTC TCTCGCTGGT TTTCCTTTCC TGGCAGTGGG TGGGGGTGGG GGTGGGGTGG CTTCCTTGTT CCTGGGGGTG TCCTCTTGCT CTGGGCTTTT CTCCCCTTTT CCTTCCTGTC TGTTTTCCTG GGGCTCTCCT CTGTCTCTGT GTCCTTGCCC TGGCCCTCTT CCCTCTCCTG TCTCCTGTCC CTGTGTTCCG CCCGTCTTCC CTCTCCTGAC CTCCTTTTCC TCCGCTGGGT GGGGCCCTGC CTGTTCTCTG CTCCCTGGCT TGGGGTTTCT TCTGTGTGTC TTCTTCCTCT GTTGGCTGGC TTTCTCCTTC TTTTGTCTTC CTGGGTGCCC CTTCTTCCTT TCTTGGGTCC TTGGTGCTTG GGCTGGG TCCCAGTTAA TACATAATCA ATATGCAATT TATTAATACA TCTCTCCATG TCCACTCCCC CTGTATCTTG CCATTCTTGA CCTGCATTTC CATCCTCCTT ACCTTCCCTA GAGGCCAACT CATTTTCTTT GAAAAACCTG GCATTTCCCA GAAAAAAAAG TGAAGGGCTG GGAGCTGTCC GTTGTCCTGA TTTGCTCCCT CTGCCCTTGC TTCCAAATGT GGTTGGAAAG AAGCACTATT GAAAAATCCC TAAACGCACC CCTGCAGGGT TGGCTCTACC CTGTAGCCAT GGACACATGC TGTTGATACC ACCTGCCTCA TGAGTCTCAC ATAATTTGCC CTTTCACACT ATCTACCCCA TCAGCCTTAC CAAAACCATA CCTGCATCCT GGGCAGCATC TGCCCTTCAA GAGACTAAGG AATCTCCTTG CAACCAAGAA TGACTAGACC AATGAGACAC CCTTTAAGGC CCCAGCACAA TATAGAAATC CCACAATATG GTAATCCCAG TAAGGAGCTA TCAAGCCATT GCAGGACCAT CTAGAATACA ACTAGAGTAT AGTTCCTTTC AATCCAGGAA CTATACTCTA ACAGCTTGGC TCACAGGAAC CAGAAGTGAA GATGATGAGG ATCAGGGCTG AGCCTGTGAG CACCAGCTCC ACCACTGACA CCAACCACAG ATTAAACAAG CATCTTGTGG ACCCCTGGGA TGGAAAGAAT AGTTGTTGCC TTATCAACCT CCCCCACAGC CCACACAGAA AAGATAAAAT CATCATGGCT ACAGTGTTAC AGAAGATGAT GACCCAAGGA GTAGGCCTGC CTGAGTGAAT GCTGAGAGTG ATAATGGGAG CAGTAGCATC TCAGAGACTA CAGCAGAAAC CATCCACATA AAGAGCTTTG CCCAAACTTA TGATAAAGGG CACCCTCAGA GACTCTCCCT ACTTTAATAT TAGCCCATTG CAGAAATGGT GAGTGGAAAG AGAAATCTTA GGAAGAACCC CTTAAAAAAG CAAAATGCTT TTTAGGTTTG TGCTGAAGAG CCTGGAAAAG AAATAAGGAC ACACACGCTG AGAAATCTTC CTCCTGCCCC AACACTGGGA TAATCTCCAA GGATCTCTCC ATATCTCATT CTCCTGGATA CACTGTCCAC TCAGAAATAT TGTGCAGAGT GCAGTAATTC AAAAGTGAGC TATTGTGTTA GGAGTGAAGG CAAGAGTATC GTAAAATAAA TCAAATTTGA AATGAATTCT CTTAAATTGC TTTATAGATG TTTAATGTAA GCCAGCAGCT ATTAAACGAT AAACCTTAAA TTCGAGAAAA ACTTGGTCAT TCAGAAACTA TAGAAACAGG CAGGACTTAT TGCGAGGGCA AACACAGAGT GAGCTCCAGC CTGCTTCAGG AAAATCTGCC AGTGCCATGA AGGATGTACT CTGTCTGCTC CACTGCACTA CTGCTCAGTA TGAGCCCATG CCATCAGCTG TCCCTGACCC ACAGGAGTTC TTTAGAAGAG ACTGGTCAAC AAAAGTTTCT AGGGTGTTTT ATACCTGCCA ACTCGAGGGT TAAAACAAGT TGCATAGAAA TGCTCAATCA

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ACACAAAGGA ATAAAACCAA CGTTTATTAA GAACCAATCA TGTGGCATTT CACATTGAGC ATCATATTTA ATTCTGAAAA
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GTGGCCCAGG GCATCGTATC CTATGGACGG TCGGATGCAA AGCCCCCTGC TGTCTTCACC CGAATCTCCC ATTACCGGCC
CTGGATCAAC CAGATCCTGC AGGCAAATTA A-3' **(FRAG. NO:1887) (SEQ. ID NO:1898)**

5'-ATCATCGGGG GCACAGAATC CAAGCCACAT TCCCGCCCCT ACATGGCCTA CCTGGAAATT GTAACTTCCA ACGGTCCCTC
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ATTACCGGCC CTGGATCAAC CAGATCCTGC AGGCAAATTA A-3' **(FRAG. NO:) (SEQ. ID NO:2467)**

5'-TCCCAGTTAA TACATAATCA ATATGCAATT TATTAATACA TCTCTCCATG TCCACTCCCC CTGTATCTTG CCATTCTTGA
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TGGTCACAAG CCCAACCTGA GACCAAGGGC ATAGTGAGAT GATTTGGGAA AGGCACTTAT ACACTACTCA TCCCCGTCTT
TGAACTAAAT GCCTTATAAA TCTCCAAGAG AAATGACAGT CCACCATGTG GACTGCTTTC TGTAAGTCCA GGGAAAATAA
AAGCTATGTG CTTGAAACCC ACTTCTGATA TTATAAGGTG TGTGATCTTT GTCATGTTAA TGGGTCTGAG TATCAATTCT
ACAATTGTAA AGTGACAGTA ATGGTGTGTC CCCAGGTTGT TGTGGAAAGC TTGATTCTTA ATGCAACAGT AGGAAACCCC
AGCCTCTCTG GAGCAAACAC CCTTCTACAT CTTTACTTCC CCTGCACATT GGCAGGACTC TATTCCTCTA TTTCTCTCTA
GTGCTAGAGC AGAAAGGGAC CTTGATTTGA TATCAGGAAA ATCTATTTCT GAACCATAAG CTATGATAGC TGATTTAAAA
AATTGACTAT CATGACATGA TAATGATCAT AATGGTAATA CATATTGATA GGGTTGCCGT GAAAGTAATA ATATATCTAA
GAGTTGTGAC AATATATGAT ACGCCTAGAC TCTCAGAAAA TGCTAATTCC AATCCCAATT GCTCTTTGCA TAAAGTTCTG
TCCTAGGGTC TGTTCTTTTC CCACATCTAC CCTCCTTGGA TCTCTCTTCT GTCTTTTTCA TGTGGTTCAG AGGAGGAGAG
AGATCCAGGT CAATGTTTTT CAAATTACAA GGAATTATCA TTTAAATGGG GAAGAAGCTC AAGTTTTGAC GTGTAGTGGA
ATTGGAGTGG AGTGGAGTGG AATGGAAACT AACAGGAAGA CACTGCACAT GGTTAAGATA AAGATTGTTT CCTGAAACCT
TTAATTTGTG CTTACATACT CACACATACA TATGTGCATG CACTGGGACT CTGCAATATG CATTTCTGAC TATGGAACAT
AGCCATAAAA GTCTTTGCAC TGAACGTTCA GTGGGCCTTT CACAAGCTGC CCTAATTGGG AAAGAAAAAC ATGGTCCCTC
CATTTCCTGC CCCCAACTCC AGAAAAGTCA CCATAGTTGA GGGTACATCT GAGAAGCCAG CACTTGGGAG TTCAGGGCTC
AAGTTCCTTT CTAGAAAAAC ACTGGGTGAT TCTAGGGGAA CTTCCGATCA GAAACAGCCA ATTCAGAGTG AGAGAAGAAA
ACGTGACCAT GCAGTTCCTG TGGTTACCAG CCTTGCCCCT CTCTTGCCTT CTGGGAGTTA TAAAACCCAA GACTGGAAAG
GAAAACCAGC ATTTGCTCAG GCAGCCTCTC TGGGAAGATG CTGCTTCTTC CTCTCCCCCT GCTGCTCTTT CTCTTGTGCT
CCAGAGCTGA AGCTGGTGAG TATCAGGGTT CTTCCCTCTG AAATCTGCAG TATCAGCTCC TGAAACAAAG ATGTTTAGTC
TGAAATAGCT GACTCCTAAA CAGGGTTCCA AGATCTCTCT TCAAGAGTCC CACAGAGGAA ATTTCCACTT GGGATGTGTG
CCACCCCACC CCCACCCCCA CCCACTGCCA TTCTCTACAG CCTAGGACAC CCCCAGGAAC AAGGAATTTC ACCTCAATTG
TAGAAAAGCC CAGAGCAAGT GGAAGGAAAA GGGGTATCCC CAGGAAAACA GACATGTCCT CTTAATCTTC TGAGCATCAG
GGCTACCCAT TACTTTGTGA CTTTCTCACT CTGTGACCAT GCTCAAGAGC TATGGAGAAA TCTAAAACAG GAACCTGGAC
AGTGGGTCCT ACACAGAGAC AGAGGAGAGT GGGCCAGGGC AAGGTGGGAG TGGGAGAAGT CTGAGATGAA
AACATCAGAA TGGAGCAGAG GCAAGAATGA GATTTCACCT GGGAGGTTAT GGGTGGGGAA AGATACGAAA TACAGGAGAC
AGGAGAGGGA AGATGGGCGG AACACAGGGT GAGAATGAGA TTCCAGGGAA GCCTAGCTCA GCTTTAACCC AATTTGTCCA
TTCATTGGAG AGAGTATCTA TGGCCGTGTT CAAACCCTGG GGTGCTCTGT TCCAGGGGAG ATCATCGGGG GCACAGAATG
CAAGCCACAT TCCCGCCCCT ACATGGCCTA CCTGGAAATT GTAACTTCCA ACGGTCCCTC AAAATTTTGT GGTGGTTTCC
TTATAAGACG GAACTTTGTG CTGACGGCTG CTCATTGTGC AGGAAGGTGA GACAACAGGG TCTATTTATC TCCAAATGGG
AGATGAACAA CCAGAGTAGC ATCCAGGAAT ACACCTGCAC TGGGGACTGA AGAGGGGGTC CTGGGTCTTG TCAACTTTCA
GGAGAGGGAA GACTTTGGGC TGAAAGACTT TAGTCTGTGT TTGAATAGTT CCTTGAGCCT CAGTCACTGA GCTAAGCTCC
CTTCGGAGGA AAAGGAGGTC CTGTCCGAAG GTCCCTCTTG TTGCAGTAGC ACCCCTCACC CCTACCCAAC TCAAGACACA
CGGCTCACTT TTCAGGGCCC CACCCAGTCT CAGGGCCACT TCCTCTATGG CCTTTTCAAG AACACTGGCT CTAGTTCTCA
GGGTCCTGAA CCCATCATTT TATGGGAGCA GAGAACAGGT CTACATAAGA CCCCCACTTT CCCGTTTTAA CTGATATCTC
CTGCTTCAGG GGCTGGCCCT CATGCAGGGT TCCCTGAATT AGGAAGTGTG AACCCTGTCC CCTGAGTCCT CCCTGGCCTG
TTCAGTCCCC AGCAATTCCA GGGGTCGTAG AAATTGTGTC TGTTTCCTGA GAAAGCTCTT TCATGAGTTA AGCCTGAGCC
CTCAAATGCC ACAAGTGGCC CATGAAAAGG GAGATGGGTA GAGTCCGGCN ACCCAGTGAC AGAGTTTAGT CCTCTTTTCT
CAGAATGAGC TCACCTCAGA AGAAACCCCA AGCCATCACT GTCGCCTCCT TTTCCTTCCT TCTTCCTCAC AGCAGGTCTA
TAACAGTCAC CCTTGGAGCC CATAACATAA CAGAGGAAGA AGACACATGG CAGAAGCTTG AGGTTATAAA GCAATTCCGT
CATCCAAAAT ATAACACTTC TACTCTTCAC CACGATATCA TGTTACTAAA GGTGACAACA CCTCTCTTCT CCCTTTCCAC
TTCCCATTCT CCTAAGCTTC TCCTTCAGGT CCTCATTGCC CTGAATTTTT CTTAGGACTT GGCTATAACA TGAAGCTACT
CACCCTGTCC CTCCCTGATC ACCTCCAACT GTCCAGAGCC CATTTCGAGG ACTGACAGTC CTTCATTCCC TTCACAGTTG
AAGGAGAAAG CCAGCCTGAC CCTGGCTGTG GGGACACTCC CCTTCCCATC ACAATTCAAC TTTGTCCCAC CTGGGAGAAT
GTGCCGGGTG GCTGGCTGGG GAAGAACAGG TGTGTTGAAG CCGGGCTCAG ACACTCTGCA AGAGGTGAAG CTGAGACTCA
TGGATCCCCA GGCCTGCAGC CACTTCAGAG ACTTTGACCA CAATCTTCAG CTGTGTGTGG GCAATCCCAG GAAGACAAAA
TCTGCATTTA AGGTGATCCT CCAACTAGGT TTCCTCTCCA AAACTCACTG TTCAGGGACC TGAATGCTCT TAGAAGGAGA
TGGGGTCAGC AGGTTGTCAG TCAGGTGACA GGGTGAGCAT CACAGGAATT GCTGTCCTCC CGTGGTCCAA GACAGCCTCT
GACCATCCAT TCCAGTCTAC TGCACTGGGG GCATGGGGTG ACTGTGGAGA ATGTGGATGA CGGTCCCAAG AAAGGAAGAA
GGGGCATCAG AACTAGATGT ATAAGTGAGG AGCTCCACCT CCTGGGTCTG ACTTTAGGTC TCACTGTGAC TCCAAGCTGG
CTGGCAGACA GGAGTGGAGG ACTTCCCGGG CTCACCTTCT TCTCTCTCTC CTCCCCCTAC AGGGAGACTC TGGGGGCCCT
CTTCTGTGTG CTGGGGTGGC CCAGGGCATC GTATCCTATG GACGGTCGGA TGCAAAGCCC CCTGCTGTCT TCACCCGAAT
CTCCCATTAC CGGCCCTGGA TCAACCAGAT CCTGCAGGCA AATTAATCCT GGATCCTGAG CCAGCCTGAA GGGAAGCTGG
AACTGGACCT TAGCAGCAAA GTGTGTGCAA CTCATTCTGG TTCTACCCTT GGTTCCCTCA GCCACAACCC TAAGCCTCCA
AGAGGTCTCC TACAGGTAAC AGAACTTTCA ATAAACTTCA GTGAAGACAC AGCTTCTAGT CGTGAGTGTG TGTCCCTCTC
TGCTGCTCTC TTCTCCTGCA CATGTGACCT GATTCCCAGC CCAAGCACCA AGGA-3' **(FRAG. NO:) (SEQ. ID NO:2467)**

5'-GGBGCBCBBG-3' **(FRAG. NO:1888) (SEQ. ID NO:1899)**

5'-GBBGCBGC-3' **(FRAG. NO:1889) (SEQ. ID NO:1900)**

5'-GGGGCBBGG CG-3' **(FRAG. NO:1890) (SEQ. ID NO:1901)**

5'-CGTTTTCTTCTCTC-3' **(FRAG. NO:1369)(SEQ. ID NO:1379)**

5'-GCTGGTTTTCCTTTCC-3' **(FRAG. NO:1370)(SEQ. ID NO:1380)**

5'-TGGCAGTGGGTGGGGGTGGGGGTGGGGTGGC-3' **(FRAG. NO:1371)(SEQ. ID NO:1381)**
5'-TTCCTTGTTCCTGGGGGTGTCCT-3' **(FRAG. NO:1372)(SEQ. ID NO:1382)**
5'-CTTGCTCTGGGCTTTTCT-3' (FRAG. NO:1373)(SEQ. ID NO:1383)
5'-CCCCTTTTCCTTCC-3' (FRAG. NO:1374)(SEQ. ID NO:1384)
5'-TGTCTGTTTTCCTGGGG-3' (FRAG. NO:1375)(SEQ. ID NO:1385)
5'-CTCTCCTCTGTCTCTGTGT-3' (FRAG. NO:1376)(SEQ. ID NO:1386)
5'-CCTTGCCCTGGCCC-3' (FRAG. NO:1377)(SEQ. ID NO:1387)
5'-TCTTCCCTCTCCTGTCTCCTGT-3' (FRAG. NO:1378)(SEQ. ID NO:1388)
5'-CCCTGTGTTCCGCCC-3' (FRAG. NO:1379)(SEQ. ID NO:1389)
5'-GTCTTCCCTCTCCTG-3' (FRAG. NO:1380)(SEQ. ID NO:1390)
5'-ACCTCCTTTTCCTCCG-3' (FRAG. NO:1381)(SEQ. ID NO:1391)
5'-CTGGGTGGGGCCCTG-3' (FRAG. NO:1382)(SEQ. ID NO:1392)
5'-CCTGTTCTCTGCTCCC-3' (FRAG. NO:1383)(SEQ. ID NO:1393)
5'-TGGCTTGGGGTTTCTTCTG-3' (FRAG. NO:1384)(SEQ. ID NO:1394)
5'-TGTGTCTTCTTCCTCTGTT-3' (FRAG. NO:1385)(SEQ. ID NO:1395)
5'-GGCTGGCTTTCTCCTTC-3' (FRAG. NO:1386)(SEQ. ID NO:1396)
5'-TTTTGTCTTCCTGGG-3' (FRAG. NO:1387)(SEQ. ID NO:1397)
5'-TGCCCCTTCTTCCTTTCTTGGG-3' (FRAG. NO:1388)(SEQ. ID NO:1398)
5'-TCCTTGGTGCTTGGGCTGGG-3' (FRAG. NO:1389)(SEQ. ID NO:1399)
5'-GGBGCTGBTB CTGCBGATTT CBGBGGGBBG BBCCCTGBTB CTCBCCBGCT TCBGCTCTGG BGCBCBBGBG BBBGBGCBGC BGGGGGBGBG GBBGBBGCBG CBTCTTCCCB GBGBGGCTGC CTGBGCBBBT GCTGGTTTTC CTTTCCBGTC TTGGGTTTTB TBBCTCCCBG BBGGCBBGBG BGGGGCBBGG-3' **(FRAG. NO:1891) (SEQ. ID NO:1902)**

<u>Endothelial Nitric Oxide Synthase Nucleic Acids and Antisense Oligonucleotide Fragments</u>

5'-GCGTCTTGGG GTGCBGGGCC CBTCCTGCTG CGCCTGGGCG CTGCTGTGCG TCCGTCTGCT GGGGGGCCGG GGTGGCTGGG CCCTGCTTGC CGCACGACCC CGGGCCGACC CGAGGCTCGG GGGGCTGTGT TCTGGCGCTG GTGGGCTTGG GCCCCTCTGG GGGCTGGGTT TCCTGCTGCG CCTGGGCGCT GGCGTCTTGG GGTGCGGGGC CGGGGGGCCG GGGGGCCGCT GTTCGTGGGC CTGGGGGTGC CTGTGGCTGC CGGTTGCCCC GGTTGGTGGC GCCGTCCTGC TGCCGGTCGT TGGCTGGGTC CCCCCGCCCG TTTCCTGGGG TCCGCGTGGG GTGCTCCGGT TCCTCGTGCC GCTGCTGCCT TGTCTTTCCG GCCGTGGCGG CGTGGTGGTC CGCCCCCCCT GGCCTTCTGC TCGGGGTCTG GCTGGTTGCC GGTGCCCTTG GCGGCGGTCT TCTTCCTGGT GGCTCTGGGC CCGGCCGGTC TCGGGCGTCT CGTGTTCGCT CTTGTGCTGT TCCGGCCGCT CCTTCCTCTT CCGCCGCCGC CGCTCCCCGC CCGCTCGTCG CCCTGGCCCG GCCTCCTCCT GGCCGCTGTC TCGGGCGGCG GCCTTGGCGC TCCGTTTGGG GCTGCCTCTG GCGCTTCCGG CCCTCGGCCT GGGCGCTCTC TTCCGCCTGT GCTGGTGGCC CTCGTGGGCC CCTCCTGGCC TCCGGTGTCC TGTGGTCCCC CGGCTGGTGG CCGGGCCGGT TGGGCGGGCG TGGGCGCCGG CGGGTCCTCC GGGCTGCCCT TCTCCGCCGG GGGTCCCGCG CTCCTGCTGT TCCCTGGGCT CTTCTGCCTC TCTCCTGGGT GGGTGCTGGG TGCCGGGGTC TCCGGGCTTG CCCCGCGCTG CTGGGCGTTC TGCGGTCTTG GGGTTGTCTG TGGCCCCGCT CGTGTCGCCC TCCGTCGCCC GTCGCCGGCC TCGTCCCCTC CTGGGTGCGC GGCGGGCTGG TCCTGGCGTT TTGCTCCTTC CTGGGCGTCT TGGGGTGCBG GGCCCBTCCT GCTGCGCCTG GGCGCTGCTG TGCGTCCGTC TGCTGGGGGG CCGGGGTGGC TGGGCCCTGC TTGCCGCACG ACCCCGGGCC GACCCGAGGC TCGGGGGGCT GTGTTCTGGC GCTGGTGGGC TTGGGCCCCT CTGGGGGCTG GGTTTCCTGC TGCGCCTGGG CGCTGGCGTC TTGGGGTGCG GGGCCGGGGG GCCGGGGGGC CGCTGTTCGT GGGCCTGGGG GTGCCTGTGG CTGCCGGTTG CCCCGGTTGG TGGCGCCGTC CTGCTGCCGG TCGTTGGCTG GGTCCCCCCG CCCGTTTCCT GGGGTCCGCG TGGGGTGCTC CGGTTCCTCG TGCCGCTGCT GCCTTGTCTT TCCGGCCGTG GCGGCGTGGT GGTCCGCCCC CCCTGGCCTT CTGCTCGGGG TCTGGCTGGT TGCCGGTGCC CTTGGCGGCG GTCTTCTTCC TGGTGGCTCT GGGCCCGGCC GGTCTCGGGC GTCTCGTGTT CGCTCTTGTG CTGTTCCGGC CGCTCCTTCC TCTTCCGCCG CCGCCGCTCC CCGCCCGCTC GTCGCCCTGG CCCGGCCTCC TCCTGGCCGC TGTCTCGGGC GGCGGCCTTG GCGCTCCGTT TGGGGCTGCC TCTGGCGCTT CCGGCCCTCG GCCTGGGCGC TCTCTTCCGC CTGTGCTGGT GGCCCTCGTG GGCCCCTCCT GGCCTCCGGT GTCCTGTGGT CCCCCGGCTG GTGGCCGGGC CGGTTGGGCG GGCGTGGGCG CCGGCGGGTC CTCCGGGCTG CCCTTCTCCG CCGGGGGTCC CGCGCTCCTG CTGTTCCCTG GGCTCTTCTG CCTCTCTCCT GGGTGGGTGC TGGGTGCCGG GGTCTCCGGG CTTGCCCCGC GCTGCTGGGC GTTCTGCGGT CTTGGGGTTG TCTGTGGCCC CGCTCGTGTC GCCCTCCGTC GCCCGTCGCC GGCCTCGTCC CCTCCTGGGT GCGCGGCGGG CTGGTCCTGG CGTTTTGCTC CTTCCTGG-3' **(FRAG. NO:1892) (SEQ. ID NO: 1903)**
5'-GCGGGGCCG-3' **(FRAG. NO:1893) (SEQ. ID NO: 1904)**
5'-CGGGGGGC-3' **(FRAG. NO:1894) (SEQ. ID NO: 1905)**
5'-GCGCGGCGGGC-3' **(FRAG. NO:1895) (SEQ. ID NO: 1906)**
5'-CTGTGCGTCCGTCTGCTGG **(FRAG. NO:1390)(SEQ. ID NO:1400)**
GGGGCCGGGGTGGCTGGGCCCTGCTTGCCGC (FRAG. NO:1391)(SEQ. ID NO:1401)
ACGACCCCGGGCCGACCCGAG (FRAG. NO:1392)(SEQ. ID NO:1402)
GCTCGGGGGGCTGTGTTCTGGCGCTGGTGGG (FRAG. NO:1393)(SEQ. ID NO:1403)
CTTGGGCCCCTCTGGGGGCTGGGTT (FRAG. NO:1394)(SEQ. ID NO:1404)
TCCTGCTGCGCCTGGGCGCTG (FRAG. NO:1395)(SEQ. ID NO:1405)
GCGTCTTGGGGTGC (FRAG. NO:1396)(SEQ. ID NO:1406)
GGGGCCGGGGGGCCGGGGG (FRAG. NO:1397)(SEQ. ID NO:1407)
GCCGCTGTTCGTGGGCCTGGG (FRAG. NO:1398)(SEQ. ID NO:1408)
GGTGCCTGTGGCTGCC (FRAG. NO:1399)(SEQ. ID NO:1409)
GGTTGCCCCGGTTGGTGGC (FRAG. NO:1400)(SEQ. ID NO:1410)
GCCGTCCTGCTGCCGGT (FRAG. NO:1401)(SEQ. ID NO:1411)
CGTTGGCTGGGTCCCCCCGC (FRAG. NO:1402)(SEQ. ID NO:1412)
CCGTTTCCTGGGGTCC (FRAG. NO:1403)(SEQ. ID NO:1413)
GCGTGGGGTGCTCC (FRAG. NO:1404)(SEQ. ID NO:1414)
GGTTCCTCGTGCCG (FRAG. NO:1405)(SEQ. ID NO:1415)
CTGCTGCCTTGTCTTTCC (FRAG. NO:1406)(SEQ. ID NO:1416)

GGCCGTGGCGGCGTGGTGGTCC (FRAG. NO:1407)(SEQ. ID NO:1417)
GCCCCCCCTGGCCTTCTGCTC (FRAG. NO:1408)(SEQ. ID NO:1418)
GGGGTCTGGCTGGT (FRAG. NO:1409)(SEQ. ID NO:1419)
TGCCGGTGCCCTTGGCGGC (FRAG. NO:1410)(SEQ. ID NO:1420)
GGTCTTCTTCCTGGTG (FRAG. NO:1411)(SEQ. ID NO:1421)
GCTCTGGGCCCGGCCGGTCTCGG (FRAG. NO:1412)(SEQ. ID NO:1422)
GCGTCTCGTGTTCG (FRAG. NO:1413)(SEQ. ID NO:1423)
CTCTTGTGCTGTTCCGGCCG (FRAG. NO:1414)(SEQ. ID NO:1424)
CTCCTTCCTCTTCCGCCGCC (FRAG. NO:1415)(SEQ. ID NO:1425)
GCCGCTCCCCGCCC (FRAG. NO:1416)(SEQ. ID NO:1426)
GCTCGTCGCCCTGGCCC (FRAG. NO:1417)(SEQ. ID NO:1427)
GGCCTCCTCCTGGCCGC (FRAG. NO:1418)(SEQ. ID NO:1428)
TGTCTCGGGCGGCGGCCTTGGC (FRAG. NO:1419)(SEQ. ID NO:1429)
GCTCCGTTTGGGGCTG (FRAG. NO:1420)(SEQ. ID NO:1430)
CCTCTGGCGCTTCC (FRAG. NO:1421)(SEQ. ID NO:1431)
GGCCCTCGGCCTGGGCGCTC (FRAG. NO:1422)(SEQ. ID NO:1432)
TCTTCCGCCTGTGC (FRAG. NO:1423)(SEQ. ID NO:1433)
TGGTGGCCCTCGTGG (FRAG. NO:1424)(SEQ. ID NO:1434)
GCCCCTCCTGGCCTCCGGTGTCC (FRAG. NO:1425)(SEQ. ID NO:1435)
TGTGGTCCCCCGGCTGGT (FRAG. NO:1426)(SEQ. ID NO:1436)
GGCCGGGCCGGTTGGGCGGGC (FRAG. NO:1427)(SEQ. ID NO:1437)
GTGGGCGCCGGCGGGTCCTCC (FRAG. NO:1428)(SEQ. ID NO:1438)
GGGCTGCCCTTCTCC (FRAG. NO:1429)(SEQ. ID NO:1439)
GCCGGGGGTCCCGC (FRAG. NO:1430)(SEQ. ID NO:1440)
GCTCCTGCTGTTCCCTGGGCTCTTCTGCC (FRAG. NO:1431)(SEQ. ID NO:1441)
TCTCTCCTGGGTGGGTGCTGGGTGCCG (FRAG. NO:1432)(SEQ. ID NO:1442)
GGGTCTCCGGGCTTG (FRAG. NO:1433)(SEQ. ID NO:1443)
CCCCGCGCTGCTGGGCGTTCTGC (FRAG. NO:1434)(SEQ. ID NO:1444)
GGTCTTGGGGTTGTC (FRAG. NO:1435)(SEQ. ID NO:1445)
TGTGGCCCCGCTCG (FRAG. NO:1436)(SEQ. ID NO:1446)
TGTCGCCCTCCGTCGCC (FRAG. NO:1437)(SEQ. ID NO:1447)
CGTCGCCGGCCTCGTCC (FRAG. NO:1438)(SEQ. ID NO:1448)
CCTCCTGGGTGCGC (FRAG. NO:1439)(SEQ. ID NO:1449)
GGCGGGCTGGTCCT (FRAG. NO:1440)(SEQ. ID NO:1450)
GGCGTTTTGCTCCTTCCTGG (FRAG. NO:1441)(SEQ. ID NO:1451)
5'-GCGTCTTGGGGTGCBGGGCCCBTCCTGCTGCGCCTGGGCGCTG-3' (FRAG. NO:1896) (SEQ. ID NO: 1907)

<u>Inducible Nitric Oxide Synthase Nucleic Acids and Antisense Oligonucleotide Fragments</u>

5'-CTGCCCCBGT TTTTGBTCCT CBCBTGCCGT GGGGBGGBCB BTGGCTGCCT CCCCGGGGTT TCTGCTGCTT GCTGCTTCTT
TCCCGTCTCC CTTCTTTCCC GTCTCCTTTT TGCCTCTTTG GGTTCCTGTT GTTTCTGGCC TGCTTGGTGG CGGCTTGTGC
GTTTCCTCTC TCTTCTCTTG GGTCTCCGCT TCTCGTCCTG CCTTTTCCTG TCTCTGTCGC GCCGTTCCTC CTCCGGCGTC
CTCCTGCCCT GTGCTGTTTG CCTCGGGTGG TGCGGGTCCC GGTGCTCCCC CGGCGGGCCG GCTGGTTGCC TGGGCCTGTC
TGGTGGGGTG TGGGGCCGCT GGGTTGGGGG TGTGGTGGGC TCTTCTGTGG CCTGTGGGGC TGTTGGTGTC TCTGTGGGCG
TGTGCTGGGT CTTGGGGCTT CCTCCCTTGT GCTGGGTGCG GCCTCCCCGC CCCCCTTCTG GGCCGGTGGC CTGGCTCCTT
GTGGGCGCTT CTGGCTCTTG CCCTGTCCTT CTTCGCCTCG TGGCTGCTGG GCTGC CATATGTATG GGAATACTGT
ATTTCAGGCA TTATAAGGAA TGAAATTATA GGCCGGGCAT TGTGGCTAAC CCTTGTAATC CTAGCACTTT
GAGAGGCTGA AGTGGGCAGA TCACTTGAGC TTCAGAGTTC GAGACCAGCA TGGACAACAT GGTGAAACCC
AGTCTCTACC AAAAACACAA AAATATTAGC TGGGTGTGGT GGTGCATGCC TGTAGTCCCA GCTACTCAGG
AGGCTGAGGT GGGAGGATCG CTTGAGCCTG GGAGGCAGAA GTTGCAATGA GCAGAGATCG TGCCACTCCG
CTCCAGTCTT GGTGACAGAA TGAGACTCCA TCTCAAAAAT AAATAAATAA ATAAATAAAA TAAATGAAAT
GAAATTATAA GAAATTACCA CTTTTTCATG TAAGAAGTGA TCATTTCCAT TATAAGGGAA GGAATTTAAT
CCTACCTGCC ATTCCACCAA AGCTTACCTA GTGCTAAAGG ATGAGGTGTT AGTAAGACCA ACATCTCAGA
GGCCTCTCTG TGCCAATAGC CTTCCTTCCT TTCCCTTCCA AAAACCTCAA GTGACTAGTT CAGAGGCCTG
TCTGGAATAA TGGCATCATC TAATATCACT GGCCTTCTGG AACCTGGGCA TTTTCCAGTG TGTTCCATAC
TGTCAATATT CCCCCAGCTT CCTGGACTCC TGTCACAAGC TGGAAAAGTG AGAGGATGGA CAGGGATTAA
CCAGAGAGCT CCCTGCTGAG GAAAAAATCT CCCAGATGCT GAAAGTGAGG CCATGTGGCT TGGCCAAATA
AAACCTGGCT CCGTGGTGCC TCTGTCTTAG CAGCCACCCT GCTGATGAAC TGCCACCTTG GACTTGGGAC
CAGAAAGAGG TGGGTTGGGT GAAGAGGCAC CACACAGAGT GATGTAACAG CAAGATCAGG TCACCCACAG
GCCCTGGCAG TCACAGTCAT AAATTAGCTA ACTGTACACA AGCTGGGGAC ACTCCCTTTG GAAACCAAAA
AAAAAAAAAA AAAAAAGAGA CCTTTATGCA AAAACAACTC TCTGGATGGC ATGGGGTGAG TATAAATACT
TCTTGGCTGC CAGTGTGTTC ATAACTTTGT AGCGAGTCGA AAACTGAGGC TCCGGCCGCA GAGAACTCAG
CCTCATTCCT GCTTTAAAAT CTCTCGGCCA CCTTTGATGA GGGGACTGGG CAGTTCTAGA CAGTCCCGAA
GTTCTCAAGG CACAGGTCTC TTCCTGGTTT GACTGTCCTT ACCCCGGGGA GGCAGTGCAG CCAGCTGCAA
GGTGAGTTGC C CATATGTATG GGAATACTGT ATTTCAGGCA TTATAAGGAA TGAAATTATA GGCCGGGCAT
TGTGGCTAAC CCTTGTAATC CTAGCACTTT GAGAGGCTGA AGTGGGCAGA TCACTTGAGC TTCAGAGTTC
GAGACCAGCA TGGACAACAT GGTGAAACCC AGTCTCTACC AAAAACACAA AAATATTAGC TGGGTGTGGT
GGTGCATGCC TGTAGTCCCA GCTACTCAGG AGGCTGAGGT GGGAGGATCG CTTGAGCCTG GGAGGCAGAA
GTTGCAATGA GCAGAGATCG TGCCACTCCG CTCCAGTCTT GGTGACAGAA TGAGACTCCA TCTCAAAAAT
AAATAAATAA ATAAATAAAA TAAATGAAAT GAAATTATAA GAAATTACCA CTTTTTCATG TAAGAAGTGA
TCATTTCCAT TATAAGGGAA GGAATTTAAT CCTACCTGCC ATTCCACCAA AGCTTACCTA GTGCTAAAGG

ATGAGGTGTT AGTAAGACCA ACATCTCAGA GGCCTCTCTG TGCCAATAGC CTTCCTTCCT TTCCCTTCCA
AAAACCTCAA GTGACTAGTT CAGAGGCCTG TCTGGAATAA TGGCATCATC TAATATCACT GGCCTTCTGG
AACCTGGGCA TTTTCCAGTG TGTTCCATAC TGTCAATATT CCCCCAGCTT CCTGGACTCC TGTCACAAGC
TGGAAAAGTG AGAGGATGGA CAGGGATTAA CCAGAGAGCT CCCTGCTGAG GAAAAAATCT CCCAGATGCT
GAAAGTGAGG CCATGTGGCT TGGCCAAATA AAACCTGGCT CCGTGGTGCC TCTGTCTTAG CAGCCACCCT
GCTGATGAAC TGCCACCTTG GACTTGGGAC CAGAAAGAGG TGGGTTGGGT GAAGAGGCAC CACACAGAGT
GATGTAACAG CAAGATCAGG TCACCCACAG GCCCTGGCAG TCACAGTCAT AAATTAGCTA ACTGTACACA
AGCTGGGGAC ACTCCCTTTG GAAACCAAAA AAAAAAAAAA AAAAAAGAGA CCTTTATGCA AAAACAACTC
TCTGGATGGC ATGGGGTGAG TATAAATACT TCTTGGCTGC CAGTGTGTTC ATAACTTTGT AGCGAGTCGA
AAACTGAGGC TCCGGCCGCA GAGAACTCAG CCTCATTCCT GCTTTAAAAT CTCTCGGCCA CCTTTGATGA
GGGGACTGGG CAGTTCTAGA CAGTCCCGAA GTTCTCAAGG CACAGGTCTC TTCCTGGTTT GACTGTCCTT
ACCCCGGGGA GGCAGTGCAG CCAGCTGCAA GGTGAGTTGC C-3' (FRAG. NO:_)(SEQ. ID NO: 2506)
5'-CTGCTTTAAA ATCTCTCGGC CACCTTTGAT GAGGGGACTG GGCAGTTCTA GACAGTCCCG AAGTTCTCAA GGCACAGGTC
TCTTCCTGGT TTGACTGTCC TTACCCCGGG GAGGCAGTGC AGCCAGCTGC AAGCCCCACA GTGAAGAACA TCTGAGCTCA
AATCCAGATA AGTGACATAA GTGACCTGCT TTGTAAAGCC ATAGAGATGG CCTGTCCTTG GAAATTTCTG TTCAAGACCA
AATTCCACCA GTATGCAATG AATGGGGAAA AAGACATCAA CAACAATGTG GAGAAAGCCC CCTGTGCCAC CTCCAGTCCA
GTGACACAGG ATGACCTTCA GTATCACAAC CTCAGCAAGC AGCAGAATGA GTCCCCGCAG CCCCTCGTGG AGACGGGAAA
GAAGTCTCCA GAATCTCTGG TCAAGCTGGA TGCAACCCCA TTGTCCTCCC CACGGCATGT GAGGATCAAA AACTGGGGCA
GCGGGATGAC TTTCCAAGAC ACACTTCACC ATAAGGCCAA AGGGATTTTA ACTTGCAGGT CCAAATCTTG CCTGGGGTCC
ATTATGACTC CCAAAAGTTT GACCAGAGGA CCCAGGGACA AGCCTACCCC TCCAGATGAG CTTCTACCTC AAGCTATCGA
ATTTGTCAAC CAATATTACG GCTCCTTCAA AGAGGCAAAA ATAGAGGAAC ATCTGGCCAG GGTGGAAGCG GTAACAAAGG
AGATAGAAAC AACAGGAACC TACCAACTGA CGGGAGATGA GCTCATCTTC GCCACCAAGC AGGCCTGGCG CAATGCCCCA
CGCTGCATTG GGAGGATCCA GTGGTCCAAC CTGCAGGTCT TCGATGCCCG CAGCTGTTCC ACTGCCCGGG AAATGTTTGA
ACACATCTGC AGACACGTGC GTTACTCCAC CAACAATGGC AACATCAGGT CGGCCATCAC CGTGTTCCCC CAGCGGAGTG
ATGGCAAGCA CGACTTCCGG GTGTGGAATG CTCAGCTCAT CCGCTATGCT GGCTACCAGA TGCCAGATGG CAGCATCAGA
GGGGACCCTG CCAACGTGGA ATTCACTCAG CTGTGCATCG ACCTGGGCTG GAAGCCCAAG TACGGCCGCT TCGATGTGGT
CCCCCTGGTC CTGCAGGCCA ATGGCCGTGA CCCTGAGCTC TTCGAAATCC CACCTGACCT TGTGCTTGAG GTGGCCATGG
AACATCCCAA ATACGAGTGG TTTCGGGAAC TGGAGCTAAA GTGGTACGCC CTGCCTGCAG TGGCCAACAT GCTGCTTGAG
GTGGGCGGCC TGGAGTTCCC AGGGTGCCCC TTCAATGGCT GGTACATGGG CACAGAGATC GGAGTCCGGG ACTTCTGTGA
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AGCGTCAGTT GCGGGGCGCA GTGCCCTGGG CGTTCGACCC TCCCGGCTCA GACACCAACA GCCCCTGAGA GCCGCCTGGC
TTTCCCTTCC AGTTCCGGGA GAGCGGCTGC CCGACTCAGG TCCGCCCGAC CAGGATCAGC CCCGCTCCTC CCCTCTTGAG
GTGGTGCCTT CTCACATCTG TCCAGAGGCT GCAAGGATTC AGCATTATTC CTCCAGGAAG GAGCAAAACG CCTCTTTTCC
CTCTCTAGGC CTGTTGCCTC GGGCCTGGGT CCGCCTTAAT CTGGAAGGCC CCTCCCAGCA GCGGTACCCC AGGGCCTACT
GCCACCCGCT TCCTGTTTCT TAGTCCGAAT GTTAGATTCC TCTTGCCTCT CTCAGGAGTA TCTTACCTGT AAAGTCTAAT
CTCTAAATCA AGTATTTATT ATTGAAGATT TACCATAAGG GACTGTGCCA GATGTTAGGA GAACTACTAA AGTGCCTACC
CCAGCTC-3' (FRAG. NO:_) (SEQ. ID NO:2508)

5'-CCCCGGGG-3' **(FRAG. NO:1898) (SEQ. ID NO: 1909)**
5'-GGGGCCGCTGGG-3' **(FRAG. NO:1899) (SEQ. ID NO:1910)**
5'-GGGGGTGTGG-3' **(FRAG. NO:1900) (SEQ. ID NO: 1911)**
5'-CTGCCTCCCCGGGGT-3' **(FRAG. NO:1442)(SEQ. ID NO:1452)**
5'-TTCTGCTGCTTGCTG-3' **(FRAG. NO:1443)(SEQ. ID NO:1453)**
5'-CTTCTTTCCCGTCTCC-3' **(FRAG. NO:1444)(SEQ. ID NO:1454)**
5'-CTTCTTTCCCGTCTCC-3' **(FRAG. NO:1445)(SEQ. ID NO:1455)**
5'-TTTTTGCCTCTTTG-3' **(FRAG. NO:1446)(SEQ. ID NO:1456)**
5'-GGTTCCTGTTGTTTCT-3' **(FRAG. NO:1447)(SEQ. ID NO:1457)**
5'-GGCCTGCTTGGTGGCG-3' **(FRAG. NO:1448)(SEQ. ID NO:1458)**
5'-GCTTGTGCGTTTCC-3' **(FRAG. NO:1449)(SEQ. ID NO:1459)**
5'-TCTCTCTTCTCTTGGGTCTCCGCTTCTCGTCCTGCC-3' **(FRAG. NO:1450)(SEQ. ID NO:1460)**
5'-TTTTCCTGTCTCTGTCGC-3' **(FRAG. NO:1451)(SEQ. ID NO:1461)**
5'-GCCGTTCCTCCTCC-3' **(FRAG. NO:1452)(SEQ. ID NO:1462)**
5'-GGCGTCCTCCTGCCC-3' **(FRAG. NO:1453)(SEQ. ID NO:1463)**
5'-TGTGCTGTTTGCCTCGG-3' (FRAG. NO:1454)(SEQ. ID NO:1464)
5'-GTGGTGCGGGTCCC-3' (FRAG. NO:1455)(SEQ. ID NO:1465)
5'-GGTGCTCCCCCGGC-3' (FRAG. NO:1456)(SEQ. ID NO:1466)
5'-GGGCCGGCTGGTTGCCTGGGC-3' (FRAG. NO:1457)(SEQ. ID NO:1467)
5'-CTGTCTGGTGGGGTGTGGGGCC-3' (FRAG. NO:1458)(SEQ. ID NO:1468)
5'-GCTGGGTTGGGGGTGTGGTG-3' (FRAG. NO:1459)(SEQ. ID NO:1469)
5'-GGCTCTTCTGTGGCC-3' (FRAG. NO:1460)(SEQ. ID NO:1470)
5'-TGTGGGGCTGTTGGTG-3' (FRAG. NO:1461)(SEQ. ID NO:1471)
5'-TCTCTGTGGGCGTGTG-3' (FRAG. NO:1462)(SEQ. ID NO:1472)
5'-CTGGGTCTTGGGGCTTC-3' (FRAG. NO:1463)(SEQ. ID NO:1473)
5'-CTCCCTTGTGCTGGG-3' (FRAG. NO:1464)(SEQ. ID NO:1474)
5'-TGCGGCCTCCCCGC-3' (FRAG. NO:1465)(SEQ. ID NO:1475)
5'-CCCCCTTCTGGGCC-3' (FRAG. NO:1466)(SEQ. ID NO:1476)
5'-GGTGGCCTGGCTCCTTGTGG-3' (FRAG. NO:1467)(SEQ. ID NO:1477)
5'-GCGCTTCTGGCTCTTG-3' (FRAG. NO:1468)(SEQ. ID NO:1478)
5'-CCCTGTCCTTCTTCGCCTCGT-3' (FRAG. NO:1469)(SEQ. ID NO:1479)
5'-GGCTGCTGGGCTGC-3' (FRAG. NO:1470)(SEQ. ID NO:1480)
5'-CTGCCCCBGTTTTTGBTCCTCBCBTGCCGTGGGGBGGBCBBTGG-3' **(FRAG. NO:1901) (SEQ. ID NO: 1912)**

<u>**NF-kB Nucleic Acids and Antisense Oligonucleotide Fragments**</u>

5'-CGGCCCTTCT CACTGGAGGC ACCGGGCAGT CCTCCATGGG AGGGTTGGGC TTGGCCGGGG CTGCCCGGTG CCTCCTCTTG
GCTGGTCCCT CGTTGTCCTT GGGCCCCGC TCCCGCTGCT CGGCCTCCGT GTTCTTTGGC CTCTTGCTCC GCCTGCTGTC

TTGTCCCGTC CCCTCCTCGC TTGCGTTTCC CTCTTCCTTG TCTTCCAGGC CTTCCTCCGC TTCCGCTGCT GGGGCCCGCG CCGGGGGGGC GCTCGGCTCC GCGGCTTCCT CCCCGGCTGG GGGGTCCTGG TCTCCGGGGC CTGCGGCTCG CGGGCTCGGG GCTGCGTGCG CCGCGCGCGG CGTCCGCGGT GGGTGGCGCT GTCCCGCCGT GGTGTGTCTC CGTTCTCGTC CTGCGCCGTC CTGGTCTGCC CGTGGGGTCC TGGGCGTGGT GGGGGGCGTC TGGTGCCTCG TCTGCCCCGT GGGGCTTCGG GCTCGGGGCT GTTCGTCCCC CCTGCCGCTC TGTGGCCTCC GGGGCTCCTC GTTTTCGCTG CTTCGGGTGT CCTTCTCGGC GTGTGGCCCC GGGTCCCGGC CCTGCTGGGC TGGGCGGGGT CGCTGCCCTG GGCTTCTGGC CCGTCTGGTT GTCTGTCGGT GCTTGTCTCG GGTTTCTGGC CTCTGTGCTG GGCGCTTCTC TGCCTCCTGC TCCGCCCTCC TGGTGGCTCG GCTGGGGGTG CCCGTGCGGG GGTGGGTGTG GGGTGTTTTC GGGGTCCTCC CCTTCCC-3' **(FRAG. NO:1902) (SEQ. ID NO:1913)**

5'-GGGCGGGGTCGC-3' **(FRAG. NO:1903) (SEQ. ID NO:1914)**
5'-GCGCCGTCC-3' **(FRAG. NO:1904) (SEQ. ID NO:1915)**
5'-GGGCGTGGTGG-3' **(FRAG. NO:1905) (SEQ. ID NO:1916)**
5'-GTTGGGCTTGGCCGGGG-3' (FRAG. NO:1471)(SEQ. ID NO:1481)
5'-CTGCCCGGTGCCTCC-3' (FRAG. NO:1472)(SEQ. ID NO:1482)
5'-TCTTGGCTGGTCCCTCGT-3' (FRAG. NO:1473)(SEQ. ID NO:1483)
5'-TGTCCTTGGGCCCC-3' (FRAG. NO:1474)(SEQ. ID NO:1484)
5'-GCTCCCGCTGCTCGGCCTCCGT-3' (FRAG. NO:1475)(SEQ. ID NO:1485)
5'-GTTCTTTGGCCTCTTGCTCC-3' (FRAG. NO:1476)(SEQ. ID NO:1486)
5'-GCCTGCTGTCTTGTCC-3' (FRAG. NO:1477)(SEQ. ID NO:1487)
5'-CGTCCCCTCCTCGCTTGCGTTTC-3' (FRAG. NO:1478)(SEQ. ID NO:1488)
5'-CCTCTTCCTTGTCTTCCA-3' (FRAG. NO:1479)(SEQ. ID NO:1489)
5'-GGCCTTCCTCCGCTTCCGCTGC-3' (FRAG. NO:1480)(SEQ. ID NO:1490)
5'-TGGGGCCCGCGCCGG-3' (FRAG. NO:1481)(SEQ. ID NO:1491)
5'-GGGGGCGCTCGGCTCCGCGGCTTCCTCCCCGG-3' (FRAG. NO:1482)(SEQ. ID NO:1492)
5'-CTGGGGGGTCCTGG-3' (FRAG. NO:1483)(SEQ. ID NO:1493)
5'-TCTCCGGGGCCTGCGGCTCGC-3' (FRAG. NO:1484)(SEQ. ID NO:1494)
5'-GGGCTCGGGGCTGCGTGCGCC-3' (FRAG. NO:1485)(SEQ. ID NO:1495)
5'-GCGCGCGGCGTCCGCGGTG-3' (FRAG. NO:1486)(SEQ. ID NO:1496)
5'-GGTGGCGCTGTCCCGCC-3' (FRAG. NO:1487)(SEQ. ID NO:1497)
5'-GTGGTGTGTCTCCGTTCTCGTCCTGCGCCGTC-3' (FRAG. NO:1488)(SEQ. ID NO:1498)
5'-CTGGTCTGCCCGTGG-3' (FRAG. NO:1489)(SEQ. ID NO:1499)
5'-GGTCCTGGGCGTGGTGG-3' (FRAG. NO:1490)(SEQ. ID NO:1500)
5'-GGGGCGTCTGGTGC-3' (FRAG. NO:1491)(SEQ. ID NO:1501)
5'-CTCGTCTGCCCCGTG-3' (FRAG. NO:1492)(SEQ. ID NO:1502)
5'-GGGCTTCGGGCTCGG-3' (FRAG. NO:1493)(SEQ. ID NO:1503)
5'-GGCTGTTCGTCCCCCCTGCCGCTCTGTGGCCTCC-3' (FRAG. NO:1494)(SEQ. ID NO:1504)
5'-GGGGCTCCTCGTTTTC-3' (FRAG. NO:1495)(SEQ. ID NO:1505)
5'-GCTGCTTCGGGTGTCCTTCTC-3' (FRAG. NO:1496)(SEQ. ID NO:1506)
5'-GGCGTGTGGCCCCGG-3' (FRAG. NO:1497)(SEQ. ID NO:1507)
5'-GTCCCGGCCCTGCTGGGCTGGGCGGGGTC-3' (FRAG. NO:1498)(SEQ. ID NO:1508)
5'-GCTGCCCTGGGCTTCTGGCCCGTCT-3' (FRAG. NO:1499)(SEQ. ID NO:1509)
5'-GGTTGTCTGTCGGT-3' (FRAG. NO:1500)(SEQ. ID NO:1510)
5'-GCTTGTCTCGGGTTTCTGG-3' (FRAG. NO:1501)(SEQ. ID NO:1511)
5'-CCTCTGTGCTGGGC-3' (FRAG. NO:1502)(SEQ. ID NO:1512)
5'-GCTTCTCTGCCTCCTGCTCC-3' (FRAG. NO:1503)(SEQ. ID NO:1513)
5'-GCCCTCCTGGTGGCTC-3' (FRAG. NO:1504)(SEQ. ID NO:1514)
5'-GGCTGGGGGTGCCCGTGCG-3' (FRAG. NO:1505)(SEQ. ID NO:1515)
5'-GGGGTGGGTGTGGGGTGTT-3' (FRAG. NO:1506)(SEQ. ID NO:1516)
5'-TTCGGGGTCCTCCCCTTCCC-3' (FRAG. NO:1507)(SEQ. ID NO:1517)
5'-CGGCCCTTCTCACTGGAGGCACCGGGCAGTCCTCCATGGGAGG-3' **(FRAG. NO:1906) (SEQ. ID NO:1917)**

Human Major Basic Protein Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GTT TCA TCT TGG CTT TAT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT CCC TCC CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG GGA GTT TCA TCT TGG GTT TCB TCT TGG CTT TBT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT CCC TCC CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG GGB GTT TCB TCT TGG-3' **(FRAG. ID:1907) (SEQ. ID NO:1918)**

5'-GGG GGA GTT-3' **(FRAG. ID:1908) (SEQ. ID NO:1919)**
5'-G CCC TGG GCC C-3' **(FRAG. ID:1909) (SEQ. ID NO:1920)**
5'-GTT TCA TCT TGG CTT TAT CC-3' **(FRAG. NO:1508) (SEQ. ID NO:1518)**
5'-TCT CCC CTT GTT CCT CCC C-3' **(FRAG. NO:1509)(SEQ. ID NO:1519)**
5'-TCT CCT GCT CTG GRG TCT CCT C-3' **(FRAG. NO:1510)(SEQ. ID NO:1520)**
5'-TTC CCT CCC TCC CCT GCC-3' (FRAG. NO:1511)(SEQ. ID NO:1521)
5'-GTG TTG TCT GTG GGT GTC C-3' (FRAG. NO:1512)(SEQ. ID NO:1522)
5'-GTT TCG CTC TTG TTG CCC-3' (FRAG. NO:1513)(SEQ. ID NO:1523)
5'-TGG GCC CTT CCC TGC TGG-3' (FRAG. NO:1514)(SEQ. ID NO:1524)
5'-GGG GGA GTT TCA TCT TGG-3' (FRAG. NO:1515)(SEQ. ID NO:1525)
5'-GTT TCA TCT TGG CTT TAT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT CCC TCC CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG GGA GTT TCA TCT TGG-3' **(FRAG. ID:1910) (SEQ. ID NO:1921)**
5'-GTT TCB TCT TGG CTT TBT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT CCC TCC

CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG GGB GTT TCB TCT TGG-3' (FRAG. ID:1911) (SEQ. ID NO:1922)

Human Eosinophil Major Basic Protein Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GGG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1516)(SEQ. ID NO:1526)
5'-GGG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1517)(SEQ. ID NO:1527)
5'-GGG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1518)(SEQ. ID NO:1528)
5'-GGG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1519)(SEQ. ID NO:1529)
5'-GGG GGB GTT TCB TCT TGG-3' (FRAG. NO:1520)(SEQ. ID NO:1530)
5'-GGG GGB GTT TCB TCT TG-3' (FRAG. NO:1521)(SEQ. ID NO:1531)
5'-GGG GGB GTT TCB TCT T-3' (FRAG. NO:1522)(SEQ. ID NO:1532)
5'-GGG GGB GTT TCB TCT-3' (FRAG. NO:1523)(SEQ. ID NO:1533)
5'-GGG GGB GTT TCB TC-3' (FRAG. NO:1524)(SEQ. ID NO:1534)
5'-GGG GGB GTT TCB T-3' (FRAG. NO:1525)(SEQ. ID NO:1535)
5'-GGG GGB GTT TCB-3' (FRAG. NO:1526)(SEQ. ID NO:1536)
5'-GG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1527)(SEQ. ID NO:1537)
5'-GG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1528)(SEQ. ID NO:1538)
5'-GG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1529)(SEQ. ID NO:1539)
5'-GG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1530)(SEQ. ID NO:1540)
5'-GG GGB GTT TCB TCT TGG-3' (FRAG. NO:1531)(SEQ. ID NO:1541)
5'-GG GGB GTT TCB TCT TG-3' (FRAG. NO:1532)(SEQ. ID NO:1542)
5'-GG GGB GTT TCB TCT T-3' (FRAG. NO:1533)(SEQ. ID NO:1543)
5'-GG GGB GTT TCB TCT-3' (FRAG. NO:1534)(SEQ. ID NO:1544)
5'-GG GGB GTT TCB TC-3' (FRAG. NO:1535)(SEQ. ID NO:1545)
5'-GG GGB GTT TCB T-3' (FRAG. NO:1536)(SEQ. ID NO:1546)
5'-G GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1537)(SEQ. ID NO:1547)
5'-G GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1538)(SEQ. ID NO:1548)
5'-G GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1539)(SEQ. ID NO:1549)
5'-G GGB GTT TCB TCT TGG C-3' (FRAG. NO:1540)(SEQ. ID NO:1550)
5'-G GGB GTT TCB TCT TGG-3' (FRAG. NO:1541)(SEQ. ID NO:1551)
5'-G GGB GTT TCB TCT TG-3' (FRAG. NO:1542)(SEQ. ID NO:1552)
5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1543)(SEQ. ID NO:1553)
5'-G GGB GTT TCB TCT-3' (FRAG. NO:1544)(SEQ. ID NO:1554)
5'-G GGB GTT TCB TC-3' (FRAG. NO:1545)(SEQ. ID NO:1555)
5'-GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1546)(SEQ. ID NO:1556)
5'-GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1547)(SEQ. ID NO:1557)
5'-GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1548)(SEQ. ID NO:1558)
5'-GGB GTT TCB TCT TGG C-3' (FRAG. NO:1549)(SEQ. ID NO:1559)
5'-GGB GTT TCB TCT TGG-3' (FRAG. NO:1550)(SEQ. ID NO:1560)
5'-GGB GTT TCB TCT TG-3' (FRAG. NO:1551)(SEQ. ID NO:1561)
5'-GGB GTT TCB TCT T-3' (FRAG. NO:1552)(SEQ. ID NO:1562)
5'-GGB GTT TCB TCT-3' (FRAG. NO:1553)(SEQ. ID NO:1563)
5'-GB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1554)(SEQ. ID NO:1564)
5'-GB GTT TCB TCT TGG CTT-3' (FRAG. NO:1555)(SEQ. ID NO:1565)
5'-GB GTT TCB TCT TGG CT-3' (FRAG. NO:1556)(SEQ. ID NO:1566)
5'-GB GTT TCB TCT TGG C-3' (FRAG. NO:1557)(SEQ. ID NO:1567)
5'-GB GTT TCB TCT TGG-3' (FRAG. NO:1558)(SEQ. ID NO:1568)
5'-GB GTT TCB TCT TG-3' (FRAG. NO:1559)(SEQ. ID NO:1569)
5'-GB GTT TCB TCT T-3' (FRAG. NO:1560)(SEQ. ID NO:1570)
5'-B GTT TCB TCT TGG CTT T-3' (FRAG. NO:1561)(SEQ. ID NO:1571)
5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1562)(SEQ. ID NO:1572)
5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1563)(SEQ. ID NO:1573)
5'-B GTT TCB TCT TGG CT-3' (FRAG. NO:1564)(SEQ. ID NO:1574)
5'-B GTT TCB TCT TGG C-3' (FRAG. NO:1565)(SEQ. ID NO:1575)
5'-B GTT TCB TCT TGG-3' (FRAG. NO:1565)(SEQ. ID NO:1576)
5'-B GTT TCB TCT TG-3' (FRAG. NO:1567)(SEQ. ID NO:1577)
5'-GTT TCB TCT TGG CTT T-3' (FRAG. NO:1568)(SEQ. ID NO:1578)
5'-GTT TCB TCT TGG CTT-3' (FRAG. NO:1569)(SEQ. ID NO:1579)
5'-GTT TCB TCT TGG CT-3' (FRAG. NO:1570)(SEQ. ID NO:1580)
5'-GTT TCB TCT TGG C-3' (FRAG. NO:1571)(SEQ. ID NO:1581)
5'-GTT TCB TCT TGG-3' (FRAG. NO:1572)(SEQ. ID NO:1582)
5'-TT TCB TCT TGG CTT T-3' (FRAG. NO:1573)(SEQ. ID NO:1583)
5'-TT TCB TCT TGG CTT-3' (FRAG. NO:1574)(SEQ. ID NO:1584)
5'-TT TCB TCT TGG CT-3' (FRAG. NO:1575)(SEQ. ID NO:1585)
5'-TT TCB TCT TGG C-3' (FRAG. NO:1576)(SEQ. ID NO:1586)
5'-T TCB TCT TGG CTT T-3' (FRAG. NO:1577)(SEQ. ID NO:1587)
5'-T TCB TCT TGG CTT-3' (FRAG. NO:1578)(SEQ. ID NO:1588)
5'-T TCB TCT TGG CT-3' (FRAG. NO:1579)(SEQ. ID NO:1589)
5'-TCB TCT TGG CTT T-3' (FRAG. NO:1580)(SEQ. ID NO:1590)
5'-TCB TCT TGG CTT-3' (FRAG. NO:1581)(SEQ. ID NO:1591)

5'-GGG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1582)(SEQ. ID NO:1592)
5'-GG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1583)(SEQ. ID NO:1593)
5'-G GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1584)(SEQ. ID NO:1594)
5'-GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1585)(SEQ. ID NO:1595)
5'-GB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1586)(SEQ. ID NO:1596)
5'-B GTT TCB TCT TGG CTT T-3' (FRAG. NO:1587)(SEQ. ID NO:1597)
5'-GTT TCB TCT TGG CTT T-3' (FRAG. NO:1588)(SEQ. ID NO:1598)
5'-TT TCB TCT TGG CTT T-3' (FRAG. NO:1589)(SEQ. ID NO:1599)
5'-T TCB TCT TGG CTT T-3' (FRAG. NO:1590)(SEQ. ID NO:1600)
5'-TCB TCT TGG CTT T-3' (FRAG. NO:1591)(SEQ. ID NO:1601)
5'-CB TCT TGG CTT T-3' (FRAG. NO:1592)(SEQ. ID NO:1602)
5'-GGG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1593)(SEQ. ID NO:1603)
5'-GG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1594)(SEQ. ID NO:1604)
5'-G GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1595)(SEQ. ID NO:1605)
5'-GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1596)(SEQ. ID NO:1606)
5'-GB GTT TCB TCT TGG CTT-3' (FRAG. NO:1597)(SEQ. ID NO:1607)
5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1598)(SEQ. ID NO:1608)
5'-GTT TCB TCT TGG CTT-3' (FRAG. NO:1599)(SEQ. ID NO:1609)
5'-TT TCB TCT TGG CTT-3' (FRAG. NO:1600)(SEQ. ID NO:1610)
5'-T TCB TCT TGG CTT-3' (FRAG. NO:1601)(SEQ. ID NO:1611)
5'-TCB TCT TGG CTT-3' (FRAG. NO:1602)(SEQ. ID NO:1612)
5'-GGG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1603)(SEQ. ID NO:1613)
5'-GG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1604)(SEQ. ID NO:1614)
5'-G GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1605)(SEQ. ID NO:1615)
5'-GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1606)(SEQ. ID NO:1616)
5'-GB GTT TCB TCT TGG CT-3' (FRAG. NO:1607)(SEQ. ID NO:1617)
5'-B GTT TCB TCT TGG CT-3' (FRAG. NO:1608)(SEQ. ID NO:1618)
5'-GTT TCB TCT TGG CT-3' (FRAG. NO:1609)(SEQ. ID NO;1619)
5'-TT TCB TCT TGG CT-3' (FRAG. NO:1610)(SEQ. ID NO:1620)
5'-T TCB TCT TGG CT-3' (FRAG. NO:1611)(SEQ. ID NO:1621)
5'-GGG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1612)(SEQ. ID NO:1622)
5'-GG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1613)(SEQ. ID NO:1623)
5'-G GGB GTT TCB TCT TGG C-3' (FRAG. NO:1614)(SEQ. ID NO:1624)
5'-GGB GTT TCB TCT TGG C-3' (FRAG. NO:1615)(SEQ. ID NO:1625)
5'-GB GTT TCB TCT TGG C-3' (FRAG. NO:1616)(SEQ. ID NO:1626)
5'-B GTT TCB TCT TGG C-3' (FRAG. NO:1617)(SEQ. ID NO:1627)
5'-GTT TCB TCT TGG C-3' (FRAG. NO:1618)(SEQ. ID NO:1628)
5'-TT TCB TCT TGG C-3' (FRAG. NO:1619)(SEQ. ID NO:1629)
5'-GGG GGB GTT TCB TCT TGG-3' (FRAG. NO:1620)(SEQ. ID NO:1630)
5'-GG GGB GTT TCB TCT TGG-3' (FRAG. NO:1621)(SEQ. ID NO:1631)
5'-G GGB GTT TCB TCT TGG-3' (FRAG. NO:1622)(SEQ. ID NO:1632)
5'-GGB GTT TCB TCT TGG-3' (FRAG. NO:1623)(SEQ. ID NO:1633)
5'-GB GTT TCB TCT TGG-3' (FRAG. NO:1624)(SEQ. ID NO:1634)
5'-B GTT TCB TCT TGG-3' (FRAG. NO:1625)(SEQ. ID NO:1635)
5'-GTT TCB TCT TGG-3' (FRAG. NO:1626)(SEQ. ID NO:1636)
5'-GGG GGB GTT TCB TCT TG-3' (FRAG. NO:1627)(SEQ. ID NO:1637)
5'-GG GGB GTT TCB TCT TG-3' (FRAG. NO:1628)(SEQ. ID NO:1638)
5'-G GGB GTT TCB TCT TG-3' (FRAG. NO:1629)(SEQ. ID NO:1639)
5'-GGB GTT TCB TCT TG-3' (FRAG. NO:1630)(SEQ. ID NO:1640)
5'-GB GTT TCB TCT TG-3' (FRAG. NO:1631)(SEQ. ID NO:1641)
5'-B GTT TCB TCT TG-3' (FRAG. NO:1632)(SEQ. ID NO:1642)
5'-GGG GGB GTT TCB TCT T-3' (FRAG. NO:1633)(SEQ. ID NO:1643)
5'-GG GGB GTT TCB TCT T-3' (FRAG. NO:1634)(SEQ. ID NO:1644)
5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1635)(SEQ. ID NO:1645)
5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1636)(SEQ. ID NO:1646)
5'-GGB GTT TCB TCT T-3' (FRAG. NO:1637)(SEQ. ID NO:1647)
5'-GB GTT TCB TCT T-3' (FRAG. NO:1638)(SEQ. ID NO:1648)
5'-GGG GGB GTT TCB TCT-3' (FRAG. NO:1639)(SEQ. ID NO:1649)
5'-GG GGB GTT TCB TCT-3' (FRAG. NO:1640)(SEQ. ID NO:1650)
5'-G GGB GTT TCB TCT-3' (FRAG. NO:1641)(SEQ. ID NO:1651)
5'-GGB GTT TCB TCT-3' (FRAG. NO:1642)(SEQ. ID NO:1652)
5'-GGG GGB GTT TCB TC-3' (FRAG. NO:1643)(SEQ. ID NO:1653)
5'-GG GGB GTT TCB TC-3' (FRAG. NO:1644)(SEQ. ID NO:1654)
5'-G GGB GTT TCB TC-3' (FRAG. NO:1645)(SEQ. ID NO:1655)
5'-GGG GGB GTT TCB T-3' (FRAG. NO:1646)(SEQ. ID NO:1656)
5'-GG GGB GTT TCB T-3' (FRAG. NO:1647)(SEQ. ID NO:1657)
5'-GGG GGB GTT TCB-3' (FRAG. NO:1648)(SEQ. ID NO:1658)
5'-TCT CCC CTT GTT CCT CCC C-3' (FRAG. NO:1649)(SEQ. ID NO:1659)
5'-TCT CCT GCT CTG GTG TCT CCT C-3' (FRAG. NO:1650)(SEQ. ID NO:1660)

5'-TTC CCT CCC TCC CCT GCC-3' (FRAG. NO:1651)(SEQ. ID NO:1661)
5'-GTG TTG TCT GTG GGT GTC C-3' (FRAG. NO:1652)(SEQ. ID NO:1662)
5'-GTT TCG CTC TTG TTG CCC-3' -3' (FRAG. NO:1653)(SEQ. ID NO:1663)
5'-TGG GCC CTT CCC TGC TGG-3' (FRAG. NO:1654)(SEQ. ID NO:1664)
5'-GGG GGB G-3' (FRAG. NO:1912)(SEQ. ID NO:1923)
5'-GTG GGT GTC C-3' (FRAG. NO:1913) (SEQ. ID NO:1924)

BP-1 Nucleic Acids and Antisense Oligonucleotide Fragments

5'-CCGTGTTGTC BGTGGTGCTG CCCGTTTGBG GTBTGGCGCT CCBCCBBTTC CCTTTTCTCC TTGTTTTCCG TTTCTCTTGC CGTCTGTGGT T-3' (FRAG. NO:1914) (SEQ. ID NO:1925)
5'-CCCGTTTGBGGTBTGGC-3'(FRAG. NO:1915) (SEQ. ID NO:1926)
5'-GCTCCBCCBBTTCCCTTTTCTCC-3'(FRAG. NO:1916) (SEQ. ID NO:1927)
5'-TTGTTTTCCGTTTCTCTTG-3'(FRAG. NO:1917) (SEQ. ID NO:1928)
5'-CCGTCTGTGGTT-3'(FRAG. NO:1918) (SEQ. ID NO:1929)
5'-CCCGTTTGAGGTATGGC-3'(FRAG. NO:1919) (SEQ. ID NO:1930)
5'-GCTCCBCCAATTCCCTTTTCTCC-3'(FRAG. NO:1920) (SEQ. ID NO:1931)

C/EBPNucleic Acids and Antisense Oligonucleotide Antisense Oligonucleotide Fragments

5'-GGGCCCBGCCCCGCCGCCTTTTCTBGCCCC GGCC-3' (FRAG. NO:1921) (SEQ. ID NO:1932)
5'-GGGCCCBGCCCCGCCGCCTTTTCTBGCCCC GGC-3' (FRAG. NO:1922) (SEQ. ID NO:1933)
5'-GGGCCCB GCCCCGCCGCCTTTTCTBGCCCCGG-3' (FRAG. NO:1923) (SEQ. ID NO:1934)
5'-GGGCCCBGCCCCGCCGCCTTTTCTBGCCCCG-3' (FRAG. NO:1924) (SEQ. ID NO:1935)
5'-GGGCCCBGCCCCGCCGCCTTTTCTBGCCCC-3' (FRAG. NO:1925) (SEQ. ID NO:1936)
5'-GGGCCCBGCCCCGCCGCCTTTTCTBGCCC-3' (FRAG. NO:1926) (SEQ. ID NO:1937)
5'-GGGCCCBGCCCCGCCGCCTTTTCTBGCC-3' (FRAG. NO:1927) (SEQ. ID NO:1938)
5'-GGGCCCBGCCCCGCCGCCTTTTCTBGC-3' (FRAG. NO:1928) (SEQ. ID NO:1939)
5'-GGGCCCBGCCCCGCCGCCTTTTCTBG-3' (FRAG. NO:1929) (SEQ. ID NO:1940)
5'-GGGCCCBGCCCCGCCGCCTTTTCTB-3' (FRAG. NO:1930) (SEQ. ID NO:1941)
5'-GGGCCCBGCCCCGCCGCCTTTTCT-3' (FRAG. NO:1931) (SEQ. ID NO:1942)
5'-GGGCCCBGCCCCGCCGCCTTTTC-3' (FRAG. NO:1932) (SEQ. ID NO:1943)
5'-GGGCCCBGCCCCGCCGCCTTTT-3' (FRAG. NO:1933) (SEQ. ID NO:1944)
5'-GGGCCCBGCCCCGCCGCCTTT-3' (FRAG. NO:1934) (SEQ. ID NO:1945)
5'-GGGCCCBGCCCCGCCGCCTT-3' (FRAG. NO:1935) (SEQ. ID NO:1946)
5'-GGGCCCBGCCCCGCCGCCT-3' (FRAG. NO:1936) (SEQ. ID NO:1947)
5'-GGGCCCBGCCCCGCCGCC-3' (FRAG. NO:1937) (SEQ. ID NO:1948)
5'-GGGCCCBGCCCCGCCGC-3' (FRAG. NO:1938) (SEQ. ID NO:1949)
5'-GGGCCCBGCCCCGCCG-3' (FRAG. NO:1939) (SEQ. ID NO:1950)
5'-GGGCCCBGCCCCGCC-3' (FRAG. NO:1940) (SEQ. ID NO:1951)
5'-GGGCCCBGCCCCGC-3' (FRAG. NO:1941) (SEQ. ID NO:1952)
5'-GGGCCCBGCCCCG-3' (FRAG. NO:1942) (SEQ. ID NO:1953)
5'-GGGCCCBGCCCC-3' (FRAG. NO:1943) (SEQ. ID NO:1954)
5'-GGGCCCBGCCC-3' (FRAG. NO:1944) (SEQ. ID NO:1955)
5'-GGCCCBGCCCCGCCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1945) (SEQ. ID NO:1956)
5'-GCCCBGCCCCGCCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1946) (SEQ. ID NO:1957)
5'-CCCBGCCCCGCCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1947) (SEQ. ID NO:1958)
5'-CCBGCCCCGCCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1948) (SEQ. ID NO:1959)
5'-CBGCCCCGCCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1948) (SEQ. ID NO:1960)
5'-BGCCCCGCCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1950) (SEQ. ID NO:1961)
5'-GCCCCGCCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1951) (SEQ. ID NO:1962)
5'-CCCCGCCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1952) (SEQ. ID NO:1963)
5'-CCCGCCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1953) (SEQ. ID NO:1964)
5'-CCGCCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1954) (SEQ. ID NO:1965)
5'-CGCCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1955) (SEQ. ID NO:1966)
5'-GCCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1956) (SEQ. ID NO:1967)
5'-CCGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1957) (SEQ. ID NO:1968)
5'-CGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1958) (SEQ. ID NO:1969)
5'-GCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1959) (SEQ. ID NO:1970)
5'-CCTTTTCTBGCCCCGGC-3' (FRAG. NO:1960) (SEQ. ID NO:1971)
5'-CTTTTCTBGCCCCGGC-3' (FRAG. NO:1961) (SEQ. ID NO:1972)
5'-TTTTCTBGCCCCGGC-3' (FRAG. NO:1962) (SEQ. ID NO:1973)
5'-TTTCTBGCCCCGGC-3' (FRAG. NO:1963) (SEQ. ID NO:1974)
5'-TTCTBGCCCCGGC-3' (FRAG. NO:1964) (SEQ. ID NO:1975)
5'-TCTBGCCCCGGC-3' (FRAG. NO:1965) (SEQ. ID NO:1976)
5'-CTBGCCCCGGC-3' (FRAG. NO:1966) (SEQ. ID NO:1977)
5'-GCGBGGCTGTCBCCTCGCTGGGCCC-3' (FRAG. NO:1967) (SEQ. ID NO:1978)
5'-GCGBGGCTGTCBCCTCGCTGGGCC-3' (FRAG. NO:1968) (SEQ. ID NO:1979)
5'-GCGBGGCTGTCBCCTCGCTGGGC-3' (FRAG. NO:1969) (SEQ. ID NO:1980)

5'-GCGBGGCTGTCBCCTCGCTGGG-3' **(FRAG. NO:1970) (SEQ. ID NO:1981)**
5'-GCGBGGCTGTCBCCTCGCTGG-3' **(FRAG. NO:1971) (SEQ. ID NO:1982)**
5'-GCGBGGCTGTCBCCTCGCTG-3' **(FRAG. NO:1972) (SEQ. ID NO:1983)**
5'-GCGBGGCTGTCBCCTCGCT-3' **(FRAG. NO:1973) (SEQ. ID NO:1984)**
5'-GCGBGGCTGTCBCCTCGC-3' **(FRAG. NO:1974) (SEQ. ID NO:1985)**
5'-GCGBGGCTGTCBCCTCG-3' **(FRAG. NO:1975) (SEQ. ID NO:1986)**
5'-GCGBGGCTGTCBCCTC-3' **(FRAG. NO:1976) (SEQ. ID NO:1987)**
5'-GCGBGGCTGTCBCCT-3' **(FRAG. NO:1977) (SEQ. ID NO:1988)**
5'-GCGBGGCTGTCBCC-3' **(FRAG. NO:1978) (SEQ. ID NO:1989)**
5'-GCGBGGCTGTCBC-3' **(FRAG. NO:1979) (SEQ. ID NO:1990)**
5'-GCGBGGCTGTCB-3' **(FRAG. NO:1980) (SEQ. ID NO:1991)**
5'-GCGBGGCTGTC-3' **(FRAG. NO:1981) (SEQ. ID NO:1992)**
5'-GCGBGGCTGT-3' **(FRAG. NO:1982) (SEQ. ID NO:1993)**
5'-CGBGGCTGTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1983) (SEQ. ID NO:1994)**
5'-GBGGCTGTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1984) (SEQ. ID NO:1995)**
5'-BGGCTGTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1985) (SEQ. ID NO:1996)**
5'-GGCTGTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1986) (SEQ. ID NO:1997)**
5'-GCTGTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1987) (SEQ. ID NO:1998)**
5'-CTGTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1988) (SEQ. ID NO:1999)**
5'-TGTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1989) (SEQ. ID NO:2000)**
5'-GTCBCCTCGCTGGGCCC-3' **(FRAG. NO:1990) (SEQ. ID NO:2001)**
5'-TCBCCTCGCTGGGCCC-3' **(FRAG. NO:1991) (SEQ. ID NO:2002)**
5'-CBCCTCGCTGGGCCC-3' **(FRAG. NO:1992) (SEQ. ID NO:2003)**
5'-BCCTCGCTGGGCCC-3' **(FRAG. NO:1993) (SEQ. ID NO:2004)**
5'-CCTCGCTGGGCCC-3' **(FRAG. NO:1994) (SEQ. ID NO:2005)**
5'-CTCGCTGGGCCC-3' **(FRAG. NO:1995) (SEQ. ID NO:2006)**
5'-TCGCTGGGCCC-3' **(FRAG. NO:1996) (SEQ. ID NO:2007)**
5'-CGCTGGGCCC-3' **(FRAG. NO:1997) (SEQ. ID NO:2008)**
5'-GCGCGGCCGTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:1998) (SEQ. ID NO:2009)**
5'-GCGCGGCCGTCBTGGCGGCGTCGGGCCGGG-3' **(FRAG. NO:1999) (SEQ. ID NO:2010)**
5'-GCGCGGCCGTCBTGGCGGCGTCGGGCCGG-3' **(FRAG. NO:2000) (SEQ. ID NO:2011)**
5'-GCGCGGCCGTCBTGGCGGCGTCGGGCCG-3' **(FRAG. NO:2001) (SEQ. ID NO:2012)**
5'-GCGCGGCCGTCBTGGCGGCGTCGGGCC-3' **(FRAG. NO:2002) (SEQ. ID NO:2013)**
5'-GCGCGGCCGTCBTGGCGGCGTCGGGC-3' **(FRAG. NO:2003) (SEQ. ID NO:2014)**
5'-GCGCGGCCGTCBTGGCGGCGTCGGG-3' **(FRAG. NO:2004) (SEQ. ID NO:2015)**
5'-GCGCGGCCGTCBTGGCGGCGTCGG-3' **(FRAG. NO:2005) (SEQ. ID NO:2016)**
5'-GCGCGGCCGTCBTGGCGGCGTCG-3' **(FRAG. NO:2006) (SEQ. ID NO:2017)**
5'-GCGCGGCCGTCBTGGCGGCGTC-3' **(FRAG. NO:2007) (SEQ. ID NO:2018)**
5'-GCGCGGCCGTCBTGGCGGCGT-3' **(FRAG. NO:2008) (SEQ. ID NO:2019)**
5'-GCGCGGCCGTCBTGGCGGCG-3' **(FRAG. NO:2009) (SEQ. ID NO:2020)**
5'-GCGCGGCCGTCBTGGCGGC-3' **(FRAG. NO:2010) (SEQ. ID NO:2021)**
5'-GCGCGGCCGTCBTGGCGG-3' **(FRAG. NO:2011) (SEQ. ID NO:2022)**
5'-GCGCGGCCGTCBTGGCG-3' **(FRAG. NO:2012) (SEQ. ID NO:2023)**
5'-GCGCGGCCGTCBTGGC-3' **(FRAG. NO:2013) (SEQ. ID NO:2024)**
5'-GCGCGGCCGTCBTGG-3' **(FRAG. NO:2014) (SEQ. ID NO:2025)**
5'-GCGCGGCCGTCBTG-3' **(FRAG. NO:2015) (SEQ. ID NO:2026)**
5'-GCGCGGCCGTCBT-3' **(FRAG. NO:2016) (SEQ. ID NO:2027)**
5'-GCGCGGCCGTCB-3' **(FRAG. NO:2017) (SEQ. ID NO:2028)**
5'-GCGCGGCCGTC-3' **(FRAG. NO:2018) (SEQ. ID NO:2029)**
5'-GCGCGGCCGT-3' **(FRAG. NO:2019) (SEQ. ID NO:2030)**
5'-CGCGGCCGTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2020) (SEQ. ID NO:2031)**
5'-GCGGCCGTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2021) (SEQ. ID NO:2032)**
5'-CGGCCGTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2022) (SEQ. ID NO:2033)**
5'-GGCCGTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2023) (SEQ. ID NO:2034)**
5'-GCCGTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2024) (SEQ. ID NO:2035)**
5'-CCGTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2025) (SEQ. ID NO:2036)**
5'-CGTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2026) (SEQ. ID NO:2037)**
5'-GTCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2027) (SEQ. ID NO:2038)**
5'-TCBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2028) (SEQ. ID NO:2039)**
5'-CBTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2029) (SEQ. ID NO:2040)**
5'-BTGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2030) (SEQ. ID NO:2041)**
5'-TGGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2031) (SEQ. ID NO:2042)**
5'-GGCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2032) (SEQ. ID NO:2043)**
5'-GCGGCGTCGGGCCGGGC-3' **(FRAG. NO:2033) (SEQ. ID NO:2044)**
5'-CGGCGTCGGGCCGGGC-3' **(FRAG. NO:2034) (SEQ. ID NO:2045)**

5'-GGCGTCGGGCCGGGC-3' (FRAG. NO:2035) (SEQ. ID NO:2046)
5'-GCGTCGGGCCGGGC-3' (FRAG. NO:2036) (SEQ. ID NO:2047)
5'-CGTCGGGCCGGGC-3' (FRAG. NO:2037) (SEQ. ID NO:2048)
5'-GTCGGGCCGGGC-3' (FRAG. NO:2038) (SEQ. ID NO:2049)
5'-TCGGGCCGGGC-3' (FRAG. NO:2039) (SEQ. ID NO:2050)
5'-CGGGCCGGGC-3' (FRAG. NO:2040) (SEQ. ID NO:2051)
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2041) (SEQ. ID NO:2052)
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCGGGCC-3' (FRAG. NO:2042) (SEQ. ID NO:2053)
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCGGGC-3' (FRAG. NO:2043) (SEQ. ID NO:2054)
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCGGG-3' (FRAG. NO:2044) (SEQ. ID NO:2055)
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCGG-3' (FRAG. NO:2045) (SEQ. ID NO:2056)
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCG-3' (FRAG. NO:2046) (SEQ. ID NO:2057)
5'-CCGCBGGCCBGGGCGCGCCGCCGGCC-3' (FRAG. NO:2047) (SEQ. ID NO:2058)
5'-CCGCBGGCCBGGGCGCGCCGCCGGC-3' (FRAG. NO:2048) (SEQ. ID NO:2059)
5'-CCGCBGGCCBGGGCGCGCCGCCGG-3' (FRAG. NO:2049) (SEQ. ID NO:2060)
5'-CCGCBGGCCBGGGCGCGCCGCCG-3' (FRAG. NO:2050) (SEQ. ID NO:2061)
5'-CCGCBGGCCBGGGCGCGCCGCC-3' (FRAG. NO:2051) (SEQ. ID NO:2062)
5'-CCGCBGGCCBGGGCGCGCCGC-3' (FRAG. NO:2052) (SEQ. ID NO:2063)
5'-CCGCBGGCCBGGGCGCGCCG-3' (FRAG. NO:2053) (SEQ. ID NO:2064)
5'-CCGCBGGCCBGGGCGCGCC-3' (FRAG. NO:2054) (SEQ. ID NO:2065)
5'-CCGCBGGCCBGGGCGCGC-3' (FRAG. NO:2055) (SEQ. ID NO:2066)
5'-CCGCBGGCCBGGGCGCG-3' (FRAG. NO:2056) (SEQ. ID NO:2067)
5'-CCGCBGGCCBGGGCGC-3' (FRAG. NO:2057) (SEQ. ID NO:2068)
5'-CCGCBGGCCBGGGCG-3' (FRAG. NO:2058) (SEQ. ID NO:2069)
5'-CCGCBGGCCBGGGC-3' (FRAG. NO:2059) (SEQ. ID NO:2070)
5'-CCGCBGGCCBGGG-3' (FRAG. NO:2060) (SEQ. ID NO:2071)
5'-CCGCBGGCCBGG-3' (FRAG. NO:2061) (SEQ. ID NO:2072)
5'-CCGCBGGCCBG-3' (FRAG. NO:2062) (SEQ. ID NO:2073)
5'-CCGCBGGCCB-3' (FRAG. NO:2063) (SEQ. ID NO:2074)
5'-CCGCBGGCC-3' (FRAG. NO:2064) (SEQ. ID NO:2075)
5'-CGCBGGCCBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2065) (SEQ. ID NO:2076)
5'-GCBGGCCBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2066) (SEQ. ID NO:2077)
5'-CBGGCCBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2067) (SEQ. ID NO:2078)
5'-BGGCCBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2068) (SEQ. ID NO:2079)
5'-GGCCBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2069) (SEQ. ID NO:2080)
5'-GCCBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2070) (SEQ. ID NO:2081)
5'-CCBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2071) (SEQ. ID NO:2082)
5'-CBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2072) (SEQ. ID NO:2083)
5'-BGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2073) (SEQ. ID NO:2084)
5'-GGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2074) (SEQ. ID NO:2085)
5'-GGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2075) (SEQ. ID NO:2086)
5'-GCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2076) (SEQ. ID NO:2087)
5'-CGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2077) (SEQ. ID NO:2088)
5'-GCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2078) (SEQ. ID NO:2089)
5'-CGCCGCCGGCCGGGCCG-3' (FRAG. NO:2079) (SEQ. ID NO:2090)
5'-GCCGCCGGCCGGGCCG-3' (FRAG. NO:2080) (SEQ. ID NO:2091)
5'-CCGCCGGCCGGGCCG-3' (FRAG. NO:2081) (SEQ. ID NO:2092)
5'-CGCCGGCCGGGCCG-3' (FRAG. NO:2082) (SEQ. ID NO:2093)
5'-GCCGGCCGGGCCG-3' (FRAG. NO:2083) (SEQ. ID NO:2094)
5'-CCGGCCGGGCCG-3' (FRAG. NO:2084) (SEQ. ID NO:2095)
5'-CGGCCGGGCCG-3' (FRAG. NO:2085) (SEQ. ID NO:2096)
5'-GGCCGGGCCG-3' (FRAG. NO:2086) (SEQ. ID NO:2097)
5'-GGGCGCBGGCTCCGCB-3' (FRAG. NO:2087) (SEQ. ID NO:2098)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2088) (SEQ. ID NO:2099)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2089) (SEQ. ID NO:2100)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCC-3' (FRAG. NO:2090) (SEQ. ID NO:2101)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCC-3' (FRAG. NO:2091) (SEQ. ID NO:2102)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGC-3' (FRAG. NO:2092) (SEQ. ID NO:2103)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGG-3' (FRAG. NO:2093) (SEQ. ID NO:2104)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCG-3' (FRAG. NO:2094) (SEQ. ID NO:2105)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCC-3' (FRAG. NO:2095) (SEQ. ID NO:2106)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCC-3' (FRAG. NO:2096) (SEQ. ID NO:2107)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGC-3' (FRAG. NO:2097) (SEQ. ID NO:2108)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCG-3' (FRAG. NO:2098) (SEQ. ID NO:2109)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCC-3' (FRAG. NO:2099) (SEQ. ID NO:2110)

5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCC-3' (FRAG. NO:2100) (SEQ. ID NO:2111)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGC-3' (FRAG. NO:2101) (SEQ. ID NO:2112)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTTG-3' (FRAG. NO:2102) (SEQ. ID NO:2113)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCTT-3' (FRAG. NO:2103) (SEQ. ID NO:2114)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGCT-3' (FRAG. NO:2104) (SEQ. ID NO:2115)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGGC-3' (FRAG. NO:2105) (SEQ. ID NO:2116)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCGG-3' (FRAG. NO:2106) (SEQ. ID NO:2117)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCCG-3' (FRAG. NO:2107) (SEQ. ID NO:2118)
5'-GGGCCCCTGGCTCGGCCCCGCGGCCC-3' (FRAG. NO:2108) (SEQ. ID NO:2119)
5'-GGGCCCCTGGCTCGGCCCCGCGGCC-3' (FRAG. NO:2109) (SEQ. ID NO:2120)
5'-GGGCCCCTGGCTCGGCCCCGCGGC-3' (FRAG. NO:2110) (SEQ. ID NO:2121)
5'-GGGCCCCTGGCTCGGCCCCGCGG-3' (FRAG. NO:2111) (SEQ. ID NO:2122)
5'-GGGCCCCTGGCTCGGCCCCGCG-3' (FRAG. NO:2112) (SEQ. ID NO:2123)
5'-GGGCCCCTGGCTCGGCCCCGC-3' (FRAG. NO:2113) (SEQ. ID NO:2124)
5'-GGGCCCCTGGCTCGGCCCCG-3' (FRAG. NO:2114) (SEQ. ID NO:2125)
5'-GGGCCCCTGGCTCGGCCCC-3' (FRAG. NO:2115) (SEQ. ID NO:2126)
5'-GGGCCCCTGGCTCGGCCC-3' (FRAG. NO:2116) (SEQ. ID NO:2127)
5'-GGGCCCCTGGCTCGGCC-3' (FRAG. NO:2117) (SEQ. ID NO:2128)
5'-GGGCCCCTGGCTCGGC-3' (FRAG. NO:2118) (SEQ. ID NO:2129)
5'-GGGCCCCTGGCTCGG-3' (FRAG. NO:2119) (SEQ. ID NO:2130)
5'-GGGCCCCTGGCTCG-3' (FRAG. NO:2120) (SEQ. ID NO:2131)
5'-GGGCCCCTGGCTC-3' (FRAG. NO:2121) (SEQ. ID NO:2132)
5'-GGGCCCCTGGCT-3' (FRAG. NO:2122) (SEQ. ID NO:2133)
5'-GGCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2123) (SEQ. ID NO:2134)
5'-GCCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2124) (SEQ. ID NO:2135)
5'-CCCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2125) (SEQ. ID NO:2136)
5'-CCCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2126) (SEQ. ID NO:2137)
5'-CCTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2127) (SEQ. ID NO:2138)
5'-CTGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2128) (SEQ. ID NO:2139)
5'-TGGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2129) (SEQ. ID NO:2140)
5'-GGCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2130) (SEQ. ID NO:2141)
5'-GCTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2131) (SEQ. ID NO:2142)
5'-CTCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2132) (SEQ. ID NO:2143)
5'-TCGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2133) (SEQ. ID NO:2144)
5'-CGGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2134) (SEQ. ID NO:2145)
5'-GGCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2135) (SEQ. ID NO:2146)
5'-GCCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2136) (SEQ. ID NO:2147)
5'-CCCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2137) (SEQ. ID NO:2148)
5'-CCCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2138) (SEQ. ID NO:2149)
5'-CCGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2139) (SEQ. ID NO:2150)
5'-CGCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2140) (SEQ. ID NO:2151)
5'-GCGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2141) (SEQ. ID NO:2152)
5'-CGGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2142) (SEQ. ID NO:2153)
5'-GGCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2143) (SEQ. ID NO:2154)
5'-GCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2144) (SEQ. ID NO:2155)
5'-CCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2145) (SEQ. ID NO:2156)
5'-CCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2146) (SEQ. ID NO:2157)
5'-CGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2147) (SEQ. ID NO:2158)
5'-GGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2148) (SEQ. ID NO:2159)
5'-GCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2149) (SEQ. ID NO:2160)
5'-CTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2150) (SEQ. ID NO:2161)
5'-TTGCCCGCCCGGCCCGG-3' (FRAG. NO:2151) (SEQ. ID NO:2162)
5'-TGCCCGCCCGGCCCGG-3' (FRAG. NO:2152) (SEQ. ID NO:2163)
5'-GCCCGCCCGGCCCGG-3' (FRAG. NO:2153) (SEQ. ID NO:2164)
5'-CCCGCCCGGCCCGG-3' (FRAG. NO:2154) (SEQ. ID NO:2165)
5'-CCGCCCGGCCCGG-3' (FRAG. NO:2155) (SEQ. ID NO:2166)
5'-CGCCCGGCCCGG-3' (FRAG. NO:2156) (SEQ. ID NO:2167)
5'-GCCCGGCCCGG-3' (FRAG. NO:2157) (SEQ. ID NO:2168)
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2158) (SEQ. ID NO:2169)
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCC-3' (FRAG. NO:2159) (SEQ. ID NO:2170)
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCC-3' (FRAG. NO:2160) (SEQ. ID NO:2171)
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTBGGGC-3' (FRAG. NO:2161) (SEQ. ID NO:2172)
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTBGGG-3' (FRAG. NO:2162) (SEQ. ID NO:2173)
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTBGG-3' (FRAG. NO:2163) (SEQ. ID NO:2174)
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTBG-3' (FRAG. NO:2164) (SEQ. ID NO:2175)

5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCTB-3' (FRAG. NO:2165) (SEQ. ID NO:2176)
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCCT-3' (FRAG. NO:2166) (SEQ. ID NO:2177)
5'-GGCGGGGGCGGCGGCGCCTGGCTCGCC-3' (FRAG. NO:2167) (SEQ. ID NO:2178)
5'-GGCGGGGGCGGCGGCGCCTGGCTCGC-3' (FRAG. NO:2168) (SEQ. ID NO:2179)
5'-GGCGGGGGCGGCGGCGCCTGGCTCG-3' (FRAG. NO:2169) (SEQ. ID NO:2180)
5'-GGCGGGGGCGGCGGCGCCTGGCTC-3' (FRAG. NO:2170) (SEQ. ID NO:2181)
5'-GGCGGGGGCGGCGGCGCCTGGCT-3' (FRAG. NO:2171) (SEQ. ID NO:2082)
5'-GGCGGGGGCGGCGGCGCCTGGC-3' (FRAG. NO:2172) (SEQ. ID NO:2183)
5'-GGCGGGGGCGGCGGCGCCTGG-3' (FRAG. NO:2173) (SEQ. ID NO:2184)
5'-GGCGGGGGCGGCGGCGCCTG-3' (FRAG. NO:2174) (SEQ. ID NO:2185)
5'-GGCGGGGGCGGCGGCGCCT-3' (FRAG. NO:2175) (SEQ. ID NO:2186)
5'-GGCGGGGGCGGCGGCGCC-3' (FRAG. NO:2176) (SEQ. ID NO:2187)
5'-GGCGGGGGCGGCGGCGC-3' (FRAG. NO:2177) (SEQ. ID NO:2188)
5'-GGCGGGGGCGGCGGCG-3' (FRAG. NO:2178) (SEQ. ID NO:2189)
5'-GGCGGGGGCGGCGGC-3' (FRAG. NO:2179) (SEQ. ID NO:2190)
5'-GGCGGGGGCGGCGG-3' (FRAG. NO:2180) (SEQ. ID NO:2191)
5'-GGCGGGGGCGGCG-3' (FRAG. NO:2181) (SEQ. ID NO:2192)
5'-GGCGGGGGCGGC-3' (FRAG. NO:2182) (SEQ. ID NO:2193)
5'-GGCGGGGGCGG-3' (FRAG. NO:2183) (SEQ. ID NO:2194)
5'-GCGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2184) (SEQ. ID NO:2195)
5'-CGGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2185) (SEQ. ID NO:2196)
5'-GGGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2186) (SEQ. ID NO:2197)
5'-GGGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2187) (SEQ. ID NO:2198)
5'-GGGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2188) (SEQ. ID NO:2199)
5'-GGCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2189) (SEQ. ID NO:2200)
5'-GCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2190) (SEQ. ID NO:2201)
5'-CGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2191) (SEQ. ID NO:2202)
5'-GGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2192) (SEQ. ID NO:2203)
5'-GCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2193) (SEQ. ID NO:2204)
5'-CGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2194) (SEQ. ID NO:2205)
5'-GGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2195) (SEQ. ID NO:2206)
5'-GCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2196) (SEQ. ID NO:2207)
5'-CGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2197) (SEQ. ID NO:2208)
5'-GCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2198) (SEQ. ID NO:2209)
5'-CCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2199) (SEQ. ID NO:2210)
5'-CTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2200) (SEQ. ID NO:2211)
5'-TGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2201) (SEQ. ID NO:2212)
5'-GGCTCGCCTBGGGCCCC-3' (FRAG. NO:2202) (SEQ. ID NO:2213)
5'-GCTCGCCTBGGGCCCC-3' (FRAG. NO:2203) (SEQ. ID NO:2214)
5'-CTCGCCTBGGGCCCC-3' (FRAG. NO:2204) (SEQ. ID NO:2215)
5'-TCGCCTBGGGCCCC-3' (FRAG. NO:2205) (SEQ. ID NO:2216)
5'-CGCCTBGGGCCCC-3' (FRAG. NO:2206) (SEQ. ID NO:2217)
5'-GCCTBGGGCCCC-3' (FRAG. NO:2207) (SEQ. ID NO:2218)
5'-CCTBGGGCCCC-3' (FRAG. NO:2208) (SEQ. ID NO:2219)
5'-CTBGGGCCCC-3' (FRAG. NO:2209) (SEQ. ID NO:2220)
5'-GGGTGGGCBCGGCGGCC-3' (FRAG. NO:2210) (SEQ. ID NO:2221)
5'-GGTCGGCGBBGBGCTCGTCGTGGC-3' (FRAG. NO:2211) (SEQ. ID NO:2222)
5'-GGTCGGCGBBGBGCTCGTCGTGG-3' (FRAG. NO:2212) (SEQ. ID NO:2223)
5'-GGTCGGCGBBGBGCTCGTCGTG-3' (FRAG. NO:2213) (SEQ. ID NO:2224)
5'-GGTCGGCGBBGBGCTCGTCGT-3' (FRAG. NO:2214) (SEQ. ID NO:2225)
5'-GGTCGGCGBBGBGCTCGTCG-3' (FRAG. NO:2215) (SEQ. ID NO:2226)
5'-GGTCGGCGBBGBGCTCGTC-3' (FRAG. NO:2216) (SEQ. ID NO:2227)
5'-GGTCGGCGBBGBGCTCGT-3' (FRAG. NO:2217) (SEQ. ID NO:2228)
5'-GGTCGGCGBBGBGCTCG-3' (FRAG. NO:2218) (SEQ. ID NO:2229)
5'-GGTCGGCGBBGBGCTC-3' (FRAG. NO:2219) (SEQ. ID NO:2230)
5'-GGTCGGCGBBGBGCT-3' (FRAG. NO:2220) (SEQ. ID NO:2231)
5'-GGTCGGCGBBGBGC-3' (FRAG. NO:2221) (SEQ. ID NO:2232)
5'-GGTCGGCGBBGBG-3' (FRAG. NO:2222) (SEQ. ID NO:2233)
5'-GGTCGGCGBBGB-3' (FRAG. NO:2223) (SEQ. ID NO:2234)
5'-GGTCGGCGBBG-3' (FRAG. NO:2224) (SEQ. ID NO:2235)
5'-GTCGGCGBBGBGCTCGTCGTGGC-3' (FRAG. NO:2225) (SEQ. ID NO:2236)
5'-TCGGCGBBGBGCTCGTCGTGGC-3' (FRAG. NO:2226) (SEQ. ID NO:2237)
5'-CGGCGBBGBGCTCGTCGTGGC-3' (FRAG. NO:2227) (SEQ. ID NO:2238)
5'-GGCGBBGBGCTCGTCGTGGC-3' (FRAG. NO:2228) (SEQ. ID NO:2239)
5'-GCGBBGBGCTCGTCGTGGC-3' (FRAG. NO:2229) (SEQ. ID NO:2240)

5'-CGBBGBGCTCGTCGTGGC-3' (FRAG. NO:2230) (SEQ. ID NO:2241)
5'-GBBGBGCTCGTCGTGGC-3' (FRAG. NO:2231) (SEQ. ID NO:2242)
5'-BBGBGCTCGTCGTGGC-3' (FRAG. NO:2232) (SEQ. ID NO:2243)
5'-BGBGCTCGTCGTGGC-3' (FRAG. NO:2233) (SEQ. ID NO:2244)
5'-GBGCTCGTCGTGGC-3' (FRAG. NO:2234) (SEQ. ID NO:2245)
5'-BGCTCGTCGTGGC-3' (FRAG. NO:2235) (SEQ. ID NO:2246)
5'-GCTCGTCGTGGC-3' (FRAG. NO:2236) (SEQ. ID NO:2247)
5'-CTCGTCGTGGC-3' (FRAG. NO:2237) (SEQ. ID NO:2248)
5'-TCGTCGTGGC-3' (FRAG. NO:2238) (SEQ. ID NO:2249)
5'-GGGGCCCCGCGCCGCCCGCC-3' (FRAG. NO:2239) (SEQ. ID NO:2250)
5'-GGGGCCCCGCGCCGCCCGC-3' (FRAG. NO:2240) (SEQ. ID NO:2251)
5'-GGGGCCCCGCGCCGCCCG-3' (FRAG. NO:2241) (SEQ. ID NO:2252)
5'-GGGGCCCCGCGCCGCCC-3' (FRAG. NO:2242) (SEQ. ID NO:2253)
5'-GGGGCCCCGCGCCGCC-3' (FRAG. NO:2243) (SEQ. ID NO:2254)
5'-GGGGCCCCGCGCCGC-3' (FRAG. NO:2244) (SEQ. ID NO:2255)
5'-GGGGCCCCGCGCCG-3' (FRAG. NO:2245) (SEQ. ID NO:2256)
5'-GGGGCCCCGCGCC-3' (FRAG. NO:2246) (SEQ. ID NO:2257)
5'-GGGGCCCCGCGC-3' (FRAG. NO:2247) (SEQ. ID NO:2258)
5'-GGGCCCCGCGCCGCCCGCC-3' (FRAG. NO:2248) (SEQ. ID NO:2259)
5'-GGCCCCGCGCCGCCCGCC-3' (FRAG. NO:2249) (SEQ. ID NO:2260)
5'-GCCCCGCGCCGCCCGCC-3' (FRAG. NO:2250) (SEQ. ID NO:2261)
5'-CCCCGCGCCGCCCGCC-3' (FRAG. NO:2251) (SEQ. ID NO:2262)
5'-CCCGCGCCGCCCGCC-3' (FRAG. NO:2252) (SEQ. ID NO:2263)
5'-CCGCGCCGCCCGCC-3' (FRAG. NO:2253) (SEQ. ID NO:2264)
5'-CGCGCCGCCCGCC-3' (FRAG. NO:2254) (SEQ. ID NO:2265)
5'-GCGCCGCCCGCC-3' (FRAG. NO:2255) (SEQ. ID NO:2266)
5'-CGCCGCCCGCC-3' (FRAG. NO:2256) (SEQ. ID NO:2267)
5'-GCCGCCCGCC-3' (FRAG. NO:2257) (SEQ. ID NO:2268)
5'-GGGGCGCGCGGGGCCGCCGGG-3' (FRAG. NO:2258) (SEQ. ID NO:2269)
5'-GGCGGGGBGCGGCBGGGCCCGGGCCC-3' (FRAG. NO:2259) (SEQ. ID NO:2270)
5'-GGCGCGTCGCCGTCGCCCCBGTCGGGCTCGCGC-3' (FRAG. NO:2260) (SEQ. ID NO:2271)
5'-GCGCGGGCBBCBGCGBGCCGGGCGCG-3' (FRAG. NO:2261) (SEQ. ID NO:2272)
5'-GCGCBCGGGCCCBCCTGCGCGGGC-3' (FRAG. NO:2262) (SEQ. ID NO:2273)
5'-GGGCGGGGTGGGCTGCCCTGCGGCCGCC-3' (FRAG. NO:2263) (SEQ. ID NO:2274)
5'-GGGCTGCTGCGCGGCGGCTCCGGCGA-3' (FRAG. NO:2264) (SEQ. ID NO:2275)
5'-CTCCCGGGCGGGGCCGGGCGCGGGG-3' (FRAG. NO:2265) (SEQ. ID NO:2276)
5'-GGGCTGCCGCGGTCCGGGCCCCTCTTGCCGGCG-3' (FRAG. NO:2266) (SEQ. ID NO:2277)
5'-GCGCTCGCGCCGCTGCCGG-3' (FRAG. NO:2267) (SEQ. ID NO:2278)
5'-GCGCCGCTTGGCCTTGTCGCGGC-3' (FRAG. NO:2268) (SEQ. ID NO:2279)
5'-GCTGCTCCBCGCGCTGG-3' (FRAG. NO:2269) (SEQ. ID NO:2280)
5'-GCCGGBGGCCGGCCBGGTCCCGCG-3' (FRAG. NO:2270) (SEQ. ID NO:2281)
5'-CCCGGCGGCCGGCBGGBBGGGCGGGCTGGGC-3' (FRAG. NO:2271) (SEQ. ID NO:2282)
5'-GTCTCTCCCGCCCCGGCCGCGCG-3' (FRAG. NO:2272) (SEQ. ID NO:2283)
5'-GGGCGTCCGCTCCGGGCCGTCGGG-3' (FRAG. NO:2273) (SEQ. ID NO:2284)
5'-GCGGGCACGCGGCGGCTCTGGCGTCGGC-3' (FRAG. NO:2274) (SEQ. ID NO:2285)

<u>Bradykinin Receptor Nucleic Acids and Antisense Oligonucleotide Fragments</u>

5'-GGTGBCBTTG BGCBTGTCGG CGCGGTCCCG TTBBGBGTGG GCCCGCCAGC CCAGCCACTC CACTTGGGGG CGGGTGGCCA GCACGAACAG CACCCAGAGG AAGGGGGGCG GCCCAGAAGG GCAGCCCGCA GGCCAGGATC AGGTCTGCTG CGGCCGGAGA TAATGGCATT CACCACGCGG CGGCCCAGCG CACGCCGCGC ATCCGGCCCG GGTTCTGACC TGCAGCCCCC GTCTCCTTGG CATTCCTGGG CCCCAGTCAC TCCTCTCCCT GCCCCCCTTG CTGGGGCAGG GACGGGGTG BCBTTGBGCB TGTCGGCGCG GTCCCGTTBB GBGTGGGCCC GCCAGCCCAG CCACTCCACT TGGGGGCGGG TGGCCAGCAC GAACAGCACC CAGAGGAAGG GGGGCGGCCC AGAAGGGCAG CCCGCAGGCC AGGATCAGGT CTGCTGCGGC CGGAGATAAT GGCATTCACC ACGCGGCGGC CCAGCGCACG CCGCGCATCC GGCCCGGGTT CTGACCTGCA GCCCCCGTCT CCTTGGCATT CCTGGGCCCC AGTCACTCCT CTCCCTGCCC CCCTTGCTGG GGCAGGGACG GCCGTGTTGT CBGTGGTGCT GCCCGTTTGB GGTBTGGCGC TCCBCCBBTT CCCTTTTCTC CTTGTTTTCC GTTTCTCTTG CCGTCTGTGG TT CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTTGATG TCTCCGGTAA AACACCGGAG ACTAATTCCT GCCCTGCCCA ATTTTGCAGG GAGCATGGCT GTGAGGATGG GGTGAACTCA CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT TCTTATTTGC TGCCACACCT GAGCCAGCCT GCTCCTTCCC AGGAGTGGAG GAGGCCTGGG GGGAGGGAGA GGAGTGACTG AGCTTCCCTC CCGTGTGTTC TCCGTCCCTG CCCCAGCAAG ACAACTTAGA TCTCCAGGAG AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGCACAAG TGAGTTGTTG CCCTGGGTTT CTTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC CCTGATAACA ACCTGGAGAC CAGGATTTTA TGGCTCCCCT CACTGATGGA CAAGGAGGTC TGTGCCAAAG AAGAATCCAA TAAGCACATA TTGAGCACTT GCTGTATATG CAGTATTGAG CACTGTAGGC AAGACCCAAG AAAGAGAAGG AGCCATCTCC ATCTTGAAGG AACTCAAAGA CTCAAGTGGG AACGACTGGG CACTGCCACC ACCAGAAAGC TGTTCGACGA GACGGTCGAG CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCA GCTCAACCAA TAACTATTGC ACAACCACCT GTCCCTGCCT CAGTTCCCTT TTATGTAACA TGAAGTCGTT

GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG TGCTACGTAC ATGTGAGGCA TCATTACGCA
GACGTAACTG GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGAA ATAGCTCCGT GGAGCAGAAT CAGTATTGGG
AGCCGGTGGC GGTGTGAAGC ACCAGTGTCT GGCACACAGT AGGTGCTCAT TGGCTCCCTT CCACCTGTCA TTCCCACCAC
CCTGAGGCCC CAACCGCCAC ACACACAGGA GCATTTGGAG AGAAGGCCAT GTCTTCAAAG TCTGATTTGT GATGAGGCAG
AGGAAGATAT TTCTAATCGG TCTTGCCCAG AGGATCACAG TGCTGAGACC CCCCACCACC AGCCGGTACC TGGGAAGGGG
GAGAGTGCAG GCCTGCTCAG GGACTGTTCC TGTCTCAGCA ACCAAGGGAT TGTTCCTGTC AATCAATGGT TTATTGGAAG
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TCACATGGCG GCTCACATCC TTCCAAGTAA GCAATGCAAA AGGCCAAGAA AGATGCTGCA AAGATGTTAT GACCTAGCCT
CAGAAATCAC ACACCATCCC TGCCACCATT AGTAAGAAGT CCAGCCCACG TCCAGGAGAA GAGGAAGCAG ATTCCTCCTT
TTGAAATGAA GAATATCAAG TAATTCGGGG GGCATATGAA AGCCACCACA CACCACAGGG ATCTTTTTAG AGCATACTTC
TTATACCATC ACTGTAGTTC CTTAAGACTC AGGGGCAAAG CCTCACTTCC TTAGCACCCA GTGAAGACCA CGCTTACTCC
CTCACTCAAC CTCTTGCTAC TTCCCACCTC TCCTGTCCAA CATCTAGTGT CACTTTCCAG AACATACCAA CAGCTTCCCC
AGTTCTGTGC CTCTGCTCAG GCTGTTCCCC CTGCCTGGTC CACTTGTCCT CCTTCTTGTC CGGTCAAAAT GCTTCTTATC
CTTCAAGACC CAGCTCTAGA GTCACCTCCA ACCCCTTACC CACCAGCCCC CTCTCCAAGT CTGTGTCCCA CAACCCCCCT
GCTCCCTCCA GGGCACCCTC CACCCTCTGG GCCACAGTTG TCAGGAGTCA GGCAGGGCAG GGGCCGGGTG GTGTCTTCTT
TGTGTTCTTG CACTCAGGGC AGAGCTCAGC ACAGAGCAGA CGCTCAAAAA ACATTTAAAG GATAGAAGCA TTGATTTGTG
GGTCCCCCAG TCTGGCTCCA GGATGCCAGC CAGCTGCTCC TAGAAGCAAA CGGACTTTTC CTGGGAAATC CCAGAGGTGA
TGATCAGTAA TCTCTCCCGT GACTCGTAGT TCAGCTCTTC CTCCATGAGC CTGACTATCA GTGGACCTTC CAGAAAGAGC
CCCTTTTCCT TCTCTCACCC ACAGCACAGG GCACTGGGAA AATGCCCAAT GAGTCCTGCC TCTGGGTTGT GCTTTGGACT
TTTCAGTGTG TCTCGCATCC ACTCTTCAAC TTGAATGTTG CAACAGCCAT GAAAAAAGAA ATGCAAAGCG ATTCAGGATG
AGAGCAATAC CCTACTCCAA AGAAGGCAAC ATAGAAGCTC AGAGAGATCA AGCAATTTGC CCAAGACCAC ACAGCTAGGA
GTGGAACTCA TGGCTGTCCA AGCCCCATGC CTCTGCTGAA GGTAGAGATG AATTACAGCA ACAAGTCTAG AAAGGTGCCT
GCCCTATGGT CTGTGAGTCT TGCCTAAGAA TGAAAGAGGA GCCAGTGGGT TAAAGATGAG GTCACCAACA ACGGTGGTGT
TGGAGTTTAC CACTGATAAT AAGGGTGCAA AATGTAAATT ACTAATGTTT ATTGAGCCTA GTGCAGTGCG TGGGGCATTT
TGCACATTGT CTCTGATCCC TATGACAACC CTGAGAGGTA GTGGTTTTAA CTGCCATGTT ACAGGTGAGG TCATTGTGGT
TCAAGGACGT TAAGTAACTT CCCCAGCGTG ACACGGCTTA TAAGTAAGGC AGCCAGGATG TGAACCCAGT AGGACTATCT
GGCTGCAAAG TCCCCACCCC CCTCGCCATC TGTATCCTCC AATCACTTCA GTGCTTTGCT GCATAGAAGG TAACGGAAAT
CACGATGCCA CAGACTGTCC AGGAAGACAG AAACTAGGCA GATGGGCTGG CCATGGTCTC CAAGCCAGAC TGGAATCTCC
AGGTCTGGAA TGATATCATT TTTCTCTTTT AATAAATTAA CTCACCCACC ACACGGCTTT GAGAGGCTCA AAGTTGACCA
ACTCCCTTGG GAGGGCCCCG GTTGATAAGG AAGGAACGTG AATCCTCCCA TCACGGAAGC TTCAAGGAGG TCAAGGGTCC
AACACTTGAG ATTGTTAGTG CTGTTGGTGG ATACTGGCCA AGGAAATATC CCAGTGGAGC CTCGAGATGA AGAACATGAG
GCCCCCGTTT AGAACCAAGG ATCAGAGGGG GCTCTGTAAG ACCCAGGGGA GTCAGGTGCA CTGGAGCGCG GGCATGCAGA
AAACAGCCTG AGCTCCACCT CGGCTTCTCC TTGTCCTGGC TGGTTGTCCT TAACCCCTGT CTCCTTCTGG ACCAGTTTTT
GTCCTTCCCT TGTGACCGCT GAGGGGTAAC AGCCTCTTTC CACTTTCTTT CAGCGCCGAC ATGCTCAATG TCACCTTGCA
AGGGCCCACT CTTAACGGGA CCTTTGCCCA GAGCAAATGC CCCCAAGTGG AGTGGCTGGG CTGGCTCAAC ACCATCCAGC
CCCCCTTCCT CTGGGTGCTG TTCGTGCTGG CCACCCTAGA GAACATCTTT GTCCTCAGCG TCTTCTGCCT GCACAAGAGC
AGCTGCACGG TGGCAGAGAT CTACCTGGGG AACCTGGCCG CAGCAGACCT GATCCTGGCC TGCGGGCTGC CCTTCTGGGC
CATCACCATC TCCAACAACT TCGACTGGCT CTTTGGGGAG ACGCTCTGCC GCGTGGTGAA TGCCATTATC TCCATGAACC
TGTACAGCAG CATCTGTTTC CTGATGCTGG TGAGCATCGA CCGCTACCTG GCCCTGGTGA AAACCATGTC CATGGGCCGG
ATGCGCGGCG TGCGCTGGGC CAAGCTCTAC AGCTTGGTGA TCTGGGGGTG TACGCTGCTC CTGAGCTCAC CCATGCTGGT
GTTCCGGACC ATGAAGGAGT ACAGCGATGA GGGCCACAAC GTCACCGCTT GTGTCATCAG CTACCCATCC CTCATCTGGG
AAGTGTTCAC CAACATGCTC CTGAATGTCG TGGGCTTCCT GCTGCCCCTG AGTGTCATCA CCTTCTGCAC GATGCAGATC
ATGCAGGTGC TGCGGAACAA CGAGATGCAG AAGTTCAAGG AGATCCAGAC GGAGAGGAGG GCCACGGTGC TAGTCCTGGT

TGTGCTGCTG CTATTCATCA TCTGCTGGCT GCCCTTCCAG ATCAGCACCT TCCTGGATAC GCTGCATCGC CTCGGCATCC
TCTCCAGCTG CCAGGACGAG CGCATCATCG ATGTAATCAC ACAGATCGCC TCCTTCATGG CCTACAGCAA CAGCTGCCTC
AACCCACTGG TGTACGTGAT CGTGGGCAAG CGCTTCCGAA AGAAGTCTTG GGAGGTGTAC CAGGGAGTGT GCCAGAAAGG
GGGCTGCAGG TCAGAACCCA TTCAGATGGA GAACTCCATG GGCACACTGC GGACCTCCAT CTCCGTGGAA CGCCAGATTC
ACAAACTGCA GGACTGGGCA GGGAGCAGAC AGTGAGCAAA CGCCAGCAGG GCTGCTGTGA ATTTGTGTAA GGATTGAGGG
ACAGTTGCTT TTCAGCATGG GCCCAGGAAT GCCAAGGAGA CATCTATGCA CGACCTTGGG AAATGAGTTG ATGTCTCCGG
TAAAACACCG GAGACTAATT CCTGCCCTGC CCAATTTTGC AGGGAGCATG GCTGTGAGGA TGGGGTGAAC TCACGCACAG
CCAAGGACTC CAAAATCACA ACAGCATTAC TGTTCTTATT TGCTGCCACA CCTGAGCCAG CCTGCTCCTT CCCAGGAGTG
GAGGAGGCCT GGGGGCAGGG AGAGGAGTGA CTGAGCTTCC CTCCCGTGTG TTCTCCGTCC CTGCCCCAGC AAGACAACTT
AGATCTCCAG GAGAACTGCC ATCCAGCTTT GGTGCAATGG CTGAGTGCAC AAGTGAGTTG TTGCCCTGGG TTTCTTTAAT
CTATTCAGCT AGAACTTTGA AGGACAATTT CTTGCATTAA TAAAGGTTAA GCCCTGAGGG GTCCCTGATA ACAACCTGGA
GACCAGGATT TTATGGCTCC CCTCACTGAT GGACAAGGAG GTCTGTGCCA AAGAAGAATC CAATAAGCAC ATATTGAGCA
CTTGCTGTAT ATGCAGTATT GAGCACTGTA GGCAAGAGGG AAGAAAGAGA AGGAGCCATC TCCATCTTGA AGGAACTCAA
AGACTCAAGT GGGAACGACT GGGCACTGCC ACCACCAGAA AGCTGTTCGA TGAGACGGTC GAGCAGGGTG CTGTGGGTGA
TATGGACAGC AGAAGGGGGA GCCAGGTTCC AGCTCACCAA TACTATTGCA CACCACCTGT CCTGCCTC TGATCCTATC
ACAACCTGAG AGTAGTTTTT ACTCCATTTA CAGGTGAGGT CATTGTGGTT CAAGGACGTT AAGTAACTTC CCCAGCTCAC
ACGGCTTATA AGTAAGGCAG CCAGGATGTG AACCCAGTAG GACTATCTGG CTGCAAAGTC CCCACCCTCC CTCGCCATCT
GTATCCTCCA ATCATCTTCA GTGCTTTGCT GATAGAAGGT ACGGAAATAC GATGCCACAG ACTGTCCAGG AAGACAGAAA
CTAGGCAGAT GGGCTGGCCA TGGTCTCCAA GCCAGACTGG AATCTCCAGG TCTGGAATGA TATCATTTTT CTCTTTTAAT
AAATTAACTC ACCCACCACA CGGCTTTGAG AGGCTCAAAG GTGACCAACT CCCTTGGGAG GGCCCCGGTT GATAAGGAAG
GAATGTGAAT CCTCCCATCA CGGAAGCTTC AAGGAGGTCA AGGGTCCAAC ACTTGAGATT GTTAGTGCTG TTGGTGGATA
CTGCAGAATA TCCAGTGGAG CCTCAGATGA AGAACATGAG GCCCCGTTTA GATCCAAGGA TCAGAGGGGG CTCTGTAAGA
CCCAGGGGAG TCAGGTGCAC TGGAGCGCGG GCTGCAGAAA ACAGCCTGAG CTCCACCTCG GCTTCTCCTT GCCCTGGCTG
GTTGTCCTTA ACCCCTGTCT CCTTCTGGAC CAGTTTTTGT CCTTCCCTTG TGACCTGAGG GGTAACAGCC TCTTTTCCAC
TTTCTTTCAG CGCCGACATG CTCAATGTCA CCTTGCAAGG GCCCACTCTT AACGGGACCT TTGCCCAGAG CAAATGCCCC
CAAGTGGAGT GGCTGGGCTG GCTCAACACC ATCCAGCCCC CCTTCCTCTG GGTGCTGTTC GTGCTGGCCA CCCTAGAGAA
CATCTTTGTC CTCAGCGTCT TCTGCCTGCA CAAGAGCAGC TGCACGGTGG CAGAGATCTA CCTGGGGAAC CTGGCCGCAG
CAGACCTGAT CCTGGCCTGC GGGCTGCCCT TCTGGGCCAT CACCATCTCC AACAACTTCG ACTGGCTCTT TGGGGAGACG
CTCTGCCGCG TGGTGAATGC CATTATCTCC ATGAACCTGT ACAGCAGCAT CTGTTTCCTG ATGCTGGTGA GCATCGACCG
CTACCTGGCC CTGGTGAAAA CCATGTCCAT GGGCCGGATG CGCGGCGTGC GCTGGGCCAA GCTCTACAGC TTGGTGATCT
GGGGGTGTAC GCTGCTCCTG AGCTCACCCA TGCTGGTGTT CCGGACCATG AAGGAGTACA GCGATGAGGG CCACAACGTC
ACCGCTTGTG TCATCAGCTA CCCATCCCTC ATCTGGGAAG TGTTCACCAA CATGCTCCTG AATGTCGTGG GCTTCCTGCT
GCCCCTGAGT GTCATCACCT TCTGCACGAT GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG TTCAAGGAGA
TCCAGACGGA GAGGAGGGCC ACGGTGCTAG TCCTGGTTGT GCTGCTGCTA TTCATCATCT GCTGGCTGCC CTTCCAGATC
AGCACCTTCC TGGATACGCT GCATCGCCTC GGCATCCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG TAATCACACA
GATCGCCTCC TTCATGGCCT ACAGCAACAG CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGGCAAGCGC TTCCGAAAGA
AGTCTTGGGA GGTGTACCAG GGAGTGTGCC AGAAAGGGGG CTGCAGGTCA GAACCCATTC AGATGGAGAA CTCCATGGGC
ACACTGCGGA CCTCCATCTC CGTGGAACGC CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC
CAGCAGGGCT GCTGTGAATT TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT
CTATGCACGA CCTTGGGAAA TGAGTGTTGA TGTCTCCGGT AAAACACCGG AGACTAATTC CTGCCCTGCC CAATTTTCGA
GGGAGCATGG CTGTGAGGAT GGGGTGAACT CACGCACAGC CAAGGACTCC AAAATCACAA CAGCATTACT GTTCTTATTT
GCTGCCACAC CTGAGCCAGC CTGCTCCTTC CCAGGAGTGG AGGAGGCCTG GGGGAGGGAG AGGAGTGACT GAGCTTCCCT
CCCGTGTGTT CTCCGTCCCT GCCCCAGCAA GACAACTTAG ATCTCCAGGA GAACTGCCAT CCACGTTTGG TGCAATGGCT
GAGTGCACAA GTGAGTTGTT GCCCTGGGTT TCTTTAATCT ATCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA
AGGTTAAGCC CTGAGGGGTC CCTTGATAAC AACCTGGAGA CCAGGATTTT ATGGCTCCCC TCACTGATGG ACAAGGAGGT
CTGTGCCAAA GAAGAATCAA TAAGCACATA TGAGCACTTC TGTATATCAG TATTGAGCAC TGTAGGCA ATGTTCTCTC
CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCCACC ACGGCCTCTT TCAGCGCCGA CATGCTCAAT
GTCACCTTGC AAGGGCCCAC TCTTAACGGG ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA
CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC GTCTTCTGCC
TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC GCAGCAGACC TGATCCTGGC CTGCGGGCTG
CCCTTCTGGG CCATCACCAT CTCCAACAAC TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT
CTCCATGAAC CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG AAAACCATGT
CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG ATCTGGGGGT GTACGCTGCT CCTGAGCTCA
CCCATGCTGG TGTTCCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC
CCTCATCTGG GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC ACCTTCTGCA
CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG GAGATCCAGA CGGAGAGGAG GGCCACGGTG
CTAGTCCTGG TTGTGCTGCT GCTATTCATC ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG
CCTCGGCATC CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG GCCTACAGCA
ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG
TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA
ACGCCAGATT CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG AATTTGTGTA
AGGATTGAGG GACAGTTGCT T ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGACTC CGTGCCCACC
ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG ACCTTTGCCC AGAGCAAATG
CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG
AGAACATCTT TGTCCTCAGC GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC
GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC TTCGACTGGC TCTTTGGGGA
GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG
ACCGCTACCT GGCCCTGGTG AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG
ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA

CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG AATTTGTGTA AGGATTGAGG GACAGTTGCT T GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA CGGTGGGGAC ATCAGGCTGC CCCGCAGTAC CAGGGAGCGA CTGAAGTGCC CATGCCGCTT GCTCCGGAGA AGGTGGGTGC CGGGCAGGGG CTGCTCCAGC CGCCTCACCT CTGCTGGGAG GACAAACTGT CCCAGCACAG AGGGAGGGAG GGAGGGCAGG CAGCGGGGAG AAGTTTCCCT GTGGTCGTGG GGAGTT GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CCGCAGTACC AGGGAGCGAC TGAAGTGCCC ATGCCGCTTG CTCCGGAGAA GGTGGGTGCC GGGCAGGGGC TGCTCCAGCC GCCTCACCTC TGCTGGGAGG ACAAACTGTC CCAGCACAGA GGGAGGGAGG GAGGGCAGGC AGCGGGGAGA AGTTTCCCTG TGGTCGTGGG GAGTT GAGCTCTTCA ATATTTTAGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA CACACCTTTT CAGAGGGCTT GTGGACTCTG GGCAGCCTGT CCATAGACCT CTGTCCCCAA CTGGCAAGTC AGGAAACTCC AGATTAAGGA GCCCCAATGT GGTTGAACAG CCAGGTGCAC AGATGAGTCA ACCACACAGC CAGGCCAGGG AGGGCCTTCA CTCAAGAGCC TACAGCCAGT TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCCATAAAC TGATCTGAGA CTCTGTTTCC CTGTCTCCAT GATGATGGGA TCAGGCTTGA TTGCTGGTTT GTAGGCTTGT TATGAATCAA GTCACAGGGA AGAGGAGCTG ATGGGCTGGG GGGACGTCCT CTGGCCCTCC TGTCTCTTCC CCAGATCCAC TGGGCCCACT CTTATCTGTT CTCTTCTGAA GGAAGGGTTT TAAGGCTTCA AAAAAAAATG TTTTGAAAGT CCCTGCCCTT TCCAGCTCCT ACCGTCTCAG CCCTGGGAGT GTAAAGTGCT GCAGATAGTT AGTAAGTCTT TGAGCAAAAC TGAGAAAGCC AGCCTGAGCC TTGACATGGG AGAAACCTCC GCCATACATC TCCGAAGAAA CGGCCGCGTG TCTCAGGGGA GCGCAAACAC CCGTACCCAG GAAACAGGAC AGCTTCTGCC ACTGTCGCCC TTGGGAGCCG TACGTGGCAT GACAAAGAAA TCCCAGGACT CCGCCTGCCC ACCTGGCCAC CCTCTGTTTA CACCTTCCGC GTAAACGCCC ACTGTTTACA TCCAAAACTC AGACACAAAA TAACCACCTC AAGAAGATAA ATAATGATAA GAAATAAATG TTACGCGAGG CAAATTTATT CACATGGGGC TTCCCAGGCC ACTTTGTGGT CAGCCGGGAG GGACGTTTTT GCCGTCCCAC GACTCCAACG GGCAGCCGGG CCTACGCAAA CATGGAAATC TTCCAAGAGC CTCCCTGGCC CCCAGGGCTC AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG CCGCAGCCTT CCCGGCCCCA CAGCCAGCCT GGCTCCAGCT GGGCAGGAGT GCAGAGCTCA GCTGGAGGCG AGGGGGAAGT GCCCAGGAGG CTGATGACAT CACTACCCAG CCCTTCAAAG ATGAGCTGTT CCCGCCGCCA CTCCAGCTCT GGCTTCTGGG CTCCGAGGAG GGGTGGGGAC GGTGGTGACG GTGGGGACAT CAGGCTGCCC CGCAGTACCA GGGAGCGACT GAAGTGCCCA TGCCGCTTGC TCCGGAGAAG GTGGGTGCCG GGCAGGGGCT GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAAACTGTCC CAGCACAGAG GGAGGGAGGG AGGGCAGGCA GCGGGGAGAA GTTTCCCTGT GGTCGTGGGG AGTTGGGAAA AGTTCCCTTC CTTCCGGAGG GAGG -3' **(FRAG. NO:2275) (SEQ. ID NO:2286)**

5'- GAGCTCTTCA ATATTTTAGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA CACACCTTTT CAGAGGGCTT GTGGACTCTG GGCAGCCTGT CCATAGACCT CTGTCCCCAA CTGGCAAGTC AGGAAACTCC AGATTAAGGA GCCCCAATGT GGTTGAACAG CCAGGTGCAC AGATGAGTCA ACCACACAGC CAGGCCAGGG AGGGCCTTCA CTCAAGAGCC TACAGCCAGT TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCCATAAAC TGATCTGAGA CTCTGTTTCC CTGTCTCCAT GATGATGGGA TCAGGCTTGA TTGCTGGTTT GTAGGCTTGT TATGAATCAA GTCACAGGGA AGAGGAGCTG ATGGGCTGGG GGGACGTCCT CTGGCCCTCC TGTCTCTTCC CCAGATCCAC TGGGCCCACT CTTATCTGTT CTCTTCTGAA GGAAGGGTTT TAAGGCTTCA AAAAAAAATG TTTTGAAAGT CCCTGCCCTT TCCAGCTCCT ACCGTCTCAG CCCTGGGAGT GTAAAGTGCT GCAGATAGTT AGTAAGTCTT TGAGCAAAAC TGAGAAAGCC AGCCTGAGCC TTGACATGGG AGAAACCTCC GCCATACATC TCCGAAGAAA CGGCCGCGTG TCTCAGGGGA GCGCAAACAC CCGTACCCAG GAAACAGGAC AGCTTCTGCC ACTGTCGCCC TTGGGAGCCG TACGTGGCAT GACAAAGAAA TCCCAGGACT CCGCCTGCCC ACCTGGCCAC CCTCTGTTTA CACCTTCCGC GTAAACGCCC ACTGTTTACA TCCAAAACTC AGACACAAAA TAACCACCTC AAGAAGATAA ATAATGATAA GAAATAAATG TTACGCGAGG CAAATTTATT CACATGGGGC TTCCCAGGCC ACTTTGTGGT CAGCCGGGAG GGACGTTTTT GCCGTCCCAC GACTCCAACG GGCAGCCGGG CCTACGCAAA CATGGAAATC TTCCAAGAGC CTCCCTGGCC CCCAGGGCTC AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG CCGCAGCCTT CCCGGCCCCA CAGCCAGCCT GGCTCCAGCT GGGCAGGAGT GCAGAGCTCA GCTGGAGGCG AGGGGGAAGT GCCCAGGAGG CTGATGACAT CACTACCCAG CCCTTCAAAG ATGAGCTGTT CCCGCCGCCA CTCCAGCTCT GGCTTCTGGG CTCCGAGGAG GGGTGGGGAC GGTGGTGACG GTGGGGACAT CAGGCTGCCC CGCAGTACCA GGGAGCGACT GAAGTGCCCA TGCCGCTTGC TCCGGAGAAG GTGGGTGCCG GGCAGGGGCT GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAAACTGTCC CAGCACAGAG GGAGGGAGGG AGGGCAGGCA GCGGGGAGAA GTTTCCCTGT GGTCGTGGGG AGTTGGGAAA AGTTCCCTTC CTTCCGGAGG GAGG -3' **(FRAG. NO:2275) (SEQ. ID NO:2461)**

5'- GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CCGCAGTACC AGGGAGCGAC TGAAGTGCCC ATGCCGCTTG CTCCGGAGAA GGTGGGTGCC GGGCAGGGGC TGCTCCAGCC GCCTCACCTC TGCTGGGAGG ACAAACTGTC CCAGCACAGA GGGAGGGAGG GAGGGCAGGC AGCGGGGAGA AGTTTCCCTG TGGTCGTGGG GAGTT -3' **(FRAG. NO:2275) (SEQ. ID NO:2460)**

5'- GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA CGGTGGGGAC ATCAGGCTGC CCCGCAGTAC CAGGGAGCGA CTGAAGTGCC CATGCCGCTT GCTCCGGAGA AGGTGGGTGC CGGGCAGGGG CTGCTCCAGC CGCCTCACCT CTGCTGGGAG GACAAACTGT CCCAGCACAG AGGGAGGGAG GGAGGGCAGG CAGCGGGGAG AAGTTTCCCT GTGGTCGTGG GGAGTT -3' **(FRAG. NO:2275) (SEQ. ID NO:2459)**

5'- ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGACTC CGTGCCCACC ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA

GCTACCCATC CCTCATCTGG GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC
ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG GAGATCCAGA CGGAGAGGAG
GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA
CGCTGCATCG CCTCGGCATC CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG
GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGTA
CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA
TCTCCGTGGA ACGCCAGATT CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG
AATTTGTGTA AGGATTGAGG GACAGTTGCT T -3' **(FRAG. NO:2275) (SEQ. ID NO:2458)**

5'- ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCCACC ACGGCCTCTT TCAGCGCCGA
CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG
GCTGGCTCAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC
GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC GCAGCAGACC TGATCCTGGC
CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA
ATGCCATTAT CTCCATGAAC CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG
AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG ATCTGGGGGT GTACGCTGCT
CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA
GCTACCCATC CCTCATCTGG GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC
ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG GAGATCCAGA CGGAGAGGAG
GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA
CGCTGCATCG CCTCGGCATC CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG
GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGTA
CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA
TCTCCGTGGA ACGCCAGATT CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG
AATTTGTGTA AGGATTGAGG GACAGTTGCT T -3' **(FRAG. NO:2275) (SEQ. ID NO:2457)**

5'- TGATCCTATC ACAACCTGAG AGTAGTTTTT ACTCCATTTA CAGGTGAGGT CATTGTGGTT CAAGGACGTT AAGTAACTTC
CCCAGCTCAC ACGGCTTATA AGTAAGGCAG CCAGGATGTG AACCCAGTAG GACTATCTGG CTGCAAAGTC CCCACCCTCC
CTCGCCATCT GTATCCTCCA ATCATCTTCA GTGCTTTGCT GATAGAAGGT ACGGAAATAC GATGCCACAG ACTGTCCAGG
AAGACAGAAA CTAGGCAGAT GGGCTGGCCA TGGTCTCCAA GCCAGACTGG AATCTCCAGG TCTGGAATGA TATCATTTTT
CTCTTTTAAT AAATTAACTC ACCCACCACA CGGCTTTGAG AGGCTCAAAG GTGACCAACT CCCTTGGGAG GGCCCCGGTT
GATAAGGAAG GAATGTGAAT CCTCCCATCA CGGAAGCTTC AAGGAGGTCA AGGGTCCAAC ACTTGAGATT GTTAGTGCTG
TTGGTGGATA CTGCAGAATA TCCAGTGGAG CCTCAGATGA AGAACATGAG GCCCCGTTTA GATCCAAGGA TCAGAGGGGG
CTCTGTAAGA CCCAGGGGAG TCAGGTGCAC TGGAGCGCGG GCTGCAGAAA ACAGCCTGAG CTCCACCTCG GCTTCTCCTT
GCCCTGGCTG GTTGTCCTTA ACCCCTGTCT CCTTCTGGAC CAGTTTTTGT CCTTCCCTTG TGACCTGAGG GGTAACAGCC
TCTTTTCCAC TTTCTTTCAG CGCCGACATG CTCAATGTCA CCTTGCAAGG GCCCACTCTT AACGGGACCT TTGCCCAGAG
CAAATGCCCC CAAGTGGAGT GGCTGGGCTG GCTCAACACC ATCCAGCCCC CCTTCCTCTG GGTGCTGTTC GTGCTGGCCA
CCCTAGAGAA CATCTTTGTC CTCAGCGTCT TCTGCCTGCA CAAGAGCAGC TGCACGGTGG CAGAGATCTA CCTGGGGAAC
CTGGCCGCAG CAGACCTGAT CCTGGCCTGC GGGCTGCCCT TCTGGGCCAT CACCATCTCC AACAACTTCG ACTGGCTCTT
TGGGGAGACG CTCTGCCGCG TGGTGAATGC CATTATCTCC ATGAACCTGT ACAGCAGCAT CTGTTTCCTG ATGCTGGTGA
GCATCGACCG CTACCTGGCC CTGGTGAAAA CCATGTCCAT GGGCCGGATG CGCGGCGTGC GCTGGGCCAA GCTCTACAGC
TTGGTGATCT GGGGGTGTAC GCTGCTCCTG AGCTCACCCA TGCTGGTGTT CCGGACCATG AAGGAGTACA GCGATGAGGG
CCACAACGTC ACCGCTTGTG TCATCAGCTA CCCATCCCTC ATCTGGGAAG TGTTCACCAA CATGCTCCTG AATGTCGTGG
GCTTCCTGCT GCCCCTGAGT GTCATCACCT TCTGCACGAT GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG
TTCAAGGAGA TCCAGACGGA GAGGAGGGCC ACGGTGCTAG TCCTGGTTGT GCTGCTGCTA TTCATCATCT GCTGGCTGCC
CTTCCAGATC AGCACCTTCC TGGATACGCT GCATCGCCTC GGCATCCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG
TAATCACACA GATCGCCTCC TTCATGGCCT ACAGCAACAG CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGGCAAGCGC
TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC AGAAAGGGGG CTGCAGGTCA GAACCCATTC AGATGGAGAA
CTCCATGGGC ACACTGCGGA CCTCCATCTC CGTGGAACGC CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT
GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC
AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTGTTGA TGTCTCCGGT AAAACACCGG AGACTAATTC CTGCCCTGCC
CAATTTTCGA GGGAGCATGG CTGTGAGGAT GGGGTGAACT CACGCACAGC CAAGGACTCC AAAATCACAA CAGCATTACT
GTTCTTATTT GCTGCCACAC CTGAGCCAGC CTGCTCCTTC CCAGGAGTGG AGGAGGCCTG GGGGAGGGAG AGGAGTGACT
GAGCTTCCCT CCCGTGTGTT CTCCGTCCCT GCCCCAGCAA GACAACTTAG ATCTCCAGGA GAACTGCCAT CCACGTTTGG
TGCAATGGCT GAGTGCACAA GTGAGTTGTT GCCCTGGGTT TCTTTAATCT ATCAGCTAGA ACTTTGAAGG ACAATTTCTT
GCATTAATAA AGGTTAAGCC CTGAGGGGTC CCTTGATAAC AACCTGGAGA CCAGGATTTT ATGGCTCCCC TCACTGATGG
ACAAGGAGGT CTGTGCCAAA GAAGAATCAA TAAGCACATA TGAGCACTTC TGTATATCAG TATTGAGCAC TGTAGGCA -3'
(FRAG. NO:2275) (SEQ. ID NO:2456)

5'- CTGCAGAAAA CAGCCTGAGC TCCACCTCGG CTTCTCCTTG CCCTGGCTGG TTGTCCTTAA CCCCTGTCTC CTTCTGGACC
AGTTTTTGTC CTTCCCTTGT GACCCTGAGG GGTAACAGCC TCTTTTCCAC TTTCTTTCAG CGCCGACATG CTCAATGTCA
CCTTGCAAGG GCCCACTCTT AACGGGACCT TTGCCCAGAG CAAATGCCCC CAAGTGGAGT GGCTGGGCTG GCTCAACACC
ATCCAGCCCC CCTTCCTCTG GGTGCTGTTC GTGCTGGCCA CCCTAGAGAA CATCTTTGTC CTCAGCGTCT TCTGCCTGCA
CAAGAGCAGC TGCACGGTGG CAGAGATCTA CCTGGGGAAC CTGGCCGCAG CAGACCTGAT CCTGGCCTGC GGGCTGCCCT
TCTGGGCCAT CACCATCTCC AACAACTTCG ACTGGCTCTT TGGGGAGACG CTCTGCCGCG TGGTGAATGC CATTATCTCC
ATGAACCTGT ACAGCAGCAT CTGTTTCCTG ATGCTGGTGA GCATCGACCG CTACCTGGCC CTGGTGAAAA CCATGTCCAT
GGGCCGGATG CGCGGCGTGC GCTGGGCCAA GCTCTACAGC TTGGTGATCT GGGGGTGTAC GCTGCTCCTG AGCTCACCCA
TGCTGGTGTT CCGGACCATG AAGGAGTACA GCGATGAGGG CCACAACGTC ACCGCTTGTG TCATCAGCTA CCCATCCCTC
ATCTGGGAAG TGTTCACCAA CATGCTCCTG AATGTCGTGG GCTTCCTGCT GCCCCTGAGT GTCATCACCT TCTGCACGAT
GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG TTCAAGGAGA TCCAGACGGA GAGGAGGGCC ACGGTGCTAG
TCCTGGTTGT GCTGCTGCTA TTCATCATCT GCTGGCTGCC CTTCCAGATC AGCACCTTCC TGGATACGCT GCATCGCCTC
GGCATCCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG TAATCACACA GATCGCCTCC TTCATGGCCT ACAGCAACAG

CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGGCAAGCGC TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC
AGAAAGGGGG CTGCAGGTCA GAACCCATTC AGATGGAGAA CTCCATGGGC ACACTGCGGA CCTCCATCTC CGTGGAACGC
CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGTAAGGA
TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTTGATG
TCTCCGGTAA AACACCGGAG ACTAATTCCT GNCCTGCCCA ATTTTGCAGG GAGCATGGCT GTGAGGATGG GGTGAACTCA
CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT TCTTATTTGC TGCCACACCT GAGCCAGCCT GCTCCTTCCC
AGGAGTGGAG GAGGCCTGGG GGCAGGGAGA GGAGTGACTG AGCTTCCCTC CCGTGTGTTC TCCGTCCCTG CCCCAGCAAG
ACAACTTAGA TCTCCAGGAG AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGCACAAG TGAGTTGTTG CCCTGGGTTT
CTTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC CCTGATAACA
ACCTGGAGAC CAGGATTTTA TGGCTCCCCT CACTGATGGA CAAGGGAGGT CTGTGCCAAA GAAGAATCCA ATAAGCACAT
ATTGAGCACT TGCTGTATAT GCAGTATTGA GCACTGTAGG CAAGAGGGAA GAAAGAGAAG GAGCCATCTC CATCTTGAAG
GAACTCAAAG ACTCAAGTGG GAACGACTGG CACTGCCACC ACCAGAAAGC TGTTCGACGA GACGGTCGAG CAGGGTGCTG
TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCA GCTCAACCAA TAACTATTGC ACAACCACCT GTCCCTGCCT
CAGTTCCCTC TTCTGTAACA TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG
TGCTACGTAC ATGTGAGGCA TCATTACGCA GACGTAACTG GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGA -3'

(FRAG. NO:2275) (SEQ. ID NO:2455)

5'- AAATGATAGA CCGTCAATAA TTTGTTAAAT GCTTTTTAAA ATGAATGCTT TAAGCCGGGT GCAGTGCCTC ACATCTGTAA
TCCCAGCACT TTGGAGCCGA GCGGGTGGAT TGTGTGAGGT CAGGAGTTCG AGACCAACCT GGCCAACATG GCAAAACCTC
ACTCTCTACC AAAAATACAA AAATTAGCCA GGCATGGTGG CAGGCACCTG TGATCCCAGC TACTCAGGAG GCTGAGACAG
GAGAATCGCT TGAACCCGGG AGGCAAGGTT GCAGTGAGCC AAGATTACGC CATTGTACTC CAGCCTGGGT GACAGAGAGA
GACTCCGTCT CAAAAAAAAA AAAAAAAAAA AAAAAATTAC GCTTCAAACA CATGATCTCT CACCACTGTT GAATTTTCTT
TCTATGAGCC CAGGAGGGCC TCTCAGAGAG GAAAGCTCCT AGGTCTTCCT TTCCCTCTGC AAACTCCCTG CCTTGAAGGT
TCAGAAGGAC TGTGCGTGCT CGTTGCATCC TTTGCAAGTG TCCAAACCCT GATCCCAGCT GTGCTTAGGG GTTCCTGCAA
ACCTTTTCCA GGTGTTAATT ACCTCCCACT TCATTTCCTG TTTACCAACT CAGCTTTTTG TTTTAGTGTG TTTGAATTCC
CTGAACTGAC CGTTGTCTGA TCTCCACCTC CCAACTGAAT TAGGGGAGCT GGGCTTCTGG AAACCCAGGT GCCGGGTGTT
GCAGAGTGGC TGAAAGCTGG GATGTGGCAG ATCCGTGGCT ACATTCATGC ACACACACAC ACCCACATAC CCACACATGC
ACACACACAC ACACACCCGC ACTCACACAC TTGGACATGC ATAGACCACA GCTTTCCACA CCCTTCCTAG ACAGGGGTCA
CTTGGTATCC TGGAGAGAGT GTGAAGTCCT GGAATGGAAA GAGGGGGGAT TAAGCCCCAC CTCTAGCCAT GGGACTGAGA
CAAGTCACCA CCAACCCATC TGCGCCTTGT TTACCTCCTC TGTGAGGCAA GCACAGAGCC CATGCCTGCC CCCCTGGATG
GGAGTGATGT GAAACTTGAA GGGCGGTCAG AGCAAGGGTC GGGAATGGAA GGCCCTTGGG AAAAAAGGCC CTTTCAACTA
GGGGCACAGA GGAGGCCCTG GGCTGAGAAC TTGACAGCAC CTTGTAATTG GTAAGCCAAG CCCGAAGGGA CTGGAAATAC
TCAGATGTGT CTGTCTCCCT TATTAGGTTC AAAGTCCCTC AAGACCCTGT CTCCATCACA GTGCTCCAGT CCAGACCCCT
CCTCTGAGCT CCAGACCCTG CTGGACCCAA CCAGCCCTAT GGGGTCGCAT CCCCACCTGC CTGGAATTCT CCAAAGAACC
TCCCCTTTAA CAGTTCCAGC CTTTAACAGT TCCAGTCTAA ACACATGACC TTTCTCCTCT AAATCAGCCC CCCATCTCTG
CCTTTGCAGG AGATGGAAGC CATGACACCT GCCTCGCCCC TGTCCTCACC CCATCCATGT CCAATCAAGC ACTAGGCATG
TCAGGTTTAC CCTCTAAACT CCTCTGGAAT CCAGTCTCTC AGTCTCCATC ATCCCAGGTC GAAGCTAATG GGCTAACTGG
TCCTTGCTTC CACTCTACCC CCACTGCAGT CCTGACTTCC TGAGCAGCAG CCAGGGCCTA ATCGATATTC ACACCAAGCG
CCAACCTGAC TGAGATATCC TCCTGCACCA TCATCCCTCC ACCCTGTTTA GTTCTGCTCA CCCTCAGTGT TCTCATCAAT
AATCCACTCC CCTCACAGGC GCGTTTGGGA CCCCATGTTC TATGCTCTCA CAGGACCTTT TGCTTGATTT TTCACTGTAC
TTAGGTCAGT TTGCAGTTAT TAAGTGACTG AGCAATGTCT GGCTTCTCCA GTAGACTGTC AGCTCCTAGC CATTGTATAC
CTAGCACCGC TGTGTGGGAG CACGTGACAA ACGTCCAGTG AGTCAGGGAC TCAGCAGTCT CCATTTCTCC GCCCTGCTGG
AGAATGCGTG TATTTGGCAA TCCCCAGCCC CTGTGCCATC TAACCATCTT TTCTTCTCTG TTCAGCCCAG GTGTGGCCTC
ACTCACATCC CACTCTGAGT CCAAATGTTC TCTCCCTGGA AGATATCAAT GTTTCTGTCT GTTCGTGAGG ACTCCGTGCC
CACCACGGCC TCTTTCAGGT GAGTCAAAGG GATTCCTCAG TTCACTAGTT AGGGGAGGTG GGCAGACACC CTGGAGAACT
CCCTGGAAAG CTCAACTCTC ATGCCCCGGA CAACAGTTGA AGGAACCATG GTGATGTTAA GCCCAAAGAC AAAACCTCTC
AGGTGTCCAA GTCCCTGTTG GAATCTTGGG AGCAGAGGGA ATGTTCTGTG GTCTAGAGGA AGAGGGGCTC AGGGAGGAGA
AGGGCACATT CCTGGTTGTT ATATGTTTCT ATCTATCCCA GATGAACTTG GAAGTGAAGG GAAGAGAGTT AAACATTAAA
GTAAATACCC AGTGGATCAG ACAGCAATGT GCCAGATTGC CTTGGAAACA AAATATCTCC AACACATGGC TGACATTTGG
TGGGAGATCA GAACACCCTA AAGAGAGAAT TTAAGGGGAG GGGGAGGAGG ACCTGAGCCA GAGTAGAAGC
AGAGGATAGG GAGATCTGTT CTTGGGGACA GCATTTGCAA GAAACAAGGC TGAGGGGTCC ACTCCAACCT CTCCACCCTG
CTGCAGGTGC TGCCTATGAT GAAGATGAGC AGATGGCCAT CTCAGCTGGG GCCACAGTGC ACTGGACCTA TAGTTTCCAA
TTCCGCACTC AGCAGGCATC TTTCTGATGA TCCGATGGCT TCTCAGAGCC AGGGATGGGC CAGGATCCAT CCCCTTGGCT
ACTGTCTTGC TGAGAAATTT ATAAGCAGCA TCTGGTGCTA TACTTTGGTC TCTAGTGAGT TAGCTCATGA AAGATGATAG
ACTCTCCAAG CCAGGGGTAT GCAGGAAATG GGTTTTCTGT AGCTACAGAA ATGGGGTTGA GGGTTGGACC AAGGGACTAC
CCAGGGGAAG TCTTACCTTC AGAGGACTCT GGAAAGGAGG CTGCAAGTTT TCATGGGTCA AGAATTCAGA GCCCAGTAGA
GACAGCTTAT CTCTGTTCCA AGATGTCTGG GGCCTTGGTT GGAAGATTCA AAGGCTAGGA AACCAGGAGC CACCAAAAGC
GTAACTGGGG CCAGAGGATC CACTTTCAAG GTGGCAAGTT GGTTCCCCCC ATGTGGCTGC TTGAGTATCC TCACATGGCG
GCTCACATCC TTCCAAGTAA GCAATGCAAA AGGCCAAGAA AGATGCTGCA AAGATGTTAT GACCTAGCCT CAGAAATCAC
ACACCATCCC TGCCACCATT AGTAAGAAGT CCAGCCCACG TCCAGGAGAA GAGGAAGCAG ATTCCTCCTT TTGAAATGAA
GAATATCAAG TAATTCGGGG GGCATATGAA AGCCACCACA CACCACAGGG ATCTTTTTAG AGCATACTTC TTATACCATC
ACTGTAGTTC CTTAAGACTC AGGGGCAAAG CCTCACTTCC TTAGCACCCA GTGAAGACCA CGCTTACTCC CTCACTCAAC
CTCTTGCTAC TTCCCACCTC TCCTGTCCAA CATCTAGTGT CACTTTCCAG AACATACCAA CAGCTTCCCC AGTTCTGTGC
CTCTGCTCAG GCTGTTCCCC CTGCCTGGTC CACTTGTCCT CCTTCTTGTC CGGTCAAAAT GCTTCTTATC CTTCAAGACC
CAGCTCTAGA GTCACCTCCA ACCCCTTACC CACCAGCCCC CTCTCCAAGT CTGTGTCCCA CAACCCCCCT GCTCCCTCCA
GGGCACCCTC CACCCTCTGG GCCACAGTTG TCAGGAGTCA GGCAGGGCAG GGGCCGGGTG GTGTCTTCTT TGTGTTCTTG
CACTCAGGGC AGAGCTCAGC ACAGAGCAGA CGCTCAAAAA ACATTTAAAG GATAGAAGCA TTGATTTGTG GGTCCCCCAG
TCTGGCTCCA GGATGCCAGC CAGCTGCTCC TAGAAGCAAA CGGACTTTTC CTGGGAAATC CCAGAGGTGA TGATCAGTAA
TCTCTCCCGT GACTCGTAGT TCAGCTCTTC CTCCATGAGC CTGACTATCA GTGGACCTTC CAGAAAGAGC CCCTTTTCCT
TCTCTCACCC ACAGCACAGG GCACTGGGAA AATGCCCAAT GAGTCCTGCC TCTGGGTTGT GCTTTGGACT TTTCAGTGTG

TCTCGCATCC ACTCTTCAAC TTGAATGTTG CAACAGCCAT GAAAAAAGAA ATGCAAAGCG ATTCAGGATG AGAGCAATAC CCTACTCCAA AGAAGGCAAC ATAGAAGCTC AGAGAGATCA AGCAATTTGC CCAAGACCAC ACAGCTAGGA GTGGAACTCA TGGCTGTCCA AGCCCCATGC CTCTGCTGAA GGTAGAGATG AATTACAGCA ACAAGTCTAG AAAGGTGCCT GCCCTATGGT CTGTGAGTCT TGCCTAAGAA TGAAAGAGGA GCCAGTGGGT TAAAGATGAG GTCACCAACA ACGGTGGTGT TGGAGTTTAC CACTGATAAT AAGGGTGCAA AATGTAAATT ACTAATGTTT ATTGAGCCTA GTGCAGTGCG TGGGGCATTT TGCACATTGT CTCTGATCCC TATGACAACC CTGAGAGGTA GTGGTTTTAA CTGCCATGTT ACAGGTGAGG TCATTGTGGT TCAAGGACGT TAAGTAACTT CCCCAGCGTG ACACGGCTTA TAAGTAAGGC AGCCAGGATG TGAACCCAGT AGGACTATCT GGCTGCAAAG TCCCCACCCC CCTCGCCATC TGTATCCTCC AATCACTTCA GTGCTTTGCT GCATAGAAGG TAACGGAAAT CACGATGCCA CAGACTGTCC AGGAAGACAG AAACTAGGCA GATGGGCTGG CCATGGTCTC CAAGCCAGAC TGGAATCTCC AGGTCTGGAA TGATATCATT TTTCTCTTTT AATAAATTAA CTCACCCACC ACACGGCTTT GAGAGGCTCA AAGTTGACCA ACTCCCTTGG GAGGGCCCCG GTTGATAAGG AAGGAACGTG AATCCTCCCA TCACGGAAGC TTCAAGGAGG TCAAGGGTCC AACACTTGAG ATTGTTAGTG CTGTTGGTGG ATACTGGCCA AGGAAATATC CCAGTGGAGC CTCGAGATGA AGAACATGAG GCCCCCGTTT AGAACCAAGG ATCAGAGGGG GCTCTGTAAG ACCCAGGGGA GTCAGGTGCA CTGGAGCGCG GGCATGCAGA AAACAGCCTG AGCTCCACCT CGGCTTCTCC TTGTCCTGGC TGGTTGTCCT TAACCCCTGT CTCCTTCTGG ACCAGTTTTT GTCCTTCCCT TGTGACCGCT GAGGGGTAAC AGCCTCTTTC CACTTTCTTT CAGCGCCGAC ATGCTCAATG TCACCTTGCA AGGGCCCACT CTTAACGGGA CCTTTGCCCA GAGCAAATGC CCCCAAGTGG AGTGGCTGGG CTGGCTCAAC ACCATCCAGC CCCCCTTCCT CTGGGTGCTG TTCGTGCTGG CCACCCTAGA GAACATCTTT GTCCTCAGCG TCTTCTGCCT GCACAAGAGC AGCTGCACGG TGGCAGAGAT CTACCTGGGG AACCTGGCCG CAGCAGACCT GATCCTGGCC TGCGGGCTGC CCTTCTGGGC CATCACCATC TCCAACAACT TCGACTGGCT CTTTGGGGAG ACGCTCTGCC GCGTGGTGAA TGCCATTATC TCCATGAACC TGTACAGCAG CATCTGTTTC CTGATGCTGG TGAGCATCGA CCGCTACCTG GCCCTGGTGA AAACCATGTC CATGGGCCGG ATGCGCGGCG TGCGCTGGGC CAAGCTCTAC AGCTTGGTGA TCTGGGGGTG TACGCTGCTC CTGAGCTCAC CCATGCTGGT GTTCCGGACC ATGAAGGAGT ACAGCGATGA GGGCCACAAC GTCACCGCTT GTGTCATCAG CTACCCATCC CTCATCTGGG AAGTGTTCAC CAACATGCTC CTGAATGTCG TGGGCTTCCT GCTGCCCCTG AGTGTCATCA CCTTCTGCAC GATGCAGATC ATGCAGGTGC TGCGGAACAA CGAGATGCAG AAGTTCAAGG AGATCCAGAC GGAGAGGAGG GCCACGGTGC TAGTCCTGGT TGTGCTGCTG CTATTCATCA TCTGCTGGCT GCCCTTCCAG ATCAGCACCT TCCTGGATAC GCTGCATCGC CTCGGCATCC TCTCCAGCTG CCAGGACGAG CGCATCATCG ATGTAATCAC ACAGATCGCC TCCTTCATGG CCTACAGCAA CAGCTGCCTC AACCCACTGG TGTACGTGAT CGTGGGCAAG CGCTTCCGAA AGAAGTCTTG GGAGGTGTAC CAGGGAGTGT GCCAGAAAGG GGGCTGCAGG TCAGAACCCA TTCAGATGGA GAACTCCATG GGCACACTGC GGACCTCCAT CTCCGTGGAA CGCCAGATTC ACAAACTGCA GGACTGGGCA GGGAGCAGAC AGTGAGCAAA CGCCAGCAGG GCTGCTGTGA ATTTGTGTAA GGATTGAGGG ACAGTTGCTT TTCAGCATGG GCCCAGGAAT GCCAAGGAGA CATCTATGCA CGACCTTGGG AAATGAGTTG ATGTCTCCGG TAAAACACCG GAGACTAATT CCTGCCCTGC CCAATTTTGC AGGGAGCATG GCTGTGAGGA TGGGGTGAAC TCACGCACAG CCAAGGACTC CAAAATCACA ACAGCATTAC TGTTCTTATT TGCTGCCACA CCTGAGCCAG CCTGCTCCTT CCCAGGAGTG GAGGAGGCCT GGGGGCAGGG AGAGGAGTGA CTGAGCTTCC CTCCCGTGTG TTCTCCGTCC CTGCCCCAGC AAGACAACTT AGATCTCCAG GAGAACTGCC ATCCAGCTTT GGTGCAATGG CTGAGTGCAC AAGTGAGTTG TTGCCCTGGG TTTCTTTAAT CTATTCAGCT AGAACTTTGA AGGACAATTT CTTGCATTAA TAAGGTTAA GCCCTGAGGG GTCCCTGATA ACAACCTGGA GACCAGGATT TTATGGCTCC CCTCACTGAT GGACAAGGAG GTCTGTGCCA AAGAAGAATC CAATAAGCAC ATATTGAGCA CTTGCTGTAT ATGCAGTATT GAGCACTGTA GGCAAGAGGG AAGAAAGAGA AGGAGCCATC TCCATCTTGA AGGAACTCAA AGACTCAAGT GGGAACGACT GGGCACTGCC ACCACCAGAA AGCTGTTCGA TGAGACGGTC GAGCAGGGTG CTGTGGGTGA TATGGACAGC AGAAGGGGGA GCCAGGTTCC AGCTCACCAA TACTATTGCA CACCACCTGT CCTGCCTC -3' (FRAG. NO:2275) (SEQ. ID NO:2454)

5'- CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTTGATG TCTCCGGTAA AACACCGGAG ACTAATTCCT GCCCTGCCCA ATTTTGCAGG GAGCATGGCT GTGAGGATGG GGTGAACTCA CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT TCTTATTTGC TGCCACACCT GAGCCAGCCT GCTCCTTCCC AGGAGTGGAG GAGGCCTGGG GGGAGGGAGA GGAGTGACTG AGCTTCCCTC CCGTGTGTTC TCCGTCCCTG CCCCAGCAAG ACAACTTAGA TCTCCAGGAG AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGCACAAG TGAGTTGTTG CCCTGGGTTT CTTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC CCTGATAACA ACCTGGAGAC CAGGATTTTA TGGCTCCCCT CACTGATGGA CAAGGAGGTC TGTGCCAAAG AAGAATCCAA TAAGCACATA TTGAGCACTT GCTGTATATG CAGTATTGAG CACTGTAGGC AAGACCCAAG AAAGAGAAGG AGCCATCTCC ATCTTGAAGG AACTCAAAGA CTCAAGTGGG AACGACTGGG CACTGCCACC ACCAGAAAGC TGTTCGACGA GACGGTCGAG CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCA GCTCAACCAA TAACTATTGC ACAACCACCT GTCCCTGCCT CAGTTCCCTT TTATGTAACA TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG TGCTACGTAC ATGTGAGGCA TCATTACGCA GACGTAACTG GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGAA ATAGCTCCGT GGAGCAGAAT CAGTATTGGG AGCCGGTGGC GGTGTGAAGC ACCAGTGTCT GGCACACAGT AGGTGCTCAT TGGCTCCCTT CCACCTGTCA TTCCCACCAC CCTGAGGCCC CAACCGCCAC ACACACAGGA GCATTTGGAG AGAAGGCCAT GTCTTCAAAG TCTGATTTGT GATGAGGCAG AGGAAGATAT TTCTAATCGG TCTTGCCCAG AGGATCACAG TGCTGAGACC CCCCACCACC AGCCGGTACC TGGGAAGGGG GAGAGTGCAG GCCTGCTCAG GGACTGTTCC TGTCTCAGCA ACCAAGGGAT TGTTCCTGTC AATCAATGGT TTATTGGAAG GTGGCCCAGT ATGAGCCCTA GAAGAGTGTG AAAAGGAATG GCAATGGTGT TCACCATCGG CAGTGCCAGG GCAGCACTCA TTCACTTGAT AAATGAATAT TTATTAGCTG GTTGGAGAGC TAGAACCTGG AGAGCTAGAA CCTGGAGAAC TAGAACCTGG AGGGCTAGAA CCTGGAGAGG CTAGAACCAA GAAGGGCTAG AACCTGGAGG GGCTAGAACC TAGAGAAGCT AAAACCTGAG CTAGAAGCTG GAGGACTAGA ACCTGGAGGG CTGGAATCTG AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTGG AATCTGGAGA GCTAGAACCT GGAGGGCTAG AACCTGGAGG GCTAGAACCT AGAAGGGCTA GAACCTGGAG GGCTAGAACC TGGCAGGTTA GAACCTAGAA GGGCTAGAAC CTGGAGAGCC AGAACCTGGA GGGCTAGAAC CTGGAAGGGC TAGAACCTGT AGAGCTAGAA CATGGAGAGC TAGAACCCGG CAGGCTAGAA CCTGGCAAGC TAGAACCTGG AGGGAATGAA CCTGGAGGGC TAGAACCTGG AGAATGAGAA AAATTTACAT GGCAAAGAGC CCATAAATCC TGACCAATCC AACTCTGAAT TTTAAAGCAA AAGCGTGAAA AAAAAGATTC CCTCCTTACC CCCAACCCAC TCTTTTTTCC CACCACCCAC TCTCCTCTGC CTCAGTAAGT ATCTGGAGGA AGAAAACAGG TGAAAGAAGA AGTAAAAACC ATTTAGTATT AGTATTAGAA TGAAGTCAAA CTGTGCCACA CATGGTGAAT GAAAAAAAAA AAAAAGAGGC TGTGTTTTGT CACACAGGGC AGTCATTCAG

CACCAGAGCA CGTGATGGTC TGAGACTCTC TTAGGAGCAG AGCTCTGCCG CAATGGCCAT GTGGGGATCC ACACCTGGTC TGAGGGGCAA CTGAGTCTGC GGGAGAAGAG CGGCCCTATG CATGGTGTAG ATGCCCTGAT AAAGAACATC TGTCCTGTGA AAGACTCAAT GAGCTGTTAT GTTGTAAACA GGAAGCATTT CACATCCAAA CGAGAAAATC ATGTAAACAT GTGTCTTTTC TGTAGAGCAT AATAAATGGA TGAGGTTTTT GCAAAAAAAA AAAAAAAAA -3' **(FRAG. NO:2275) (SEQ. ID NO:2453)**

5'- GAGCTCTTCA ATATTTTAGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA CACACCTTTT CAGAGGGCTT GTGGACTCTG GGCAGCCTGT CCATAGACCT CTGTCCCCAA CTGGCAAGTC AGGAAACTCC AGATTAAGGA GCCCCAATGT GGTTGAACAG CCAGGTGCAC AGATGAGTCA ACCACACAGC CAGGCCAGGG AGGGCCTTCA CTCAAGAGCC TACAGCCAGT TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCCATAAAC TGATCTGAGA CTCTGTTTCC CTGTCTCCAT GATGATGGGA TCAGGCTTGA TTGCTGGTTT GTAGGCTTGT TATGAATCAA GTCACAGGGA AGAGGAGCTG ATGGGCTGGG GGGACGTCCT CTGGCCCTCC TGTCTCTTCC CCAGATCCAC TGGGCCCACT CTTATCTGTT CTCTTCTGAA GGAAGGGTTT TAAGGCTTCA AAAAAAAATG TTTTGAAAGT CCCTGCCCTT TCCAGCTCCT ACCGTCTCAG CCCTGGGAGT GTAAAGTGCT GCAGATAGTT AGTAAGTCTT TGAGCAAAAC TGAGAAAGCC AGCCTGAGCC TTGACATGGG AGAAACCTCC GCCATACATC TCCGAAGAAA CGGCCGCGTG TCTCAGGGGA GCGCAAACAC CCGTACCCAG GAAACAGGAC AGCTTCTGCC ACTGTCGCCC TTGGGAGCCG TACGTGGCAT GACAAAGAAA TCCCAGGACT CCGCCTGCCC ACCTGGCCAC CCTCTGTTTA CACCTTCCGC GTAAACGCCC ACTGTTTACA TCCAAAACTC AGACACAAAA TAACCACCTC AAGAAGATAA ATAATGATAA GAAATAAATG TTACGCGAGG CAAATTTATT CACATGGGGC TTCCCAGGCC ACTTTGTGGT CAGCCGGGAG GGACGTTTTT GCCGTCCCAC GACTCCAACG GGCAGCCGGG CCTACGCAAA CATGGAAATC TTCCAAGAGC CTCCCTGGCC CCCAGGGCTC AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG CCGCAGCCTT CCCGGCCCCA CAGCCAGCCT GGCTCCAGCT GGGCAGGAGT GCAGAGCTCA GCTGGAGGCG AGGGGGAAGT GCCCAGGAGG CTGATGACAT CACTACCCAG CCCTTCAAAG ATGAGCTGTT CCCGCCGCCA CTCCAGCTCT GGCTTCTGGG CTCCGAGGAG GGGTGGGGAC GGTGGTGACG GTGGGGACAT CAGGCTGCCC CGCAGTACCA GGGAGCGACT GAAGTGCCCA TGCCGCTTGC TCCGGAGAAG GTGGGTGCCG GGCAGGGGCT GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAAACTGTCC CAGCACAGAG GGAGGGAGGG AGGGCAGGCA GCGGGGAGAA GTTTCCCTGT GGTCGTGGGG AGTTGGGAAA AGTTCCCTTC CTTCCGGAGG GAGG -3' **(FRAG. NO:2275) (SEQ. ID NO:2452)**

5'- GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CCGCAGTACC AGGGAGCGAC TGAAGTGCCC ATGCCGCTTG CTCCGGAGAA GGTGGGTGCC GGGCAGGGGC TGCTCCAGCC GCCTCACCTC TGCTGGGAGG ACAAACTGTC CCAGCACAGA GGGAGGGAGG GAGGGCAGGC AGCGGGGAGA AGTTTCCCTG TGGTCGTGGG GAGTT -3' **(FRAG. NO:2275) (SEQ. ID NO:2451)**

5'- GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA CGGTGGGGAC ATCAGGCTGC CCCGCAGTAC CAGGGAGCGA CTGAAGTGCC CATGCCGCTT GCTCCGGAGA AGGTGGGTGC CGGGCAGGGG CTGCTCCAGC CGCCTCACCT CTGCTGGGAG GACAAACTGT CCCAGCACAG AGGGAGGGAG GGAGGGCAGG CAGCGGGGAG AAGTTTCCCT GTGGTCGTGG GGAGTT -3' **(FRAG. NO:2275) (SEQ. ID NO:2450)**

5'- ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGACTC CGTGCCCACC ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG AATTTGTGTA AGGATTGAGG GACAGTTGCT T -3' **(FRAG. NO:2275) (SEQ. ID NO:2449)**

5'- ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCCACC ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG AATTTGTGTA AGGATTGAGG GACAGTTGCT T -3' **(FRAG. NO:2275) (SEQ. ID NO:2448)**

5'- TGATCCTATC ACAACCTGAG AGTAGTTTTT ACTCCATTTA CAGGTGAGGT CATTGTGGTT CAAGGACGTT AAGTAACTTC CCCAGCTCAC ACGGCTTATA AGTAAGGCAG CCAGGATGTG AACCCAGTAG GACTATCTGG CTGCAAAGTC CCCACCCTCC CTCGCCATCT GTATCCTCCA ATCATCTTCA GTGCTTTGCT GATAGAAGGT ACGGAAATAC GATGCCACAG ACTGTCCAGG AAGACAGAAA CTAGGCAGAT GGGCTGGCCA TGGTCTCCAA GCCAGACTGG AATCTCCAGG TCTGGAATGA TATCATTTTT CTCTTTTAAT AAATTAACTC ACCCACCACA CGGCTTTGAG AGGCTCAAAG GTGACCAACT CCCTTGGGAG GGCCCCGGTT GATAAGGAAG GAATGTGAAT CCTCCCATCA CGGAAGCTTC AAGGAGGTCA AGGGTCCAAC ACTTGAGATT GTTAGTGCTG

TTGGTGGATA CTGCAGAATA TCCAGTGGAG CCTCAGATGA AGAACATGAG GCCCCGTTTA GATCCAAGGA TCAGAGGGGG
CTCTGTAAGA CCCAGGGGAG TCAGGTGCAC TGGAGCGCGG GCTGCAGAAA ACAGCCTGAG CTCCACCTCG GCTTCTCCTT
GCCCTGGCTG GTTGTCCTTA ACCCCTGTCT CCTTCTGGAC CAGTTTTTGT CCTTCCCTTG TGACCTGAGG GGTAACAGCC
TCTTTTCCAC TTTCTTTCAG CGCCGACATG CTCAATGTCA CCTTGCAAGG GCCCACTCTT AACGGGACCT TTGCCCAGAG
CAAATGCCCC CAAGTGGAGT GGCTGGGCTG GCTCAACACC ATCCAGCCCC CCTTCCTCTG GGTGCTGTTC GTGCTGGCCA
CCCTAGAGAA CATCTTTGTC CTCAGCGTCT TCTGCCTGCA CAAGAGCAGC TGCACGGTGG CAGAGATCTA CCTGGGGAAC
CTGGCCGCAG CAGACCTGAT CCTGGCCTGC GGGCTGCCCT TCTGGGCCAT CACCATCTCC AACAACTTCG ACTGGCTCTT
TGGGGAGACG CTCTGCCGCG TGGTGAATGC CATTATCTCC ATGAACCTGT ACAGCAGCAT CTGTTTCCTG ATGCTGGTGA
GCATCGACCG CTACCTGGCC CTGGTGAAAA CCATGTCCAT GGGCCGGATG CGCGGCGTGC GCTGGGCCAA GCTCTACAGC
TTGGTGATCT GGGGGTGTAC GCTGCTCCTG AGCTCACCCA TGCTGGTGTT CCGGACCATG AAGGAGTACA GCGATGAGGG
CCACAACGTC ACCGCTTGTG TCATCAGCTA CCCATCCCTC ATCTGGGAAG TGTTCACCAA CATGCTCCTG AATGTCGTGG
GCTTCCTGCT GCCCCTGAGT GTCATCACCT TCTGCACGAT GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG
TTCAAGGAGA TCCAGACGGA GAGGAGGGCC ACGGTGCTAG TCCTGGTTGT GCTGCTGCTA TTCATCATCT GCTGGCTGCC
CTTCCAGATC AGCACCTTCC TGGATACGCT GCATCGCCTC GGCATCCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG
TAATCACACA GATCGCCTCC TTCATGGCCT ACAGCAACAG CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGGCAAGCGC
TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC AGAAAGGGGG CTGCAGGTCA GAACCCATTC AGATGGAGAA
CTCCATGGGC ACACTGCGGA CCTCCATCTC CGTGGAACGC CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT
GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC
AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTGTTGA TGTCTCCGGT AAAACACCGG AGACTAATTC CTGCCCTGCC
CAATTTTCGA GGGAGCATGG CTGTGAGGAT GGGGTGAACT CACGCACAGC CAAGGACTCC AAAATCACAA CAGCATTACT
GTTCTTATTT GCTGCCACAC CTGAGCCAGC CTGCTCCTTC CCAGGAGTGG AGGAGGCCTG GGGGAGGGAG AGGAGTGACT
GAGCTTCCCT CCCGTGTGTT CTCCGTCCCT GCCCCAGCAA GACAACTTAG ATCTCCAGGA GAACTGCCAT CCACGTTTGG
TGCAATGGCT GAGTGCACAA GTGAGTTGTT GCCCTGGGTT TCTTTAATCT ATCAGCTAGA ACTTTGAAGG ACAATTTCTT
GCATTAATAA AGGTTAAGCC CTGAGGGGTC CCTTGATAAC AACCTGGAGA CCAGGATTTT ATGGCTCCCC TCACTGATGG
ACAAGGAGGT CTGTGCCAAA GAAGAATCAA TAAGCACATA TGAGCACTTC TGTATATCAG TATTGAGCAC TGTAGGCA -3'

(FRAG. NO:2275) (SEQ. ID NO:2447)

5'- CTGCAGAAAA CAGCCTGAGC TCCACCTCGG CTTCTCCTTG CCCTGGCTGG TTGTCCTTAA CCCCTGTCTC CTTCTGGACC
AGTTTTTGTC CTTCCCTTGT GACCCTGAGG GGTAACAGCC TCTTTTCCAC TTTCTTTCAG CGCCGACATG CTCAATGTCA
CCTTGCAAGG GCCCACTCTT AACGGGACCT TTGCCCAGAG CAAATGCCCC CAAGTGGAGT GGCTGGGCTG GCTCAACACC
ATCCAGCCCC CCTTCCTCTG GGTGCTGTTC GTGCTGGCCA CCCTAGAGAA CATCTTTGTC CTCAGCGTCT TCTGCCTGCA
CAAGAGCAGC TGCACGGTGG CAGAGATCTA CCTGGGGAAC CTGGCCGCAG CAGACCTGAT CCTGGCCTGC GGGCTGCCCT
TCTGGGCCAT CACCATCTCC AACAACTTCG ACTGGCTCTT TGGGGAGACG CTCTGCCGCG TGGTGAATGC CATTATCTCC
ATGAACCTGT ACAGCAGCAT CTGTTTCCTG ATGCTGGTGA GCATCGACCG CTACCTGGCC CTGGTGAAAA CCATGTCCAT
GGGCCGGATG CGCGGCGTGC GCTGGGCCAA GCTCTACAGC TTGGTGATCT GGGGGTGTAC GCTGCTCCTG AGCTCACCCA
TGCTGGTGTT CCGGACCATG AAGGAGTACA GCGATGAGGG CCACAACGTC ACCGCTTGTG TCATCAGCTA CCCATCCCTC
ATCTGGGAAG TGTTCACCAA CATGCTCCTG AATGTCGTGG GCTTCCTGCT GCCCCTGAGT GTCATCACCT TCTGCACGAT
GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG TTCAAGGAGA TCCAGACGGA GAGGAGGGCC ACGGTGCTAG
TCCTGGTTGT GCTGCTGCTA TTCATCATCT GCTGGCTGCC CTTCCAGATC AGCACCTTCC TGGATACGCT GCATCGCCTC
GGCATCCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG TAATCACACA GATCGCCTCC TTCATGGCCT ACAGCAACAG
CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGGCAAGCGC TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC
AGAAAGGGGG CTGCAGGTCA GAACCCATTC AGATGGAGAA CTCCATGGGC ACACTGCGGA CCTCCATCTC CGTGGAACGC
CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGTAAGGA
TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTTGATG
TCTCCGGTAA AACACCGGAG ACTAATTCCT GNCCTGCCCA ATTTTGCAGG GAGCATGGCT GTGAGGATGG GGTGAACTCA
CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT TCTTATTTGC TGCCACACCT GAGCCAGCCT GCTCCTTCCC
AGGAGTGGAG GAGGCCTGGG GGCAGGGAGA GGAGTGACTG AGCTTCCCTC CCGTGTGTTC TCCGTCCCTG CCCCAGCAAG
ACAACTTAGA TCTCCAGGAG AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGCACAAG TGAGTTGTTG CCCTGGGTTT
CTTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC CCTGATAACA
ACCTGGAGAC CAGGATTTTA TGGCTCCCCT CACTGATGGA CAAGGGAGGT CTGTGCCAAA GAAGAATCCA ATAAGCACAT
ATTGAGCACT TGCTGTATAT GCAGTATTGA GCACTGTAGG CAAGAGGGAA GAAAGAGAAG GAGCCATCTC CATCTTGAAG
GAACTCAAAG ACTCAAGTGG GAACGACTGG CACTGCCACC ACCAGAAAGC TGTTCGACGA GACGGTCGAG CAGGGTGCTG
TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCA GCTCAACCAA TAACTATTGC ACAACCACCT GTCCCTGCCT
CAGTTCCCTC TTCTGTAACA TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG
TGCTACGTAC ATGTGAGGCA TCATTACGCA GACGTAACTG GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGA -3'

(FRAG. NO:2275) (SEQ. ID NO:2446)

5'- AAATGATAGA CCGTCAATAA TTTGTTAAAT GCTTTTTAAA ATGAATGCTT TAAGCCGGGT GCAGTGCCTC ACATCTGTAA
TCCCAGCACT TTGGAGCCGA GCGGGTGGAT TGTGTGAGGT CAGGAGTTCG AGACCAACCT GGCCAACATG GCAAAACCTC
ACTCTCTACC AAAAATACAA AAATTAGCCA GGCATGGTGG CAGGCACCTG TGATCCCAGC TACTCAGGAG GCTGAGACAG
GAGAATCGCT TGAACCCGGG AGGCAAGGTT GCAGTGAGCC AAGATTACGC CATTGTACTC CAGCCTGGGT GACAGAGAGA
GACTCCGTCT CAAAAAAAAA AAAAAAAAAA AAAAAATTAC GCTTCAAACA CATGATCTCT CACCACTGTT GAATTTTCTT
TCTATGAGCC CAGGAGGGCC TCTCAGAGAG GAAAGCTCCT AGGTCTTCCT TTCCCTCTGC AAACTCCCTG CCTTGAAGGT
TCAGAAGGAC TGTGCGTGCT CGTTGCATCC TTTGCAAGTG TCCAAACCCT GATCCCAGCT GTGCTTAGGG GTTCCTGCAA
ACCTTTTCCA GGTGTTAATT ACCTCCCACT TCATTTCCTG TTTACCAACT CAGCTTTTTG TTTTAGTGTG TTTGAATTCC
CTGAACTGAC CGTTGTCTGA TCTCCACCTC CCAACTGAAT TAGGGGAGCT GGGCTTCTGG AAACCCAGGT GCCGGGTGTT
GCAGAGTGGC TGAAAGCTGG GATGTGGCAG ATCCGTGGCT ACATTCATGC ACACACACAC ACCCACATAC CCACACATGC
ACACACACAC ACACACCCGC ACTCACACAC TTGGACATGC ATAGACCACA GCTTTCCACA CCCTTCCTAG ACAGGGGTCA
CTTGGTATCC TGGAGAGAGT GTGAAGTCCT GGAATGGAAA GAGGGGGGAT TAAGCCCCAC CTCTAGCCAT GGGACTGAGA
CAAGTCACCA CCAACCCATC TGCGCCTTGT TTACCTCCTC TGTGAGGCAA GCACAGAGCC CATGCCTGCC CCCCTGGATG
GGAGTGATGT GAAACTTGAA GGGCGGTCAG AGCAAGGGTC GGGAATGGAA GGCCCTTGGG AAAAAAGGCC CTTTCAACTA

GGGGCACAGA GGAGGCCCTG GGCTGAGAAC TTGACAGCAC CTTGTAATTG GTAAGCCAAG CCCGAAGGGA CTGGAAATAC
TCAGATGTGT CTGTCTCCCT TATTAGGTTC AAAGTCCCTC AAGACCCTGT CTCCATCACA GTGCTCCAGT CCAGACCCCT
CCTCTGAGCT CCAGACCCTG CTGGACCCAA CCAGCCCTAT GGGGTCGCAT CCCCACCTGC CTGGAATTCT CCAAAGAACC
TCCCCTTTAA CAGTTCCAGC CTTTAACAGT TCCAGTCTAA ACACATGACC TTTCTCCTCT AAATCAGCCC CCCATCTCTG
CCTTTGCAGG AGATGGAAGC CATGACACCT GCCTCGCCCC TGTCCTCACC CCATCCATGT CCAATCAAGC ACTAGGCATG
TCAGGTTTAC CCTCTAAACT CCTCTGGAAT CCAGTCTCTC AGTCTCCATC ATCCCAGGTC GAAGCTAATG GGCTAACTGG
TCCTTGCTTC CACTCTACCC CCACTGCAGT CCTGACTTCC TGAGCAGCAG CCAGGGCCTA ATCGATATTC ACACCAAGCG
CCAACCTGAC TGAGATATCC TCCTGCACCA TCATCCCTCC ACCCTGTTTA GTTCTGCTCA CCCTCAGTGT TCTCATCAAT
AATCCACTCC CCTCACAGGC GCGTTTGGGA CCCCATGTTC TATGCTCTCA CAGGACCTTT TGCTTGATTT TTCACTGTAC
TTAGGTCAGT TTGCAGTTAT TAAGTGACTG AGCAATGTCT GGCTTCTCCA GTAGACTGTC AGCTCCTAGC CATTGTATAC
CTAGCACCGC TGTGTGGGAG CACGTGACAA ACGTCCAGTG AGTCAGGGAC TCAGCAGTCT CCATTTCTCC GCCCTGCTGG
AGAATGCGTG TATTTGGCAA TCCCCAGCCC CTGTGCCATC TAACCATCTT TTCTTCTCTG TTCAGCCCAG GTGTGGCCTC
ACTCACATCC CACTCTGAGT CCAAATGTTC TCTCCCTGGA AGATATCAAT GTTTCTGTCT GTTCGTGAGG ACTCCGTGCC
CACCACGGCC TCTTTCAGGT GAGTCAAAGG GATTCCTCAG TTCACTAGTT AGGGGAGGTG GGCAGACACC CTGGAGAACT
CCCTGGAAAG CTCAACTCTC ATGCCCCGGA CAACAGTTGA AGGAACCATG GTGATGTTAA GCCCAAAGAC AAAACCTCTC
AGGTGTCCAA GTCCCTGTTG GAATCTTGGG AGCAGAGGGA ATGTTCTGTG GTCTAGAGGA AGAGGGGCTC AGGGAGGAGA
AGGGCACATT CCTGGTTGTT ATATGTTTCT ATCTATCCCA GATGAACTTG GAAGTGAAGG GAAGAGAGTT AAACATTAAA
GTAAATACCC AGTGGATCAG ACAGCAATGT GCCAGATTGC CTTGGAAACA AAATATCTCC AACACATGGC TGACATTTGG
TGGGAGATCA GAACACCCTA AAGAGAGAAT TTAAGGGGAG GGGGAGGAGG ACCTGAGCCA GAGTAGAAGC
AGAGGATAGG GAGATCTGTT CTTGGGGACA GCATTTGCAA GAAACAAGGC TGAGGGGTCC ACTCCAACCT CTCCACCCTG
CTGCAGGTGC TGCCTATGAT GAAGATGAGC AGATGGCCAT CTCAGCTGGG GCCACAGTGC ACTGGACCTA TAGTTTCCAA
TTCCGCACTC AGCAGGCATC TTTCTGATGA TCCGATGGCT TCTCAGAGCC AGGGATGGGC CAGGATCCAT CCCCTTGGCT
ACTGTCTTGC TGAGAAATTT ATAAGCAGCA TCTGGTGCTA TACTTTGGTC TCTAGTGAGT TAGCTCATGA AAGATGATAG
ACTCTCCAAG CCAGGGGTAT GCAGGAAATG GGTTTTCTGT AGCTACAGAA ATGGGGTTGA GGGTTGGACC AAGGGACTAC
CCAGGGGAAG TCTTACCTTC AGAGGACTCT GGAAAGGAGG CTGCAAGTTT TCATGGGTCA AGAATTCAGA GCCCAGTAGA
GACAGCTTAT CTCTGTTCCA AGATGTCTGG GGCCTTGGTT GGAAGATTCA AAGGCTAGGA AACCAGGAGC CACCAAAAGC
GTAACTGGGG CCAGAGGATC CACTTTCAAG GTGGCAAGTT GGTTCCCCCC ATGTGGCTGC TTGAGTATCC TCACATGGCG
GCTCACATCC TTCCAAGTAA GCAATGCAAA AGGCCAAGAA AGATGCTGCA AAGATGTTAT GACCTAGCCT CAGAAATCAC
ACACCATCCC TGCCACCATT AGTAAGAAGT CCAGCCCACG TCCAGGAGAA GAGGAAGCAG ATTCCTCCTT TTGAAATGAA
GAATATCAAG TAATTCGGGG GGCATATGAA AGCCACCACA CACCACAGGG ATCTTTTTAG AGCATACTTC TTATACCATC
ACTGTAGTTC CTTAAGACTC AGGGGCAAAG CCTCACTTCC TTAGCACCCA GTGAAGACCA CGCTTACTCC CTCACTCAAC
CTCTTGCTAC TTCCCACCTC TCCTGTCCAA CATCTAGTGT CACTTTCCAG AACATACCAA CAGCTTCCCC AGTTCTGTGC
CTCTGCTCAG GCTGTTCCCC CTGCCTGGTC CACTTGTCCT CCTTCTTGTC CGGTCAAAAT GCTTCTTATC CTTCAAGACC
CAGCTCTAGA GTCACCTCCA ACCCCTTACC CACCAGCCCC CTCTCCAAGT CTGTGTCCCA CAACCCCCCT GCTCCCTCCA
GGGCACCCTC CACCCTCTGG GCCACAGTTG TCAGGAGTCA GGCAGGGCAG GGGCCGGGTG GTGTCTTCTT TGTGTTCTTG
CACTCAGGGC AGAGCTCAGC ACAGAGCAGA CGCTCAAAAA ACATTTAAAG GATAGAAGCA TTGATTTGTG GGTCCCCCAG
TCTGGCTCCA GGATGCCAGC CAGCTGCTCC TAGAAGCAAA CGGACTTTTC CTGGGAAATC CCAGAGGTGA TGATCAGTAA
TCTCTCCCGT GACTCGTAGT TCAGCTCTTC CTCCATGAGC CTGACTATCA GTGGACCTTC CAGAAAGAGC CCCTTTTCCT
TCTCTCACCC ACAGCACAGG GCACTGGGAA AATGCCCAAT GAGTCCTGCC TCTGGGTTGT GCTTTGGACT TTTCAGTGTG
TCTCGCATCC ACTCTTCAAC TTGAATGTTG CAACAGCCAT GAAAAAAGAA ATGCAAAGCG ATTCAGGATG AGAGCAATAC
CCTACTCCAA AGAAGGCAAC ATAGAAGCTC AGAGAGATCA AGCAATTTGC CCAAGACCAC ACAGCTAGGA GTGGAACTCA
TGGCTGTCCA AGCCCCATGC CTCTGCTGAA GGTAGAGATG AATTACAGCA ACAAGTCTAG AAAGGTGCCT GCCCTATGGT
CTGTGAGTCT TGCCTAAGAA TGAAAGAGGA GCCAGTGGGT TAAAGATGAG GTCACCAACA ACGGTGGTGT TGGAGTTTAC
CACTGATAAT AAGGGTGCAA AATGTAAATT ACTAATGTTT ATTGAGCCTA GTGCAGTGCG TGGGGCATTT TGCACATTGT
CTCTGATCCC TATGACAACC CTGAGAGGTA GTGGTTTTAA CTGCCATGTT ACAGGTGAGG TCATTGTGGT TCAAGGACGT
TAAGTAACTT CCCCAGCGTG ACACGGCTTA TAAGTAAGGC AGCCAGGATG TGAACCCAGT AGGACTATCT GGCTGCAAAG
TCCCCACCCC CCTCGCCATC TGTATCCTCC AATCACTTCA GTGCTTTGCT GCATAGAAGG TAACGGAAAT CACGATGCCA
CAGACTGTCC AGGAAGACAG AAACTAGGCA GATGGGCTGG CCATGGTCTC CAAGCCAGAC TGGAATCTCC AGGTCTGGAA
TGATATCATT TTTCTCTTTT AATAAATTAA CTCACCCACC ACACGGCTTT GAGAGGCTCA AAGTTGACCA ACTCCCTTGG
GAGGGCCCCG GTTGATAAGG AAGGAACGTG AATCCTCCCA TCACGGAAGC TTCAAGGAGG TCAAGGGTCC AACACTTGAG
ATTGTTAGTG CTGTTGGTGG ATACTGGCCA AGGAAATATC CCAGTGGAGC CTCGAGATGA AGAACATGAG GCCCCCGTTT
AGAACCAAGG ATCAGAGGGG GCTCTGTAAG ACCCAGGGGA GTCAGGTGCA CTGGAGCGCG GGCATGCAGA AAACAGCCTG
AGCTCCACCT CGGCTTCTCC TTGTCCTGGC TGGTTGTCCT TAACCCCTGT CTCCTTCTGG ACCAGTTTTT GTCCTTCCCT
TGTGACCGCT GAGGGGTAAC AGCCTCTTTC CACTTTCTTT CAGCGCCGAC ATGCTCAATG TCACCTTGCA AGGGCCCACT
CTTAACGGGA CCTTTGCCCA GAGCAAATGC CCCCAAGTGG AGTGGCTGGG CTGGCTCAAC ACCATCCAGC CCCCCTTCCT
CTGGGTGCTG TTCGTGCTGG CCACCCTAGA GAACATCTTT GTCCTCAGCG TCTTCTGCCT GCACAAGAGC AGCTGCACGG
TGGCAGAGAT CTACCTGGGG AACCTGGCCG CAGCAGACCT GATCCTGGCC TGCGGGCTGC CCTTCTGGGC CATCACCATC
TCCAACAACT TCGACTGGCT CTTTGGGGAG ACGCTCTGCC GCGTGGTGAA TGCCATTATC TCCATGAACC TGTACAGCAG
CATCTGTTTC CTGATGCTGG TGAGCATCGA CCGCTACCTG GCCCTGGTGA AAACCATGTC CATGGGCCGG ATGCGCGGCG
TGCGCTGGGC CAAGCTCTAC AGCTTGGTGA TCTGGGGGTG TACGCTGCTC CTGAGCTCAC CCATGCTGGT GTTCCGGACC
ATGAAGGAGT ACAGCGATGA GGGCCACAAC GTCACCGCTT GTGTCATCAG CTACCCATCC CTCATCTGGG AAGTGTTCAC
CAACATGCTC CTGAATGTCG TGGGCTTCCT GCTGCCCCTG AGTGTCATCA CCTTCTGCAC GATGCAGATC ATGCAGGTGC
TGCGGAACAA CGAGATGCAG AAGTTCAAGG AGATCCAGAC GGAGAGGAGG GCCACGGTGC TAGTCCTGGT TGTGCTGCTG
CTATTCATCA TCTGCTGGCT GCCCTTCCAG ATCAGCACCT TCCTGGATAC GCTGCATCGC CTCGGCATCC TCTCCAGCTG
CCAGGACGAG CGCATCATCG ATGTAATCAC ACAGATCGCC TCCTTCATGG CCTACAGCAA CAGCTGCCTC AACCCACTGG
TGTACGTGAT CGTGGGCAAG CGCTTCCGAA AGAAGTCTTG GGAGGTGTAC CAGGGAGTGT GCCAGAAAGG GGGCTGCAGG
TCAGAACCCA TTCAGATGGA GAACTCCATG GGCACACTGC GGACCTCCAT CTCCGTGGAA CGCCAGATTC ACAAACTGCA
GGACTGGGCA GGGAGCAGAC AGTGAGCAAA CGCCAGCAGG GCTGCTGTGA ATTTGTGTAA GGATTGAGGG ACAGTTGCTT
TTCAGCATGG GCCCAGGAAT GCCAAGGAGA CATCTATGCA CGACCTTGGG AAATGAGTTG ATGTCTCCGG TAAAACACCG

GAGACTAATT CCTGCCCTGC CCAATTTTGC AGGGAGCATG GCTGTGAGGA TGGGGTGAAC TCACGCACAG CCAAGGACTC CAAAATCACA ACAGCATTAC TGTTCTTATT TGCTGCCACA CCTGAGCCAG CCTGCTCCTT CCCAGGAGTG GAGGAGGCCT GGGGGCAGGG AGAGGAGTGA CTGAGCTTCC CTCCCGTGTG TTCTCCGTCC CTGCCCCAGC AAGACAACTT AGATCTCCAG GAGAACTGCC ATCCAGCTTT GGTGCAATGG CTGAGTGCAC AAGTGAGTTG TTGCCCTGGG TTTCTTTAAT CTATTCAGCT AGAACTTTGA AGGACAATTT CTTGCATTAA TAAAGGTTAA GCCCTGAGGG GTCCCTGATA ACAACCTGGA GACCAGGATT TTATGGCTCC CCTCACTGAT GGACAAGGAG GTCTGTGCCA AAGAAGAATC CAATAAGCAC ATATTGAGCA CTTGCTGTAT ATGCAGTATT GAGCACTGTA GGCAAGAGGG AAGAAAGAGA AGGAGCCATC TCCATCTTGA AGGAACTCAA AGACTCAAGT GGGAACGACT GGGCACTGCC ACCACCAGAA AGCTGTTCGA TGAGACGGTC GAGCAGGGTG CTGTGGGTGA TATGGACAGC AGAAGGGGGA GCCAGGTTCC AGCTCACCAA TACTATTGCA CACCACCTGT CCTGCCTC -3' **(FRAG. NO:2275) (SEQ. ID NO:2445)**

5'- CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTTGATG TCTCCGGTAA AACACCGGAG ACTAATTCCT GCCCTGCCCA ATTTTGCAGG GAGCATGGCT GTGAGGATGG GGTGAACTCA CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT TCTTATTTGC TGCCACACCT GAGCCAGCCT GCTCCTTCCC AGGAGTGGAG GAGGCCTGGG GGGAGGGAGA GGAGTGACTG AGCTTCCCTC CCGTGTGTTC TCCGTCCCTG CCCCAGCAAG ACAACTTAGA TCTCCAGGAG AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGCACAAG TGAGTTGTTG CCCTGGGTTT CTTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC CCTGATAACA ACCTGGAGAC CAGGATTTTA TGGCTCCCCT CACTGATGGA CAAGGAGGTC TGTGCCAAAG AAGAATCCAA TAAGCACATA TTGAGCACTT GCTGTATATG CAGTATTGAG CACTGTAGGC AAGACCCAAG AAAGAGAAGG AGCCATCTCC ATCTTGAAGG AACTCAAAGA CTCAAGTGGG AACGACTGGG CACTGCCACC ACCAGAAAGC TGTTCGACGA GACGGTCGAG CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCA GCTCAACCAA TAACTATTGC ACAACCACCT GTCCCTGCCT CAGTTCCCTT TTATGTAACA TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG TGCTACGTAC ATGTGAGGCA TCATTACGCA GACGTAACTG GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGAA ATAGCTCCGT GGAGCAGAAT CAGTATTGGG AGCCGGTGGC GGTGTGAAGC ACCAGTGTCT GGCACACAGT AGGTGCTCAT TGGCTCCCTT CCACCTGTCA TTCCCACCAC CCTGAGGCCC CAACCGCCAC ACACACAGGA GCATTTGGAG AGAAGGCCAT GTCTTCAAAG TCTGATTTGT GATGAGGCAG AGGAAGATAT TTCTAATCGG TCTTGCCCAG AGGATCACAG TGCTGAGACC CCCCACCACC AGCCGGTACC TGGGAAGGGG GAGAGTGCAG GCCTGCTCAG GGACTGTTCC TGTCTCAGCA ACCAAGGGAT TGTTCCTGTC AATCAATGGT TTATTGGAAG GTGGCCCAGT ATGAGCCCTA GAAGAGTGTG AAAAGGAATG GCAATGGTGT TCACCATCGG CAGTGCCAGG GCAGCACTCA TTCACTTGAT AAATGAATAT TTATTAGCTG GTTGGAGAGC TAGAACCTGG AGAGCTAGAA CCTGGAGAAC TAGAACCTGG AGGGCTAGAA CCTGGAGAGG CTAGAACCAA GAAGGGCTAG AACCTGGAGG GGCTAGAACC TAGAGAAGCT AAAACCTGAG CTAGAAGCTG GAGGACTAGA ACCTGGAGGG CTGGAATCTG AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTGG AATCTGGAGA GCTAGAACCT GGAGGGCTAG AACCTGGAGG GCTAGAACCT AGAAGGGCTA GAACCTGGAG GGCTAGAACC TGGCAGGTTA GAACCTAGAA GGGCTAGAAC CTGGAGAGCC AGAACCTGGA GGGCTAGAAC CTGGAAGGGC TAGAACCTGT AGAGCTAGAA CATGGAGAGC TAGAACCCGG CAGGCTAGAA CCTGGCAAGC TAGAACCTGG AGGGAATGAA CCTGGAGGGC TAGAACCTGG AGAATGAGAA AAATTTACAT GGCAAAGAGC CCATAAATCC TGACCAATCC AACTCTGAAT TTTAAAGCAA AAGCGTGAAA AAAAAGATTC CCTCCTTACC CCCAACCCAC TCTTTTTTCC CACCACCCAC TCTCCTCTGC CTCAGTAAGT ATCTGGAGGA AGAAAACAGG TGAAAGAAGA AGTAAAAACC ATTTAGTATT AGTATTAGAA TGAAGTCAAA CTGTGCCACA CATGGTGAAT GAAAAAAAAA AAAAAGAGGC TGTGTTTTGT CACACAGGGC AGTCATTCAG CACCAGAGCA CGTGATGGTC TGAGACTCTC TTAGGAGCAG AGCTCTGCCG CAATGGCCAT GTGGGGATCC ACACCTGGTC TGAGGGGCAA CTGAGTCTGC GGGAGAAGAG CGGCCCTATG CATGGTGTAG ATGCCCTGAT AAAGAACATC TGTCCTGTGA AAGACTCAAT GAGCTGTTAT GTTGTAAACA GGAAGCATTT CACATCCAAA CGAGAAAATC ATGTAAACAT GTGTCTTTTC TGTAGAGCAT AATAAATGGA TGAGGTTTTT GCAAAAAAAA AAAAAAAAA -3' **(FRAG. NO:2275) (SEQ. ID NO:2444)**

5'- GAGCTCTTCA ATATTTTAGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA CACACCTTTT CAGAGGGCTT GTGGACTCTG GGCAGCCTGT CCATAGACCT CTGTCCCCAA CTGGCAAGTC AGGAAACTCC AGATTAAGGA GCCCCAATGT GGTTGAACAG CCAGGTGCAC AGATGAGTCA ACCACACAGC CAGGCCAGGG AGGGCCTTCA CTCAAGAGCC TACAGCCAGT TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCCATAAAC TGATCTGAGA CTCTGTTTCC CTGTCTCCAT GATGATGGGA TCAGGCTTGA TTGCTGGTTT GTAGGCTTGT TATGAATCAA GTCACAGGGA AGAGGAGCTG ATGGGCTGGG GGGACGTCCT CTGGCCCTCC TGTCTCTTCC CCAGATCCAC TGGGCCCACT CTTATCTGTT CTCTTCTGAA GGAAGGGTTT TAAGGCTTCA AAAAAAAATG TTTTGAAAGT CCCTGCCCTT TCCAGCTCCT ACCGTCTCAG CCCTGGGAGT GTAAAGTGCT GCAGATAGTT AGTAAGTCTT TGAGCAAAAC TGAGAAAGCC AGCCTGAGCC TTGACATGGG AGAAACCTCC GCCATACATC TCCGAAGAAA CGGCCGCGTG TCTCAGGGGA GCGCAAACAC CCGTACCCAG GAAACAGGAC AGCTTCTGCC ACTGTCGCCC TTGGGAGCCG TACGTGGCAT GACAAAGAAA TCCCAGGACT CCGCCTGCCC ACCTGGCCAC CCTCTGTTTA CACCTTCCGC GTAAACGCCC ACTGTTTACA TCCAAAACTC AGACACAAAA TAACCACCTC AAGAAGATAA ATAATGATAA GAAATAAATG TTACGCGAGG CAAATTTATT CACATGGGGC TTCCCAGGCC ACTTTGTGGT CAGCCGGGAG GGACGTTTTT GCCGTCCCAC GACTCCAACG GGCAGCCGGG CCTACGCAAA CATGGAAATC TTCCAAGAGC CTCCCTGGCC CCCAGGGCTC AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG CCGCAGCCTT CCCGGCCCCA CAGCCAGCCT GGCTCCAGCT GGGCAGGAGT GCAGAGCTCA GCTGGAGGCG AGGGGGAAGT GCCCAGGAGG CTGATGACAT CACTACCCAG CCCTTCAAAG ATGAGCTGTT CCCGCCGCCA CTCCAGCTCT GGCTTCTGGG CTCCGAGGAG GGGTGGGGAC GGTGGTGACG GTGGGGACAT CAGGCTGCCC CGCAGTACCA GGGAGCGACT GAAGTGCCCA TGCCGCTTGC TCCGGAGAAG GTGGGTGCCG GGCAGGGGCT GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAAACTGTCC CAGCACAGAG GGAGGGAGGG AGGGCAGGCA GCGGGGAGAA GTTTCCCTGT GGTCGTGGGG AGTTGGGAAA AGTTCCCTTC CTTCCGGAGG GAGG -3' **(FRAG. NO:2275) (SEQ. ID NO:2443)**

5'- GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CCGCAGTACC AGGGAGCGAC TGAAGTGCCC ATGCCGCTTG CTCCGGAGAA GGTGGGTGCC GGGCAGGGGC TGCTCCAGCC GCCTCACCTC TGCTGGGAGG ACAAACTGTC CCAGCACAGA GGGAGGGAGG GAGGGCAGGC AGCGGGGAGA AGTTTCCCTG TGGTCGTGGG GAGTT -3' **(FRAG. NO:2275) (SEQ. ID NO:2442)**

5'- AAATGATAGA CCGTCAATAA TTTGTTAAAT GCTTTTTAAA ATGAATGCTT TAAGCCGGGT GCAGTGCCTC ACATCTGTAA TCCCAGCACT TTGGAGCCGA GCGGGTGGAT TGTGTGAGGT CAGGAGTTCG AGACCAACCT GGCCAACATG GCAAAACCTC ACTCTCTACC AAAAATACAA AAATTAGCCA GGCATGGTGG CAGGCACCTG TGATCCCAGC TACTCAGGAG GCTGAGACAG

GAGAATCGCT TGAACCCGGG AGGCAAGGTT GCAGTGAGCC AAGATTACGC CATTGTACTC CAGCCTGGGT GACAGAGAGA
GACTCCGTCT CAAAAAAAAA AAAAAAAAAA AAAAAATTAC GCTTCAAACA CATGATCTCT CACCACTGTT GAATTTTCTT
TCTATGAGCC CAGGAGGGCC TCTCAGAGAG GAAAGCTCCT AGGTCTTCCT TTCCCTCTGC AAACTCCCTG CCTTGAAGGT
TCAGAAGGAC TGTGCGTGCT CGTTGCATCC TTTGCAAGTG TCCAAACCCT GATCCCAGCT GTGCTTAGGG GTTCCTGCAA
ACCTTTTCCA GGTGTTAATT ACCTCCCACT TCATTTCCTG TTTACCAACT CAGCTTTTTG TTTTAGTGTG TTTGAATTCC
CTGAACTGAC CGTTGTCTGA TCTCCACCTC CCAACTGAAT TAGGGGAGCT GGGCTTCTGG AAACCCAGGT GCCGGGTGTT
GCAGAGTGGC TGAAAGCTGG GATGTGGCAG ATCCGTGGCT ACATTCATGC ACACACACAC ACCCACATAC CCACACATGC
ACACACACAC ACACACCCGC ACTCACACAC TTGGACATGC ATAGACCACA GCTTTCCACA CCCTTCCTAG ACAGGGGTCA
CTTGGTATCC TGGAGAGAGT GTGAAGTCCT GGAATGGAAA GAGGGGGGAT TAAGCCCCAC CTCTAGCCAT GGGACTGAGA
CAAGTCACCA CCAACCCATC TGCGCCTTGT TTACCTCCTC TGTGAGGCAA GCACAGAGCC CATGCCTGCC CCCCTGGATG
GGAGTGATGT GAAACTTGAA GGGCGGTCAG AGCAAGGGTC GGGAATGGAA GGCCCTTGGG AAAAAAGGCC CTTTCAACTA
GGGGCACAGA GGAGGCCCTG GGCTGAGAAC TTGACAGCAC CTTGTAATTG GTAAGCCAAG CCCGAAGGGA CTGGAAATAC
TCAGATGTGT CTGTCTCCCT TATTAGGTTC AAAGTCCCTC AAGACCCTGT CTCCATCACA GTGCTCCAGT CCAGACCCCT
CCTCTGAGCT CCAGACCCTG CTGGACCCAA CCAGCCCTAT GGGGTCGCAT CCCCACCTGC CTGGAATTCT CCAAAGAACC
TCCCCTTTAA CAGTTCCAGC CTTTAACAGT TCCAGTCTAA ACACATGACC TTTCTCCTCT AAATCAGCCC CCCATCTCTG
CCTTTGCAGG AGATGGAAGC CATGACACCT GCCTCGCCCC TGTCCTCACC CCATCCATGT CCAATCAAGC ACTAGGCATG
TCAGGTTTAC CCTCTAAACT CCTCTGGAAT CCAGTCTCTC AGTCTCCATC ATCCCAGGTC GAAGCTAATG GGCTAACTGG
TCCTTGCTTC CACTCTACCC CCACTGCAGT CCTGACTTCC TGAGCAGCAG CCAGGGCCTA ATCGATATTC ACACCAAGCG
CCAACCTGAC TGAGATATCC TCCTGCACCA TCATCCCTCC ACCCTGTTTA GTTCTGCTCA CCCTCAGTGT TCTCATCAAT
AATCCACTCC CCTCACAGGC GCGTTTGGGA CCCCATGTTC TATGCTCTCA CAGGACCTTT TGCTTGATTT TTCACTGTAC
TTAGGTCAGT TTGCAGTTAT TAAGTGACTG AGCAATGTCT GGCTTCTCCA GTAGACTGTC AGCTCCTAGC CATTGTATAC
CTAGCACCGC TGTGTGGGAG CACGTGACAA ACGTCCAGTG AGTCAGGGAC TCAGCAGTCT CCATTTCTCC GCCCTGCTGG
AGAATGCGTG TATTTGGCAA TCCCCAGCCC CTGTGCCATC TAACCATCTT TTCTTCTCTG TTCAGCCCAG GTGTGGCCTC
ACTCACATCC CACTCTGAGT CCAAATGTTC TCTCCCTGGA AGATATCAAT GTTTCTGTCT GTTCGTGAGG ACTCCGTGCC
CACCACGGCC TCTTTCAGGT GAGTCAAAGG GATTCCTCAG TTCACTAGTT AGGGGAGGTG GGCAGACACC CTGGAGAACT
CCCTGGAAAG CTCAACTCTC ATGCCCCGGA CAACAGTTGA AGGAACCATG GTGATGTTAA GCCCAAAGAC AAAACCTCTC
AGGTGTCCAA GTCCCTGTTG GAATCTTGGG AGCAGAGGGA ATGTTCTGTG GTCTAGAGGA AGAGGGGCTC AGGGAGGAGA
AGGGCACATT CCTGGTTGTT ATATGTTTCT ATCTATCCCA GATGAACTTG GAAGTGAAGG GAAGAGAGTT AAACATTAAA
GTAAATACCC AGTGGATCAG ACAGCAATGT GCCAGATTGC CTTGGAAACA AAATATCTCC AACACATGGC TGACATTTGG
TGGGAGATCA GAACACCCTA AAGAGAGAAT TTAAGGGGAG GGGGAGGAGG ACCTGAGCCA GAGTAGAAGC
AGAGGATAGG GAGATCTGTT CTTGGGGACA GCATTTGCAA GAAACAAGGC TGAGGGGTCC ACTCCAACCT CTCCACCCTG
CTGCAGGTGC TGCCTATGAT GAAGATGAGC AGATGGCCAT CTCAGCTGGG GCCACAGTGC ACTGGACCTA TAGTTTCCAA
TTCCGCACTC AGCAGGCATC TTTCTGATGA TCCGATGGCT TCTCAGAGCC AGGGATGGGC CAGGATCCAT CCCCTTGGCT
ACTGTCTTGC TGAGAAATTT ATAAGCAGCA TCTGGTGCTA TACTTTGGTC TCTAGTGAGT TAGCTCATGA AAGATGATAG
ACTCTCCAAG CCAGGGGTAT GCAGGAAATG GGTTTTCTGT AGCTACAGAA ATGGGGTTGA GGGTTGGACC AAGGGACTAC
CCAGGGGAAG TCTTACCTTC AGAGGACTCT GGAAAGGAGG CTGCAAGTTT TCATGGGTCA AGAATTCAGA GCCCAGTAGA
GACAGCTTAT CTCTGTTCCA AGATGTCTGG GGCCTTGGTT GGAAGATTCA AAGGCTAGGA AACCAGGAGC CACCAAAAGC
GTAACTGGGG CCAGAGGATC CACTTTCAAG GTGGCAAGTT GGTTCCCCCC ATGTGGCTGC TTGAGTATCC TCACATGGCG
GCTCACATCC TTCCAAGTAA GCAATGCAAA AGGCCAAGAA AGATGCTGCA AAGATGTTAT GACCTAGCCT CAGAAATCAC
ACACCATCCC TGCCACCATT AGTAAGAAGT CCAGCCCACG TCCAGGAGAA GAGGAAGCAG ATTCCTCCTT TTGAAATGAA
GAATATCAAG TAATTCGGGG GGCATATGAA AGCCACCACA CACCACAGGG ATCTTTTTAG AGCATACTTC TTATACCATC
ACTGTAGTTC CTTAAGACTC AGGGGCAAAG CCTCACTTCC TTAGCACCCA GTGAAGACCA CGCTTACTCC CTCACTCAAC
CTCTTGCTAC TTCCCACCTC TCCTGTCCAA CATCTAGTGT CACTTTCCAG AACATACCAA CAGCTTCCCC AGTTCTGTGC
CTCTGCTCAG GCTGTTCCCC CTGCCTGGTC CACTTGTCCT CCTTCTTGTC CGGTCAAAAT GCTTCTTATC CTTCAAGACC
CAGCTCTAGA GTCACCTCCA ACCCCTTACC CACCAGCCCC CTCTCCAAGT CTGTGTCCCA CAACCCCCCT GCTCCCTCCA
GGGCACCCTC CACCCTCTGG GCCACAGTTG TCAGGAGTCA GGCAGGGCAG GGGCCGGGTG GTGTCTTCTT TGTGTTCTTG
CACTCAGGGC AGAGCTCAGC ACAGAGCAGA CGCTCAAAAA ACATTTAAAG GATAGAAGCA TTGATTTGTG GGTCCCCCAG
TCTGGCTCCA GGATGCCAGC CAGCTGCTCC TAGAAGCAAA CGGACTTTTC CTGGGAAATC CCAGAGGTGA TGATCAGTAA
TCTCTCCCGT GACTCGTAGT TCAGCTCTTC CTCCATGAGC CTGACTATCA GTGGACCTTC CAGAAAGAGC CCCTTTTCCT
TCTCTCACCC ACAGCACAGG GCACTGGGAA AATGCCCAAT GAGTCCTGCC TCTGGGTTGT GCTTTGGACT TTTCAGTGTG
TCTCGCATCC ACTCTTCAAC TTGAATGTTG CAACAGCCAT GAAAAAAGAA ATGCAAAGCG ATTCAGGATG AGAGCAATAC
CCTACTCCAA AGAAGGCAAC ATAGAAGCTC AGAGAGATCA AGCAATTTGC CCAAGACCAC ACAGCTAGGA GTGGAACTCA
TGGCTGTCCA AGCCCCATGC CTCTGCTGAA GGTAGAGATG AATTACAGCA ACAAGTCTAG AAAGGTGCCT GCCCTATGGT
CTGTGAGTCT TGCCTAAGAA TGAAAGAGGA GCCAGTGGGT TAAAGATGAG GTCACCAACA ACGGTGGTGT TGGAGTTTAC
CACTGATAAT AAGGGTGCAA AATGTAAATT ACTAATGTTT ATTGAGCCTA GTGCAGTGCG TGGGGCATTT TGCACATTGT
CTCTGATCCC TATGACAACC CTGAGAGGTA GTGGTTTTAA CTGCCATGTT ACAGGTGAGG TCATTGTGGT TCAAGGACGT
TAAGTAACTT CCCCAGCGTG ACACGGCTTA TAAGTAAGGC AGCCAGGATG TGAACCCAGT AGGACTATCT GGCTGCAAAG
TCCCCACCCC CCTCGCCATC TGTATCCTCC AATCACTTCA GTGCTTTGCT GCATAGAAGG TAACGGAAAT CACGATGCCA
CAGACTGTCC AGGAAGACAG AAACTAGGCA GATGGGCTGG CCATGGTCTC CAAGCCAGAC TGGAATCTCC AGGTCTGGAA
TGATATCATT TTTCTCTTTT AATAAATTAA CTCACCCACC ACACGGCTTT GAGAGGCTCA AAGTTGACCA ACTCCCTTGG
GAGGGCCCCG GTTGATAAGG AAGGAACGTG AATCCTCCCA TCACGGAAGC TTCAAGGAGG TCAAGGGTCC AACACTTGAG
ATTGTTAGTG CTGTTGGTGG ATACTGGCCA AGGAAATATC CCAGTGGAGC CTCGAGATGA AGAACATGAG GCCCCCGTTT
AGAACCAAGG ATCAGAGGGG GCTCTGTAAG ACCCAGGGGA GTCAGGTGCA CTGGAGCGCG GGCATGCAGA AAACAGCCTG
AGCTCCACCT CGGCTTCTCC TTGTCCTGGC TGGTTGTCCT TAACCCCTGT CTCCTTCTGG ACCAGTTTTT GTCCTTCCCT
TGTGACCGCT GAGGGGTAAC AGCCTCTTTC CACTTTCTTT CAGCGCCGAC ATGCTCAATG TCACCTTGCA AGGGCCCACT
CTTAACGGGA CCTTTGCCCA GAGCAAATGC CCCCAAGTGG AGTGGCTGGG CTGGCTCAAC ACCATCCAGC CCCCCTTCCT
CTGGGTGCTG TTCGTGCTGG CCACCCTAGA GAACATCTTT GTCCTCAGCG TCTTCTGCCT GCACAAGAGC AGCTGCACGG
TGGCAGAGAT CTACCTGGGG AACCTGGCCG CAGCAGACCT GATCCTGGCC TGCGGGCTGC CCTTCTGGGC CATCACCATC
TCCAACAACT TCGACTGGCT CTTTGGGGAG ACGCTCTGCC GCGTGGTGAA TGCCATTATC TCCATGAACC TGTACAGCAG

CATCTGTTTC CTGATGCTGG TGAGCATCGA CCGCTACCTG GCCCTGGTGA AAACCATGTC CATGGGCCGG ATGCGCGGCG TGCGCTGGGC CAAGCTCTAC AGCTTGGTGA TCTGGGGGTG TACGCTGCTC CTGAGCTCAC CCATGCTGGT GTTCCGGACC ATGAAGGAGT ACAGCGATGA GGGCCACAAC GTCACCGCTT GTGTCATCAG CTACCCATCC CTCATCTGGG AAGTGTTCAC CAACATGCTC CTGAATGTCG TGGGCTTCCT GCTGCCCCTG AGTGTCATCA CCTTCTGCAC GATGCAGATC ATGCAGGTGC TGCGGAACAA CGAGATGCAG AAGTTCAAGG AGATCCAGAC GGAGAGGAGG GCCACGGTGC TAGTCCTGGT TGTGCTGCTG CTATTCATCA TCTGCTGGCT GCCCTTCCAG ATCAGCACCT TCCTGGATAC GCTGCATCGC CTCGGCATCC TCTCCAGCTG CCAGGACGAG CGCATCATCG ATGTAATCAC ACAGATCGCC TCCTTCATGG CCTACAGCAA CAGCTGCCTC AACCCACTGG TGTACGTGAT CGTGGGCAAG CGCTTCCGAA AGAAGTCTTG GGAGGTGTAC CAGGGAGTGT GCCAGAAAGG GGGCTGCAGG TCAGAACCCA TTCAGATGGA GAACTCCATG GGCACACTGC GGACCTCCAT CTCCGTGGAA CGCCAGATTC ACAAACTGCA GGACTGGGCA GGGAGCAGAC AGTGAGCAAA CGCCAGCAGG GCTGCTGTGA ATTTGTGTAA GGATTGAGGG ACAGTTGCTT TTCAGCATGG GCCCAGGAAT GCCAAGGAGA CATCTATGCA CGACCTTGGG AAATGAGTTG ATGTCTCCGG TAAAACACCG GAGACTAATT CCTGCCCTGC CCAATTTTGC AGGGAGCATG GCTGTGAGGA TGGGGTGAAC TCACGCACAG CCAAGGACTC CAAAATCACA ACAGCATTAC TGTTCTTATT TGCTGCCACA CCTGAGCCAG CCTGCTCCTT CCCAGGAGTG GAGGAGGCCT GGGGGCAGGG AGAGGAGTGA CTGAGCTTCC CTCCCGTGTG TTCTCCGTCC CTGCCCCAGC AAGACAACTT AGATCTCCAG GAGAACTGCC ATCCAGCTTT GGTGCAATGG CTGAGTGCAC AAGTGAGTTG TTGCCCTGGG TTTCTTTAAT CTATTCAGCT AGAACTTTGA AGGACAATTT CTTGCATTAA TAAAGGTTAA GCCCTGAGGG GTCCCTGATA ACAACCTGGA GACCAGGATT TTATGGCTCC CCTCACTGAT GGACAAGGAG GTCTGTGCCA AAGAAGAATC CAATAAGCAC ATATTGAGCA CTTGCTGTAT ATGCAGTATT GAGCACTGTA GGCAAGAGGG AAGAAAGAGA AGGAGCCATC TCCATCTTGA AGGAACTCAA AGACTCAAGT GGGAACGACT GGGCACTGCC ACCACCAGAA AGCTGTTCGA TGAGACGGTC GAGCAGGGTG CTGTGGGTGA TATGGACAGC AGAAGGGGGA GCCAGGTTCC AGCTCACCAA TACTATTGCA CACCACCTGT CCTGCCTC -3' **(FRAQ. NO: _) (SEQ. ID NO 2441)**

5'-CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTTGATG TCTCCGGTAA AACACCGGAG ACTAATTCCT GCCCTGCCCA ATTTTGCAGG GAGCATGGCT GTGAGGATGG GGTGAACTCA CGCACAGCCA AGGACTCCAA AATCACAACA GCATTACTGT TCTTATTTGC TGCCACACCT GAGCCAGCCT GCTCCTTCCC AGGAGTGGAG GAGGCCTGGG GGGAGGGAGA GGAGTGACTG AGCTTCCCTC CCGTGTGTTC TCCGTCCCTG CCCCAGCAAG ACAACTTAGA TCTCCAGGAG AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGCACAAG TGAGTTGTTG CCCTGGGTTT CTTTAATCTA TTCAGCTAGA ACTTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC CCTGATAACA ACCTGGAGAC CAGGATTTTA TGGCTCCCCT CACTGATGGA CAAGGAGGTC TGTGCCAAAG AAGAATCCAA TAAGCACATA TTGAGCACTT GCTGTATATG CAGTATTGAG CACTGTAGGC AAGACCCAAG AAAGAGAAGG AGCCATCTCC ATCTTGAAGG AACTCAAAGA CTCAAGTGGG AACGACTGGG CACTGCCACC ACCAGAAAGC TGTTCGACGA GACGGTCGAG CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC CAAGGTTCCA GCTCAACCAA TAACTATTGC ACAACCACCT GTCCCTGCCT CAGTTCCCTT TTATGTAACA TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG TGCTACGTAC ATGTGAGGCA TCATTACGCA GACGTAACTG GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGAA ATAGCTCCGT GGAGCAGAAT CAGTATTGGG AGCCGGTGGC GGTGTGAAGC ACCAGTGTCT GGCACACAGT AGGTGCTCAT TGGCTCCCTT CCACCTGTCA TTCCCACCAC CCTGAGGCCC CAACCGCCAC ACACACAGGA GCATTTGGAG AGAAGGCCAT GTCTTCAAAG TCTGATTTGT GATGAGGCAG AGGAAGATAT TTCTAATCGG TCTTGCCCAG AGGATCACAG TGCTGAGACC CCCCACCACC AGCCGGTACC TGGGAAGGGG GAGAGTGCAG GCCTGCTCAG GGACTGTTCC TGTCTCAGCA ACCAAGGGAT TGTTCCTGTC AATCAATGGT TTATTGGAAG GTGGCCCAGT ATGAGCCCTA GAAGAGTGTG AAAAGGAATG GCAATGGTGT TCACCATCGG CAGTGCCAGG GCAGCACTCA TTCACTTGAT AAATGAATAT TTATTAGCTG GTTGGAGAGC TAGAACCTGG AGAGCTAGAA CCTGGAGAAC TAGAACCTGG AGGGCTAGAA CCTGGAGAGG CTAGAACCAA GAAGGGCTAG AACCTGGAGG GGCTAGAACC TAGAGAAGCT AAAACCTGAG CTAGAAGCTG GAGGACTAGA ACCTGGAGGG CTGGAATCTG AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTGG AATCTGGAGA GCTAGAACCT GGAGGGCTAG AACCTGGAGG GCTAGAACCT AGAAGGGCTA GAACCTGGAG GGCTAGAACC TGGCAGGTTA GAACCTAGAA GGGCTAGAAC CTGGAGAGCC AGAACCTGGA GGGCTAGAAC CTGGAAGGGC TAGAACCTGT AGAGCTAGAA CATGGAGAGC TAGAACCCGG CAGGCTAGAA CCTGGCAAGC TAGAACCTGG AGGGAATGAA CCTGGAGGGC TAGAACCTGG AGAATGAGAA AAATTTACAT GGCAAAGAGC CCATAAATCC TGACCAATCC AACTCTGAAT TTTAAAGCAA AAGCGTGAAA AAAAAGATTC CCTCCTTACC CCCAACCCAC TCTTTTTTCC CACCACCCAC TCTCCTCTGC CTCAGTAAGT ATCTGGAGGA AGAAAACAGG TGAAAGAAGA AGTAAAAACC ATTTAGTATT AGTATTAGAA TGAAGTCAAA CTGTGCCACA CATGGTGAAT GAAAAAAAAA AAAAAGAGGC TGTGTTTTGT CACACAGGGC AGTCATTCAG CACCAGAGCA CGTGATGGTC TGAGACTCTC TTAGGAGCAG AGCTCTGCCG CAATGGCCAT GTGGGGATCC ACACCTGGTC TGAGGGGCAA CTGAGTCTGC GGGAGAAGAG CGGCCCTATG CATGGTGTAG ATGCCCTGAT AAAGAACATC TGTCCTGTGA AAGACTCAAT GAGCTGTTAT GTTGTAAACA GGAAGCATTT CACATCCAAA CGAGAAAATC ATGTAAACAT GTGTCTTTTC TGTAGAGCAT AATAAATGGA TGAGGTTTTT GCAAAAAAAA AAAAAAAAA -3' **(FRAQ. NO: _) (SEQ. ID NO 2431)**

5'-GGTGBCBTTGBGCBTGTCGGCGC-3' **(FRAG. NO:2276) (SEQ. ID NO:2287)**

5'-GGTCCCGTTBBGBGTGGGCCC-3' **(FRAG. NO:2277) (SEQ. ID NO:2288)**

5'-GCCAGCCCAGCCACTCCACTTGGGGGC-3' **(FRAG. NO:2278) (SEQ. ID NO:2289)**

5'-GGGTGGCCAGCACGAACAGCACCCAGAGGAAGGGGGGC-3' **(FRAG. NO:2279) (SEQ. ID NO:2290)**

5'-GGCCCAGAAGGGCAGCCCGCAGGCCAGGATCAGGTCTGCTGCGGCC-3' **(FRAG. NO:2280) (SEQ. ID NO:2291)**

5'-GGAGATAATGGCATTCACCACGCGGC-3' **(FRAG. NO:2281) (SEQ. ID NO:2292)**

5'-GGCCCAGCGCACGCCGCGCATCCGGCCC-3' **(FRAG. NO:2282) (SEQ. ID NO:2293)**

5'-GGGTTCTGACCTGCAGCCCCC-3' **(FRAG. NO:2283) (SEQ. ID NO:2294)**

5'-GTCTCCTTGGCATTCCTGGGCCC-3' **(FRAG. NO:2284) (SEQ. ID NO:2295)**

5'-CAGTCACTCCTCTCCCTGCCCCC-3' **(FRAG. NO:2285) (SEQ. ID NO:2296)**

5'-CTTGCTGGGGCAGGGACGG-3' **(FRAG. NO:2286) (SEQ. ID NO:2297)**

5'-GGTGBCBTTGBGCBTGTCGGCGC-3' **(FRAG. NO:2287) (SEQ. ID NO:2298)**

5'-GGTCCCGTTBBGBGTGGGCCC-3' **(FRAG. NO:2288) (SEQ. ID NO:2299)**

5'-GCCAGCCCAGCCACTCCACTTGGGGGC-3' **(FRAG. NO:2289) (SEQ. ID NO:2300)**

5'-GGGTGGCCAGCACGAACAGCACCCAGAGGAAGGGGGGC-3' **(FRAG. NO:2290) (SEQ. ID NO:2301)**
5'-GGCCCAGAAGGGCAGCCCGCAGGCCAGGATCAGGTCTGCTGCGGCC-3' **(FRAG. NO:2291) (SEQ. ID NO:2302)**
5'-GGAGATAATGGCATTCACCACGCGGC-3' **(FRAG. NO:2292) (SEQ. ID NO:2303)**
5'-GGCCCAGCGCACGCCGCGCATCCGGCCC-3' **(FRAG. NO:2293) (SEQ. ID NO:2304)**
5'-GGGTTCTGACCTGCAGCCCCC-3' **(FRAG. NO:2294) (SEQ. ID NO:2305)**
5'-GTCTCCTTGGCATTCCTGGGCCC-3' **(FRAG. NO:2295) (SEQ. ID NO:2306)**
5'-CAGTCACTCCTCTCCCTGCCCCC-3' **(FRAG. NO:2296) (SEQ. ID NO:2307)**
5'-CTTGCTGGGGCAGGGACGG-3' **(FRAG. NO:2297) (SEQ. ID NO:2308)**
5'-CCGTGTTGTCBGTGGTGCTG-3' **(FRAG. NO:2298) (SEQ. ID NO:2309)**
5'-CCCGTTTGBGGTBTGGC-3' **(FRAG. NO:2299) (SEQ. ID NO:2310)**
5'-GCTCCBCCBBTTCCCTTTTCTCC-3' **(FRAG. NO:2300) (SEQ. ID NO:2311)**
5'-TTGTTTTCCGTTTCTCTTG-3' **(FRAG. NO:2301) (SEQ. ID NO:2312)**
5'-CCGTCTGTGGTT-3' **(FRAG. NO:2302) (SEQ. ID NO:2313)**

β2 Adrenergic Receptor Kinase Nucleic Acids and Antisense Oligonucleotide Fragments

5'- GCCGCCGCCG CCAAGATGGC GGACCTGGAG GCGGTGCTGG CCGACGTGAG CTACCTGATG GCCATGGAGA
AGAGCAAGGC CACGCCGGCC GCGCGCGCCA GCAAGAAGAT ACTGCTGCCC GAGCCCAGCA TCCGCAGTGT CATGCAGAAG
TACCTGGAGG ACCGGGGCGA GGTGACCTTT GAGAAGATCT TTTCCCAGAA GCTGGGGTAC CTGCTCTTCC GAGACTTCTG
CCTGAACCAC CTGGAGGAGG CCAGGCCCTT GGTGGAATTC TATGAGGAGA TCAAGAAGTA CGAGAAGCTG GAGACGGAGG
AGGAGCGTGT GGCCCGCAGC CGGGAGATCT TCGACTCATA CATCATGAAG GAGCTGCTGG CCTGCTCGCA TCCCTTCTCG
AAGAGTGCCA CTGAGCATGT CCAAGGCCAC CTGGGGAAGA AGCAGGTGCC TCCGGATCTC TTCCAGCCAT ACATCGAAGA
GATTTGTCAA AACCTCCGAG GGGACGTGTT CCAGAAATTC ATTGAGAGCG ATAAGTTCAC ACGGTTTTGC CAGTGGAAGA
ATGTGGAGCT CAACATCCAC CTGACCATGA ATGACTTCAG CGTGCATCGC ATCATTGGGC GCGGGGGCTT TGGCGAGGTC
TATGGGTGCC GGAAGGCTGA CACAGGCAAG ATGTACGCCA TGAAGTGCCT GGACAAAAAG CGCATCAAGA TGAAGCAGGG
GGAGACCCTG GCCCTGAACG AGCGCATCAT GCTCTCGCTC GTCAGCACTG GGGACTGCCC ATTCATTGTC TGCATGTCAT
ACGCGTTCCA CACGCCAGAC AAGCTCAGCT TCATCCTGGA CCTCATGAAC GGTGGGGACC TGCACTACCA CCTCTCCCAG
CACGGGGTCT TCTCAGAGGC TGACATGCGC TTCTATGCGG CCGAGATCAT CCTGGGCCTG GAGCACATGC ACAACCGCTT
CGTGGTCTAC CGGGACCTGA AGCCAGCCAA CATCCTTCTG GACGAGCATG GCCACGTGCG GATCTCGGAC CTGGGCCTGG
CCTGTGACTT CTCCAAGAAG AAGCCCCATG CCAGCGTGGG CACCCACGGG TACATGGCTC CGGAGGTCCT GCAGAAGGGC
GTGGCCTACG ACAGCAGTGC CGACTGGTTC TCTCTGGGGT GCATGCTCTT CAAGTTGCTG CGGGGGCACA GCCCCTTCCG
GCAGCACAAG ACCAAAGACA AGCATGAGAT CGACCGCATG ACGCTGACGA TGGCCGTGGA GCTGCCCGAC TCCTTCTCCC
CTGAACTACG CTCCCTGCTG GAGGGGTTGC TGCAGAGGGA TGTCAACCGG AGATTGGGCT GCCTGGGCCG AGGGGCTCAG
GAGGTGAAAG AGAGCCCCTT TTTCCGCTCC CTGGACTGGC AGATGGTCTT CTTGCAGAAG TACCCTCCCC CGCTGATCCC
CCCACGAGGG GAGGTGAACG CGGCCGACGC CTTCGACATT GGCTCCTTCG ATGAGGAGGA CACAAAAGGA ATCAAGTTAC
TGGACAGTGA TCAGGAGCTC TACCGCAACT TCCCCCTCAC CATCTCGGAG CGGTGGCAGC AGGAGGTGGC AGAGACTGTC
TTCGACACCA TCAACGCTGA GACAGACCGG CTGGAGGCTC GCAAGAAAGC CAAGAACAAG CAGCTGGGCC ATGAGGAAGA
CTACGCCCTG GGCAAGGACT GCATCATGCA TGGCTACATG TCCAAGATGG GCAACCCCTT CCTGACCCAG TGGCAGCGGC
GGTACTTCTA CCTGTTCCCC AACCGCCTCG AGTGGCGGGG CGAGGGCGAG GCCCCGCAGA GCCTGCTGAC CATGGAGGAG
ATCCAGTCGG TGGAGGAGAC GCAGATCAAG GAGCGCAAGT GCCTGCTCCT CAAGATCCGC GGTGGGAAAC AGTTCATTTT
GCAGTGCGAT AGCGACCCTG AGCTGGTGCA GTGGAAGAAG GAGCTGCGCG ACGCCTACCG CGAGGCCCAG CAGCTGGTGC
AGCGGGTGCC CAAGATGAAG AACAAGCCGC GCTCGCCCGT GGTGGAGCTG AGCAAGGTGC CGCTGGTCCA GCGCGGCAGT
GCCAACGGCC TCTGACCCGC CCACCCGCCT CCAGGAAGCT ACCTGGAGGA GGTGAGTCTT AGCGGATGAG TAGGAGTTGT
CCACGGAGGA AGGTACACAG AAGGGCTTCC AGGCCCAGGA AACAGCAGAG GCACAGAAGT GAGAATGGGT GGGTGAGTTG
GTGGGGAAAC TCCAGGTGCA GAGGATGGTA GCGAAACAAA CTGGAGCATT AAGGTCCAAG TCCTCCAAGA TCTTGACTTG
CAGATTAAGG AGTTTGTTCA CCTAATCTGC TTTGGGCAGA GTGTGGTGAG TCCTAGAGAC CCCTCTAGGT CTCTCCTCTC
AGTAGCCCCA GAAGGCCTGG AGAGCTGCTT CTGGGTGCCA AGCAGGCAGT GACTCCATCA GATCTAGATT TGGGAAAAGC
ATCCCTGGTC AGGGCCTGCA TCAGGGCAGT GGCTGGCCAT GAGGACCCTG AGAAGTAGAC AGATTCACGG AGATTCTCAG
GAGGCCAGAC AGGAGACTAT GGTGACAAAT TAGATTAGAG AAGGGGAGAG AATGAAGGAG CAGTTGGGGT
AAAAGAAAAC TGAGGCTGAC ATGGGTATAT GGGTGGCGAG TGACTCACCA CCCACTGAGA GGAGAACCTC ACAAGCTCTG
ACATGCTCTG GTTCCAGGTT CTGTTGGGGC TGATCCAAGA TGGTAGCCTA GAGGTGCACA GAGATGGGGG CCTTGCTTTG
CAAAAGGATG CTGGCTGCTG GCCCACAGCA TGGTAATGAG ATTTGAGCTT TATGTGCCCA GGGCTGGGAG GAGGGTCCTG
TCACTTTGAA AGCAAAGAGA GGCTCTAGAG AGGGGCATGT TGAGATAGGA ATGCTGCCTT GAGACACCTG GCTTTCCCCA
CTCTGGGTGG CTCTCAGCAG GGTGGGTTTC CCCTGCCAGG CAGCACTGAA CCTCTGTGCG CTTCCGGCTG GGAGAGTTTT
TACCGTAACT ACATGTGGAA CCATCCTGAA GGAACATCTG GATGGGATGG GGTACAGGGA AGGGAGCTGC CAAGAGTGCT
GGCCAGGGAC CTGGGTCTAT GAGCTGGTTG GGGGGTGGGG TTGGGTGCAG GGTACTTGAT CCTGAGTGGG CCTTCTGCGG
CCAGGATTGG TTCTAGAGTA GGAGGGGTGG GATCGGGGAT GGGGGAAGCC TGTAACTGCG CTGCAGTTGT CAGGTCCCAG
GTTCTGGGTG ACCTACTAAG GATTCTGGGT CCAGTGTGGG TCCCAGGTTA GACGTCCTAG TCCTGAGTCC GTGTCCACAG
TTCTGGGTGT TGAGTCTAGG ACAGTGATCT GGAGTTGACA GTCCAATCTA GGTCTGAGTC CTGACCCCAA GTCTAGAGTT
CAGGGTCATG GTAGTAGCCT AGGGTCAGAA TCAAGGTTGG GGTCAGTAAC CAGGATGGGA TCGAGGTCAT GGTCCAAAAT
CTGGATCTGG GGACCTGTTG GGGGTCTGAG GTGAGTGTCG CAGTCTGGGT ATGGCGTTGG AGACCCAGGG CTGTGATCTG
AGGTCATGGT TAGAGTCTCA GGTGGTGGGC CAAGGTTTGA GTCTGGGGTC CTGTTTGGAG TCTGGTGTCA GGTCGTGGAC
TGCGTCCAAG GTCAGGGAGT CCGGGGTTAT AGCCAGGGTC TGAGATGAAA GTCCCAGATG GTGTTCAGAG GTCTGAATCT
GTGTCTTGGT GAGCGTCCAG GTTCCCTGTG ATCACGTTTG GTGTCAGGGC TGCGGCCCGA CTGGGGAGCC TGGGATCCAG
AGATGTGACC CGAGGTTGTG GTCAGAGAAT GGGTCTCGGG TCGTCTTCGT GCCGGGTCCC TGTCGTGTTC CAGGCCCGGG
TCTCCGTCCA GCATCGAGGG CCGAGGTCAC GGCCAGGGTC TGAGCCCGCG GTCGCAGGTC TGGTTCGGGG TCAGATTCCG
CGCGGCCTCC AGGGGGCGCC GTCGCCGCCC GGCTCGGCCC CTCGCGGGCT CGCTGGCGTT GTGCGCGGCA GGCGGGGCCG

GAGGCGGCGG CGGCTCCGGG GGCGCGGGCC GGGCGGCGGC GGCGGCGGCG CCCCGACTGC AGTCCCGGCG GGAGCGGAGC GCGAAGCGCG GGGCCGGGCC CGGAGCCGGC GCCATGGGGC GGCGCCGCCT GTGAGCGGCG GCGAGCGGAG CCGCGGGCGC CGAGCAGGGC CAGGCGGGAG CGTCGGCGCC CGAGGCCGAG CGAGCCGCGG CCGGGCCGGG CCGAGCGCCG AGCGAGCAGG AGCGGCGGCG GCGGCGGCGG CGGCGGGAGG AGGCAGCGCC GCCGCCAAGA TGGCGGACCT GGAGGCGGTG CTGGCCGACG TGAGCTACCT GATGGCCATG GAGAAGAGCA AGGCCACGCC GGCCGCGCGC GCCAGCAAGA AGATACTGCT GCCCGAGCCC AGGTGAGGAG AAGCT-3' **(FRAG. NO:_) (SEQ. ID NO:2430)**

5'-CCAGGAAGCT ACCTGGAGGA GGTGAGTCTT AGCGGATGAG TAGGAGTTGT CCACGGAGGA AGGTACACAG AAGGGCTTCC AGGCCCAGGA AACAGCAGAG GCACAGAAGT GAGAATGGGT GGGTGAGTTG GTGGGGAAAC TCCAGGTGCA GAGGATGGTA GCGAAACAAA CTGGAGCATT AAGGTCCAAG TCCTCCAAGA TCTTGACTTG CAGATTAAGG AGTTTGTTCA CCTAATCTGC TTTGGGCAGA GTGTGGTGAG TCCTAGAGAC CCCTCTAGGT CTCTCCTCTC AGTAGCCCCA GAAGGCCTGG AGAGCTGCTT CTGGGTGCCA AGCAGGCAGT GACTCCATCA GATCTAGATT TGGGAAAAGC ATCCCTGGTC AGGGCCTGCA TCAGGGCAGT GGCTGGCCAT GAGGACCCTG AGAAGTAGAC AGATTCACGG AGATTCTCAG GAGGCCAGAC AGGAGACTAT GGTGACAAAT TAGATTAGAG AAGGGGAGAG AATGAAGGAG CAGTTGGGGT AAAAGAAAAC TGAGGCTGAC ATGGGTATAT GGGTGGCGAG TGACTCACCA CCCACTGAGA GGAGAACCTC ACAAGCTCTG ACATGCTCTG GTTCCAGGTT CTGTTGGGGC TGATCCAAGA TGGTAGCCTA GAGGTGCACA GAGATGGGGG CCTTGCTTTG CAAAAGGATG CTGGCTGCTG GCCCACAGCA TGGTAATGAG ATTTGAGCTT TATGTGCCCA GGGCTGGGAG GAGGGTCCTG TCACTTTGAA AGCAAAGAGA GGCTCTAGAG AGGGGCATGT TGAGATAGGA ATGCTGCCTT GAGACACCTG GCTTTCCCCA CTCTGGGTGG CTCTCAGCAG GGTGGGTTTC CCCTGCCAGG CAGCACTGAA CCTCTGTGCG CTTCCGGCTG GGAGAGTTTT TACCGTAACT ACATGTGGAA CCATCCTGAA GGAACATCTG GATGGGATGG GGTACAGGGA AGGGAGCTGC CAAGAGTGCT GGCCAGGGAC CTGGGTCTAT GAGCTGGTTG GGGGGTGGGG TTGGGTGCAG GGTACTTGAT CCTGAGTGGG CCTTCTGCGG CCAGGATTGG TTCTAGAGTA GGAGGGGTGG GATCGGGGAT GGGGGAAGCC TGTAACTGCG CTGCAGTTGT CAGGTCCCAG GTTCTGGGTG ACCTACTAAG GATTCTGGGT CCAGTGTGGG TCCCAGGTTA GACGTCCTAG TCCTGAGTCC GTGTCCACAG TTCTGGGTGT TGAGTCTAGG ACAGTGATCT GGAGTTGACA GTCCAATCTA GGTCTGAGTC CTGACCCCAA GTCTAGAGTT CAGGGTCATG GTAGTAGCCT AGGGTCAGAA TCAAGGTTGG GGTCAGTAAC CAGGATGGGA TCGAGGTCAT GGTCCAAAAT CTGGATCTGG GGACCTGTTG GGGGTCTGAG GTGAGTGTCG CAGTCTGGGT ATGGCGTTGG AGACCCAGGG CTGTGATCTG AGGTCATGGT TAGAGTCTCA GGTGGTGGGC CAAGGTTTGA GTCTGGGGTC CTGTTTGGAG TCTGGTGTCA GGTCGTGGAC TGCGTCCAAG GTCAGGGAGT CCGGGGTTAT AGCCAGGGTC TGAGATGAAA GTCCCAGATG GTGTTCAGAG GTCTGAATCT GTGTCTTGGT GAGCGTCCAG GTTCCCTGTG ATCACGTTTG GTGTCAGGGC TGCGGCCCGA CTGGGGAGCC TGGGATCCAG AGATGTGACC CGAGGTTGTG GTCAGAGAAT GGGTCTCGGG TCGTCTTCGT GCCGGGTCCC TGTCGTGTTC CAGGCCCGGG TCTCCGTCCA GCATCGAGGG CCGAGGTCAC GGCCAGGGTC TGAGCCCGCG GTCGCAGGTC TGGTTCGGGG TCAGATTCCG CGCGGCCTCC AGGGGGCGCC GTCGCCGCCC GGCTCGGCCC CTCGCGGGCT CGCTGGCGTT GTGCGCGGCA GGCGGGGCCG GAGGCGGCGG CGGCTCCGGG GGCGCGGGCC GGGCGGCGGC GGCGGCGGCG CCCCGACTGC AGTCCCGGCG GGAGCGGAGC GCGAAGCGCG GGGCCGGGCC CGGAGCCGGC GCCATGGGGC GGCGCCGCCT GTGAGCGGCG GCGAGCGGAG CCGCGGGCGC CGAGCAGGGC CAGGCGGGAG CGTCGGCGCC CGAGGCCGAG CGAGCCGCGG CCGGGCCGGG CCGAGCGCCG AGCGAGCAGG AGCGGCGGCG GCGGCGGCGG CGGCGGGAGG AGGCAGCGCC GCCGCCAAGA TGGCGGACCT GGAGGCGGTG CTGGCCGACG TGAGCTACCT GATGGCCATG GAGAAGAGCA AGGCCACGCC GGCCGCGCGC GCCAGCAAGA AGATACTGCT GCCCGAGCCC AGGTGAGGAG AAGCT-3' **(FRAG. NO:_) (SEQ. ID NO:2429)**

5'-GCCGCCGCCG CCAAGATGGC GGACCTGGAG GCGGTGCTGG CCGACGTGAG CTACCTGATG GCCATGGAGA AGAGCAAGGC CACGCCGGCC GCGCGCGCCA GCAAGAAGAT ACTGCTGCCC GAGCCCAGCA TCCGCAGTGT CATGCAGAAG TACCTGGAGG ACCGGGGCGA GGTGACCTTT GAGAAGATCT TTTCCCAGAA GCTGGGGTAC CTGCTCTTCC GAGACTTCTG CCTGAACCAC CTGGAGGAGG CCAGGCCCTT GGTGGAATTC TATGAGGAGA TCAAGAAGTA CGAGAAGCTG GAGACGGAGG AGGAGCGTGT GGCCCGCAGC CGGGAGATCT TCGACTCATA CATCATGAAG GAGCTGCTGG CCTGCTCGCA TCCCTTCTCG AAGAGTGCCA CTGAGCATGT CCAAGGCCAC CTGGGGAAGA AGCAGGTGCC TCCGGATCTC TTCCAGCCAT ACATCGAAGA GATTTGTCAA AACCTCCGAG GGGACGTGTT CCAGAAATTC ATTGAGAGCG ATAAGTTCAC ACGGTTTTGC CAGTGGAAGA ATGTGGAGCT CAACATCCAC CTGACCATGA ATGACTTCAG CGTGCATCGC ATCATTGGGC GCGGGGGCTT TGGCGAGGTC TATGGGTGCC GGAAGGCTGA CACAGGCAAG ATGTACGCCA TGAAGTGCCT GGACAAAAAG CGCATCAAGA TGAAGCAGGG GGAGACCCTG GCCCTGAACG AGCGCATCAT GCTCTCGCTC GTCAGCACTG GGGACTGCCC ATTCATTGTC TGCATGTCAT ACGCGTTCCA CACGCCAGAC AAGCTCAGCT TCATCCTGGA CCTCATGAAC GGTGGGGACC TGCACTACCA CCTCTCCCAG CACGGGGTCT TCTCAGAGGC TGACATGCGC TTCTATGCGG CCGAGATCAT CCTGGGCCTG GAGCACATGC ACAACCGCTT CGTGGTCTAC CGGGACCTGA AGCCAGCCAA CATCCTTCTG GACGAGCATG GCCACGTGCG GATCTCGGAC CTGGGCCTGG CCTGTGACTT CTCCAAGAAG AAGCCCCATG CCAGCGTGGG CACCCACGGG TACATGGCTC CGGAGGTCCT GCAGAAGGGC GTGGCCTACG ACAGCAGTGC CGACTGGTTC TCTCTGGGGT GCATGCTCTT CAAGTTGCTG CGGGGGCACA GCCCCTTCCG GCAGCACAAG ACCAAAGACA AGCATGAGAT CGACCGCATG ACGCTGACGA TGGCCGTGGA GCTGCCCGAC TCCTTCTCCC CTGAACTACG CTCCCTGCTG GAGGGGTTGC TGCAGAGGGA TGTCAACCGG AGATTGGGCT GCCTGGGCCG AGGGGCTCAG GAGGTGAAAG AGAGCCCCTT TTTCCGCTCC CTGGACTGGC AGATGGTCTT CTTGCAGAAG TACCCTCCCC CGCTGATCCC CCCACGAGGG GAGGTGAACG CGGCCGACGC CTTCGACATT GGCTCCTTCG ATGAGGAGGA CACAAAAGGA ATCAAGTTAC TGGACAGTGA TCAGGAGCTC TACCGCAACT TCCCCCTCAC CATCTCGGAG CGGTGGCAGC AGGAGGTGGC AGAGACTGTC TTCGACACCA TCAACGCTGA GACAGACCGG CTGGAGGCTC GCAAGAAAGC CAAGAACAAG CAGCTGGGCC ATGAGGAAGA CTACGCCCTG GGCAAGGACT GCATCATGCA TGGCTACATG TCCAAGATGG GCAACCCCTT CCTGACCCAG TGGCAGCGGC GGTACTTCTA CCTGTTCCCC AACCGCCTCG AGTGGCGGGG CGAGGGCGAG GCCCCGCAGA GCCTGCTGAC CATGGAGGAG ATCCAGTCGG TGGAGGAGAC GCAGATCAAG GAGCGCAAGT GCCTGCTCCT CAAGATCCGC GGTGGGAAAC AGTTCATTTT GCAGTGCGAT AGCGACCCTG AGCTGGTGCA GTGGAAGAAG GAGCTGCGCG ACGCCTACCG CGAGGCCCAG CAGCTGGTGC AGCGGGTGCC CAAGATGAAG AACAAGCCGC GCTCGCCCGT GGTGGAGCTG AGCAAGGTGC CGCTGGTCCA GCGCGGCAGT GCCAACGGCC TCTGACCCGC CCACCCGCCT-3' **(FRAG. NO:_) (SEQ. ID NO:2428)**

<u>**CCR-2 CC Chemokine Receptor Nucleic Acids and Antisense Oligonucleotide Fragments**</u>

5'-CTTTGTGAAG AAGGAATTGG CAACACTGAA ACCTCCAGAA CAAAGGCTGT CACTAAGGTC CCGCTGCCTT GATGGATTAT ACACTTGACC TCAGTGTGAC AACAGTGACC GACTACTACT ACCCTGATAT CTTCTCAAGC CCCTGTGATG CGGAACTTAT TCAGACAAAT GGCAAGTTGC TCCTTGCTGT CTTTTATTGC CTCCTGTTTG TATTCAGTCT TCTGGGAAAC AGCCTGGTCA TCCTGGTCCT TGTGGTCTGC AAGAAGCTGA GGAGCATCAC AGATGTATAC CTCTTGAACC TGGCCCTGTC

TGACCTGCTT TTTGTCTTCT CCTTCCCCTT TCAGACCTAC TATCTGCTGG ACCAGTGGGT GTTTGGGACT GTAATGTGCA
AAGTGGTGTC TGGCTTTTAT TACATTGGCT TCTACAGCAG CATGTTTTTC ATCACCCTCA TGAGTGTGGA CAGGTACCTG
GCTGTTGTCC ATGCCGTGTA TGCCCTAAAG GTGAGGACGA TCAGGATGGG CACAACGCTG TGCCTGGCAG TATGGCTAAC
CGCCATTATG GCTACCATCC CATTGCTAGT GTTTTACCAA GTGGCCTCTG AAGATGGTGT TCTACAGTGT TATTCATTTT
ACAATCAACA GACTTTGAAG TGGAAGATCT TCACCAACTT CAAAATGAAC ATTTTAGGCT TGTTGATCCC ATTCACCATC
TTTATGTTCT GCTACATTAA AATCCTGCAC CAGCTGAAGA GGTGTCAAAA CCACAACAAG ACCAAGGCCA TCAGGTTGGT
GCTCATTGTG GTCATTGCAT CTTTACTTTT CTGGGTCCCA TTCAACGTGG TTCTTTTCCT CACTTCCTTG CACAGTATGC
ACATCTTGGA TGGATGTAGC ATAAGCCAAC AGCTGACTTA TGCCACCCAT GTCACAGAAA TCATTTCCTT TACTCACTGC
TGTGTGAACC CTGTTATCTA TGCTTTTGTT GGGGAGAAGT TCAAGAAACA CCTCTCAGAA ATATTTCAGA AAAGTTGCAG
CCAAATCTTC AACTACCTAG GAAGACAAAT GCCTAGGGAG AGCTGTGAAA AGTCATCATC CTGCCAGCAG CACTCCTCCC
GTTCCTCCAG CGTAGACTAC ATTTTGTGAG GATCAATGAA GACTAAATAT AAAAAACATT TTCTTGAATG GCATGCTAGT
AGCAGTGAGC AAAGGTGTGG GTGTGAAAGG TTTCCAAAAA AAGTTCAGCA TGAAGGATGC CGTGTGTGTT GTTGCCAACA
CTTGGAACAC AATGACTGGA GACATAGTTG TGCATGCCTG GCACAACATC AAGCCTGTGA TTGTGTTTAT TGATGATGTT
GAACAAGTGG TGGCTTTGAG GGATTCTGTA TGCCAAGTGG AAAAAAAAGA TGTCTCCGGA ATTCGACAGG TTATCA-3'
(FRAG. NO:_) (SEQ. ID NO:2462)

CCR-4 CC Chemokine Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

5'-TTTCATCTCT CCGGGCTTAT TTGCTGGTTT CTCCGAATGC GGGCCTTGTC TGGTTCACGC TGGATCCCCA ACGCCTAGAA
CAGTGCGTGG CACGCAGTTC GTCCTTCTAT AAATATCGGA CTAAATGCAT CTCTGTGATG GTAATACCCA CACGGTGTTG
TGAGAATGAA TGAGTGATTC TGTGCAAGTT CCTAGTGATC TGTTACAAAA AGTACTGGTC GCTAAATTAC TCTTATAATA
AAGCATACTT TTAGGATAAT AAAGCACTAT TCGCGAATTG GTTACCGCTA TTATGAAATT ACTGAGCAAT ACATATCTAC
ATCTGATCAG TCTCCAGAAT TATGCCAAAT CCTACCTTCT TCTGAAAGTA TCTCCTAATT ATCTGCACCT GACCCTAGTG
ATGCTGTGAA TGTGCAAGTA TAGCTACATC CTCCGAAGGA AGGATCTTTA CTCCTTTTAC CTCCTGAATG GGCTGCGTCT
GCTGAAAGCG CGGGGGAATG GGCGGTTGGA AGCTTGGCCC TACTTCCAGC ATTGCCGCCT ACTGGTTGGG TTACTCCAGC
AAGTCACTCC CCTTCCCTGG GCCTCAGTGT CTCTACTGTA GCATTCCCAG GTCTGGAATT CCATCCACTT TAGCAAGGAT
GGACGCGCCA CAGAGAGACG CGTTCCTAGC CCGCGCTTCC CACCTGTCTT CAGGCGCATC CCGCTTCCCT CAAACTTAGG
AAATGCCTCT GGGAGGTCCT GTCCGGCTCC GGACTCACTA CCGACCACCC GCAAACAGCA GGGTCCCCTG GGCTTCCCAA
GCCGCGCACC TCTCCGCCCC GCCCCTGCGC CCTCCTTCCT CGCGTCTGCC CCTCTCCCCC ACCCCGCCTT CTCCCTCCCC
GCCCCAGCGG CGCATGCGCC GCGCTCGGAG CGTGTTTTTA TAAAAGTCCG GCCGCGGCCA GAAACTTCAG TTTGTTGGCT
GCGGCAGCAG GTAGCAAAGT GACGCCGAGG GCCTGAGTGC TCCAGTAGCC ACCGCATCTG GAGAACCAGC GGTTACCATG
GAGGGGATCA GTGTAAGTCC AGTTTCAACC TGCTTTGTCA TAAATGTACA AACGTTTGAA CTTAGAGCGC AGCCCCTCTC
CGAGCGGGCA GAAGCGGCCA GGACATTGGA GGTACCCGTA CTCCAAAAAA GGGTCACCGA AAGGAGTTTT CTTGACCATG
CCTATATAGT GCGGGTGGGT GGGGGGGGAG CAGGATTGGA ATCTTTTTCT CTGTGAGTCG AGGAGAAACG ACTGGAAAGA
GCGTTCCAGT GGCTGCATGT GTCTCCCCCT TGAGTCCCGC CGCGCGCGGC GGCTTGCACG CTGTTTGCAA ACGTAAGAAC
ATTCTGTGCA CAAGTGCAGA GAAGGCGTGC GCGCTGCCTC GGGACTCAGA CCACCGGTCT CTTCCTTGGG GAAGCGGGGA
TGTCTTGGAG CGAGTTACAT TGTCTGAATT TAGAGGCGGA GGGCGGCGTG CCTGGGCTGA CTTCCCAGGA GGAGATTGCG
CCCGCTTTAA CTTCGGGGTT AAGCGCCTGG TGACTGTTCT TGACACTGGG TGCGTGTTTG TTAAACTCTG TGCGGCCGAC
GGAGCTGTGC CAGTCTCCCA GCACAGTAGG CAGAGGGCGG GAGAGGCGGG TGGACCCACC GCGCCGATCC TCTGAGGGGA
TCGAGTGGTG GCAGCAGCTA GGAGTTGATC CGCCCGCGCG CTTTGGGTTT GAGGGGGAAA CCTTCCCGCC GTCCGAAGCG
CGCCTCTTCC CCACGGCCGC GAGTGGGTCC TGCAGTTCGA GAGTTTGGGG TCGTGCAGAG GTCAGCGGAG TGGTTTGACC
TCCCCTTTGA CACCGCGCAG CTGCCAGCCC TGAGATTTGC GCTCCGGGGA TAGGAGCGGG TACGGGGTGA GGGGCGGGGG
CGGTTAAGAC CGCACCTGGG CTGCCAGGTC GCCGCCGCGA AGACTGGCAG GTGCAAGTGG GGAAACCGTT TGGCTCTCTC
CGAGTCCAGT TGTGATGTTT AACCGTCGGT GGTTTCCAGA AACCTTTTGA AACCCTCTTG CTAGGGAGTT TTTGGTTTCC
TGCAGCGGCG CGCAATTCAA AGACGCTCGC GGCGGAGCCG CCCAGTCGCT CCCCAGCACC CTGTGGGACA GAGCCTGGCG
TGTCGCCCAG CGGAGCCCCT GCAGCGCTGC TTGCGGGCGG TTGGCGTGGG TGTAGTGGGC AGCCGCGGCG GCCCGGGGCT
GGACGACCCG GCCCCCCGCG TGCCCACCGC CTGGAGGCTT CCAGCTGCCC ACCTCCGGCC GGGTTAACTG GATCAGTGGC
GGGGTAATGG GAAGCCACCC GGGAGAGTGA GGAAATGAAA CTTGGGGCGA GGACCACGGG TGCAGACCCC GTTACCTTCT
CCACCCAGGA AAATGCCCCG CTCCCTAACG TCCCAAACGC GCCAAGTGAT AAACACGAGG ATGGCAAGAG ACCCACACAC
CGGAGGAGCG CCCGCTTGGG GGAGGAGGTG CCGTTTGTTC ATTTTCTGAC ACTCCCGCCC AATATACCCC AAGCACCGAA
GGGCCTTCGT TTTAAGACCG CATTCTCTTT ACCCACTACA AGTTGCTTGA AGCCCAGAAT GGTTTGTATT TAGGCAGGCG
TGGGAAAATT AAGTTTTTGC GCTTTAGGAG AATGAGTCTT TGCAACGCCC CCGCCCTCCC CCCGTGATCC TCCCTTCTCC
CCTCTTCCCT CCCTGGGCGA AAAACTTCTT ACAAAAAGTT AATCACTGCC CCTCCTAGCA GCACCCACCC CACCCCCCAC
GCCGCCTGGG AGTGGCCTCT TTGTGTGTAT TTTTTTTTTC CTCCTAAGGA AGGTTTTTTT TCTTCCCTCT AGTGGGCGGG
GCAGAGGAGT TAGCCAAGAT GTGACTTTGA AACCCTCAGC GTCTCAGTGC CCTTTTGTTC TAAACAAAGA ATTTTGTAAT
TGGTTCTACC AAAGAAGGAT ATAATGAAGT CACTATGGGA AAAGATGGGG AGGAGAGTTG TAGGATTCTA CATTAATTCT
CTTGTGCCCT TAGCCCACTA CTTCAGAATT TCCTGAAGAA AGCAAGCCTG AATTGGTTTT TTAAATTGCT TTAAAAATTT
TTTTTAACTG GGTTAATGCT TGCTGAATTG GAAGTGAATG TCCATTCCTT TGCCTCTTTT GCAGATATAC ACTTCAGATA
ACTACACCGA GGAAATGGGC TCAGGGGACT ATGACTCCAT GAAGGAACCC TGTTTCCGTG AAGAAAATGC TAATTTCAAT
AAAATCTTCC TGCCCACCAT CTACTCCATC ATCTTCTTAA CTGGCATTGT GGGCAATGGA TTGGTCATCC TGGTCATGGG
TTACCAGAAG AAACTGAGAA GCATGACGGA CAAGTACAGG CTGCACCTGT CAGTGGCCGA CCTCCTCTTT GTCATCACGC
TTCCCTTCTG GGCAGTTGAT GCCGTGGCAA ACTGGTACTT TGGGAACTTC CTATGCAAGG CAGTCCATGT CATCTACACA
GTCAACCTCT ACAGCAGTGT CCTCATCCTG GCCTTCATCA GTCTGGACCG CTACCTGGCC ATCGTCCACG CCACCAACAG
TCAGAGGCCA AGGAAGCTGT TGGCTGAAAA GGTGGTCTAT GTTGGCGTCT GGATCCCTGC CCTCCTGCTG ACTATTCCCG
ACTTCATCTT TGCCAACGTC AGTGAGGCAG ATGACAGATA TATCTGTGAC CGCTTCTACC CCAATGACTT GTGGGTGGTT
GTGTTCCAGT TTCAGCACAT CATGGTTGGC CTTATCCTGC CTGGTATTGT CATCCTGTCC TGCTATTGCA TTATCATCTC
CAAGCTGTCA CACTCCAAGG GCCACCAGAA GCGCAAGGCC CTCAAGACCA CAGTCATCCT CATCCTGGCT TTCTTCGCCT
GTTGGCTGCC TTACTACATT GGGATCAGCA TCGACTCCTT CATCCTCCTG GAAATCATCA AGCAAGGGTG TGAGTTTGAG
AACACTGTGC ACAAGTGGAT TTCCATCACC GAGGCCCTAG CTTTCTTCCA CTGTTGTCTG AACCCCATCC TCTATGCTTT
CCTTGGAGCC AAATTTAAAA CCTCTGCCCA GCACGCACTC ACCTCTGTGA GCAGAGGGTC CAGCCTCAAG ATCCTCTCCA
AAGGAAAGCG AGGTGGACAT TCATCTGTTT CCACTGAGTC TGAGTCTTCA AGTTTTCACT CCAGCTAACA CAGATGTAAA

AGACTTTTTT TTATACGATA AATAACTTTT TTTTAAGTTA CACATTTTTC AGATATAAAA GACTGACCAA TATTGTACAG TTTTTATTGC TTGTTGGATT TTTGTCTTGT GTTTCTTTAG TTTTTGTGAA GTTTAATTGA CTTATTTATA TAAATTTTTT TTGTTTCATA TTGATGTGTG TCTAGGCAGG ACCTGTGGCC AAGTTCTTAG TTGCTGTATG TCTCGTGGTA GGACTGTAGA AAAGGGAACT GAACATTCCA GAGCGTGTAG TGAATCACGT AAAGCTAGAA ATGATCCCCA GCTGTTTATG CATAGATAAT CTCTCCATTC CCGTGGAACG TTTTTCCTGT TCTTAAGACG TGATTTTGCT GTAGAAGATG GCACTTATAA CCAAAGCCCA AAGTGGTATA GAAATGCTGG TTTTTCAGTT TTCAGGAGTG GGTTGATTTC AGCACCTACA GTGTACAGTC TTGTATTAAG TTGTTAATAA AAGTACATGT TAAACTTACT TAGTGTTATG TTCTGATTTC TGTTGACATT CTTTTGGCTA GTAGAAGACA AAAGTAATAC ATTTATGGTA TGCAAAGCAC TATCCTAGGT ATTTCATTGT AATATTTTAC TTACCCCTTA TCACAACTCT GATAGATTCT GCTTCTGTTA CTAATTACAT TTTATAGAAG AGGAAACGGA GGCACAGAAA GCCTAAGTAA CTTGGTTAAA GGCATGTAGT AAGTATCAAA TCCTGTATTT TAAACCAGGT AACATGACTT AACGAATCTG AAGCCTTCAC CACTTTAAAT TCAAATGGAA GTTTAGAAAT GGCCAGCCAG CACCTATTTG TATGAAAGGT CATCTTTCAG AGGATAAGCA TGTATAAAGA AGAAAAGGTA TGCAGTCGTG TTTGGATTTT ACTCCACCAT C-3' **(FRAG. NO:_) (SEQ. ID NO: 2463)**

CD-34 Nucleic Acids and Antisense Oligonucleotide Fragments

5'-AGGATGATGG TGATGGGGAA CTAAATGGGG AAATATGGAA GGTCACAGGA AAAGTTAACA CAAGTTAGCA AAAGTTAAC ATAACACAAA AAGGTCTTGC AGGAAAAAAA AAAGAAAAGA AAAGAAAGAA AAAGTCTCCA AGAATGGTTT GGACAGCCAA AATGAATACT TATAGTCACG TATACCTGCT CACTCCTGAC GCTTCACTCA CACACAGCAC AGGATCTGGT GAGGCTATCA TAAATGTGC CACATTGTGG TTAAGTTTTA CCTGATTAAC GAAATGCTCA CACTTCTAAA CTGAGGTCCT TACAGTAGAT TCCTTTTGCA AGATTGTTAC TGGCTTACAA CTTAAAAATA AAGGAAAATC ACAAGGAAAG AAAAGTGGGG AAAAAATCGG AGGAAACTTG CCCCTGCCCT GGCCACCGGC AAGGCTGCCA CAAAGGGGTT AAAAGTTAAG TGGAAGTGGA GCTTGAAGAA GTGGGATGGG GCCTCTCCAG GAAAGCTGAA CGAGGCATCT GGAGCCCGAA CAAACCTCCA CCTTTTTTGG CCTCGACGGC GGCAACCCAG CCTCCCTCCT AACGCCCTCC GCCTTTGGGA CCAACCAGGG GAGCTCAAGT TAGTAGCAGC CAAGGAGAGG CGCTGCCTTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG GAAAAAAGCA AGAATCCCCC ACCCCTCTCC CGGGCGGAGG GGGCGGGAAG AGCGCGTCCT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT GCGTCTCTCT AGGAGCCGCG CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC GCGCAGGGCC CAGGATGCCG CGGGGCTGGA CCGCGCTTTG CTTGCTGAGT TTGCTGC CCTTTTTTGG CCTCGACGGC GGCAACCCAG CCTCCCTCCT AACGCCCTCC GCCTTTGGGA CCAACCAGGG GAGCTCAAGT TAGTAGCAGC CAAGGAGAGG CGCTGCCTTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG GAAAAAAGCA AGAATCCCCC ACCCCTCTCC CGGGCGGAGG GGGCGGGAAG AGCGCGTCCT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT GCGTCTCTCT AGGAGCCGCG CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC GCGAGGGCCC AGGATGCCGC GGGGCTGGAC CGCGCTTTGC TTGCTGAGTT TGCTGCCTTC TGGGTTCATG AGTCTTGACA ACAACGGTAC TGCTACCCCA GAGTTACCTA CCCAGGGAAC ATTTTCAAAT GTTTCTACAA ATGTATCCTA CCAAGAAACT ACAACACCTA GTACCCTTGG AAGTACCAGC CTGCACCCTG TGTCTCAACA TGGCAATGAG GCCACAACAA ACATCACAGA AACGACAGTC AAATTCACAT CTACCTCTGT GATAACCTCA GTTTATGGAA ACACAAACTC TTCTGTCCAG TCACAGACCT CTGTAATCAG CACAGTGTTC ACCACCCCAG CCAACGTTTC AACTCCAGAG ACAACCTTGA AGCCTAGCCT GTCACCTGGA AATGTTTCAG ACCTTTCAAC CACTAGCACT AGCCTTGCAA CATCTCCCAC TAAACCCTAT ACATCATCTT CTCCTATCCT AAGTGACATC AAGGCAGAAA TCAAATGTTC AGGCATCAGA GAAGTGAAAT TGACTCAGGG CATCTGCCTG GAGCAAAATA AGACCTCCAG CTGTGCGGAG TTTAAGAAGG ACAGGGGAGA GGGCCTGGCC CGAGTGCTGT GTGGGGAGGA GCAGGCTGAT GCTGATGCTG GGGCCCAGGT ATGCTCCCTG CTCCTTGCCC AGTCTGAGGT GAGGCCTCAG TGTCTACTGC TGGTCTTGGC CAACAGAACA GAAATTTCCA GCAAACTCCA ACTTATGAAA AAGCACCAAT CTGACCTGAA AAAGCTGGGG ATCCTAGATT TCACTGAGCA AGATGTTGCA AGCCACCAGA GCTATTCCCA AAAGACCCTG ATTGCACTGG TCACCTCGGG AGCCCTGCTG GCTGTCTTGG GCATCACTGG CTATTTCCTG ATGAATCGCC GCAGCTGGAG CCCCACAGGA GAAAGGCTGG GCGAAGACCC TTATTACACG GAAAACGGTG GAGGCCAGGG CTATAGCTCA GGACCTGGGA CCTCCCCTGA GGCTCAGGGA AAGGCCAGTG TGAACCGAGG GGCTCAGAAA AACGGGACCG GCCAGGCCAC CTCCAGAAAC GGCCATTCAG CAAGACAACA CGTGGTGGCT GATACCGAAT TGTGACTCGG CTAGGTGGGG CAAGGCTGGG CAGTGTCCGA GAGAGCACCC CTCTCTGCAT CTGACCACGT GCTACCCCCA TGCTGGAGGT GACATCTCTT ACGCCCAACC CTTCCCCACT GCACACACCT CAGAGGCTGT TCTTGGGGCC CTACACCTTG AGGAGGGGGC AGGTAAACTC CTGTCCTTTA CACATTCGGC TCCCTGGAGC CAGACTCTGG TCTTCTTTGG GTAAACGTGT GACGGGGGAA AGCCAAGGTC TGGAGAAGCT CCCAGGAACA ATCGATGGCC TTGCAGCACT CACACAGGAC CCCCTTCCCC TACCCCCTCC TCTCTGCCGC AATACAGGAA CCCCCAGGGG AAAGATGAGC TTTTCTAGGC TACAATTTTC TCCCAGGAAG CTTTGATTTT TACCGTTTCT TCCCTGTATT TTCTTTCTCT ACTTTGAGGA AACCAAAGTA ACCTTTTGCA CCTGCTCTCT TGTAATGATA TAGCCAGAAA AACGTGTTGC CTTGAACCAC TTCCCTCATC TCTCCTCCAA GACACTGTGG ACTTGGTCAC CAGCTCCTCC CTTGTTCTCT AAGTTCCACT GAGCTCCATG TGCCCCCTCT ACCATTTGCA GAGTCCTGCA CAGTTTTCTG GCTGGAGCCT AGAACAGGCC TCCCAAGTTT TAGGACAAAC AGCTCAGTTC TAGTCTCTCT GGGGCCACAC AGAAACTCTT TTTGGGCTCC TTTTTCTCCC TCTGGATCAA AGTAGGCAGG ACCATGGGAC CAGGTCTTGG AGCTGAGCCT CTCACCTGTA CTCTTCCGAA AAATCCTCTT CCTCTGAGGC TGGATCCTAG CCTTATCCTC TGATCTCCAT GGCTTCCTCC TCCCTCCTGC CGACTCCTGG GTTGAGCTGT TGCCTCAGTC CCCCAACAGA TGCTTTTCTG TCTCTGCCTC CCTCACCCTG AGCCCCTTCC TTGCTCTGCA CCCCCATATG GTCATAGCCC AGATCAGCTC CTAACCCTTA TCACCAGCTG CCTCTTCTGT GGGTGACCCA GGTCCTTGTT TGCTGTTGAT TTCTTTCCAG AGGGGTTGAG CAGGGATCCT GGTTTCAATG ACGGTTGGAA ATAGAAATTT CCAGAGAAGA GAGTATTGGG TAGATATTTT TTCTGAATAC AAAGTGATGT GTTTAAATAC TGCAATTAAA GTGATACTGA AACAC-3' **(FRAG. No:_) (SEQ. ID NO:2466)**

5'-AGGATGATGG TGATGGGGAA CTAAATGGGG AAATATGGAA GGTCACAGGA AAAGTTAACA CAAGTTAGCA AAAAGTTAAC ATAACACAAA AAGGTCTTGC AGGAAAAAAA AAAGAAAAGA AAAGAAAGAA AAAGTCTCCA AGAATGGTTT GGACAGCCAA AATGAATACT TATAGTCACG TATACCTGCT CACTCCTGAC GCTTCACTCA CACACAGCAC AGGATCTGGT GAGGCTATCA CTAAATGTGC CACATTGTGG TTAAGTTTTA CCTGATTAAC GAAATGCTCA CACTTCTAAA CTGAGGTCCT TACAGTAGAT TCCTTTTGCA AGATTGTTAC TGGCTTACAA CTTAAAAATA AAGGAAAATC ACAAGGAAAG AAAAGTGGGG AAAAAATCGG AGGAAACTTG CCCCTGCCCT GGCCACCGGC AAGGCTGCCA CAAAGGGGTT AAAAGTTAAG TGGAAGTGGA GCTTGAAGAA GTGGGATGGG GCCTCTCCAG GAAAGCTGAA CGAGGCATCT GGAGCCCGAA CAAACCTCCA CCTTTTTTGG CCTCGACGGC GGCAACCCAG CCTCCCTCCT AACGCCCTCC GCCTTTGGGA CCAACCAGGG GAGCTCAAGT TAGTAGCAGC CAAGGAGAGG CGCTGCCTTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG GAAAAAAGCA AGAATCCCCC ACCCCTCTCC CGGGCGGAGG GGGCGGGAAG AGCGCGTCCT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT GCGTCTCTCT AGGAGCCGCG CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC GCGCAGGGCC CAGGATGCCG CGGGGCTGGA CCGCGCTTTG CTTGCTGAGT TTGCTGC-3' **(FRAG. NO:_) (SEQ. ID NO:2464)**

5'-CCTTTTTTGG CCTCGACGGC GGCAACCCAG CCTCCCTCCT AACGCCCTCC GCCTTTGGGA CCAACCAGGG GAGCTCAAGT TAGTAGCAGC CAAGGAGAGG CGCTGCCTTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG GAAAAAAGCA AGAATCCCCC ACCCCTCTCC CGGGCGGAGG GGGCGGGAAG AGCGCGTCCT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT

GCGTCTCTCT AGGAGCCGCG CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC GCGAGGGCCC AGGATGCCGC GGGGCTGGAC CGCGCTTTGC TTGCTGAGTT TGCTGCCTTC TGGGTTCATG AGTCTTGACA ACAACGGTAC TGCTACCCCA GAGTTACCTA CCCAGGGAAC ATTTTCAAAT GTTTCTACAA ATGTATCCTA CCAAGAAACT ACAACACCTA GTACCCTTGG AAGTACCAGC CTGCACCCTG TGTCTCAACA TGGCAATGAG GCCACAACAA ACATCACAGA AACGACAGTC AAATTCACAT CTACCTCTGT GATAACCTCA GTTTATGGAA ACACAAACTC TTCTGTCCAG TCACAGACCT CTGTAATCAG CACAGTGTTC ACCACCCCAG CCAACGTTTC AACTCCAGAG ACAACCTTGA AGCCTAGCCT GTCACCTGGA AATGTTTCAG ACCTTTCAAC CACTAGCACT AGCCTTGCAA CATCTCCCAC TAAACCCTAT ACATCATCTT CTCCTATCCT AAGTGACATC AAGGCAGAAA TCAAATGTTC AGGCATCAGA GAAGTGAAAT TGACTCAGGG CATCTGCCTG GAGCAAAATA AGACCTCCAG CTGTGCGGAG TTTAAGAAGG ACAGGGGAGA GGGCCTGGCC CGAGTGCTGT GTGGGGAGGA GCAGGCTGAT GCTGATGCTG GGGCCCAGGT ATGCTCCCTG CTCCTTGCCC AGTCTGAGGT GAGGCCTCAG TGTCTACTGC TGGTCTTGGC CAACAGAACA GAAATTTCCA GCAAACTCCA ACTTATGAAA AAGCACCAAT CTGACCTGAA AAAGCTGGGG ATCCTAGATT TCACTGAGCA AGATGTTGCA AGCCACCAGA GCTATTCCCA AAAGACCCTG ATTGCACTGG TCACCTCGGG AGCCCTGCTG GCTGTCTTGG GCATCACTGG CTATTTCCTG ATGAATCGCC GCAGCTGGAG CCCCACAGGA GAAAGGCTGG GCGAAGACCC TTATTACACG GAAAACGGTG GAGGCCAGGG CTATAGCTCA GGACCTGGGA CCTCCCCTGA GGCTCAGGGA AAGGCCAGTG TGAACCGAGG GGCTCAGAAA AACGGGACCG GCCAGGCCAC CTCCAGAAAC GGCCATTCAG CAAGACAACA CGTGGTGGCT GATACCGAAT TGTGACTCGG CTAGGTGGGG CAAGGCTGGG CAGTGTCCGA GAGAGCACCC CTCTCTGCAT CTGACCACGT GCTACCCCCA TGCTGGAGGT GACATCTCTT ACGCCCAACC CTTCCCCACT GCACACACCT CAGAGGCTGT TCTTGGGGCC CTACACCTTG AGGAGGGGGC AGGTAAACTC CTGTCCTTTA CACATTCGGC TCCCTGGAGC CAGACTCTGG TCTTCTTTGG GTAAACGTGT GACGGGGGAA AGCCAAGGTC TGGAGAAGCT CCCAGGAACA ATCGATGGCC TTGCAGCACT CACACAGGAC CCCCTTCCCC TACCCCCTCC TCTCTGCCGC AATACAGGAA CCCCCAGGGG AAAGATGAGC TTTTCTAGGC TACAATTTTC TCCCAGGAAG CTTTGATTTT TACCGTTTCT TCCCTGTATT TTCTTTCTCT ACTTTGAGGA AACCAAAGTA ACCTTTTGCA CCTGCTCTCT TGTAATGATA TAGCCAGAAA AACGTGTTGC CTTGAACCAC TTCCCTCATC TCTCCTCCAA GACACTGTGG ACTTGGTCAC CAGCTCCTCC CTTGTTCTCT AAGTTCCACT GAGCTCCATG TGCCCCCTCT ACCATTTGCA GAGTCCTGCA CAGTTTTCTG GCTGGAGCCT AGAACAGGCC TCCCAAGTTT TAGGACAAAC AGCTCAGTTC TAGTCTCTCT GGGGCCACAC AGAAACTCTT TTTGGGCTCC TTTTTCTCCC TCTGGATCAA AGTAGGCAGG ACCATGGGAC CAGGTCTTGG AGCTGAGCCT CTCACCTGTA CTCTTCCGAA AAATCCTCTT CCTCTGAGGC TGGATCCTAG CCTTATCCTC TGATCTCCAT GGCTTCCTCC TCCCTCCTGC CGACTCCTGG GTTGAGCTGT TGCCTCAGTC CCCCAACAGA TGCTTTTCTG TCTCTGCCTC CCTCACCCTG AGCCCCTTCC TTGCTCTGCA CCCCCATATG GTCATAGCCC AGATCAGCTC CTAACCCTTA TCACCAGCTG CCTCTTCTGT GGGTGACCCA GGTCCTTGTT TGCTGTTGAT TTCTTTCCAG AGGGGTTGAG CAGGGATCCT GGTTTCAATG ACGGTTGGAA ATAGAAATTT CCAGAGAAGA GAGTATTGGG TAGATATTTT TTCTGAATAC AAAGTGATGT GTTTAAATAC TGCAATTAAA GTGATACTGA AACAC-3' **(FRAG. No:_) (SEQ. ID NO:2465)**

Eotaxin Antisense Nucleic Acids and Oligonucleotide Fragments

5'-GCATTTTTTC AAGTTTTATG ATTTATTTAA CTTGTGGAAC AAAAATAAAC CAGAAACCAC CACCTCTCAC GCCAAAGCTC ACACCTTCAG CCTCCAACAT GAAGGTCTCC GCAGCACTTC TGTGGCTGCT GCTCATAGCA GCTGCCTTCA GCCCCCAGGG GCTCGCTGGG CCAGCTTCTG TCCCAACCAC CTGCTGCTTT AACCTGGCCA ATAGGAAGAT ACCCCTTCAG CGACTAGAGA GCTACAGGAG AATCACCAGT GGCAAATGTC CCCAGAAAGC TGTGATCTTC AAGACCAAAC TGGCCAAGGA TATCTGTGCC GACCCCAAGA AGAAGTGGGT GCAGGATTCC ATGAAGTATC TGGACCAAAA ATCTCCAACT CCAAAGCCAT AAATAATCAC CATTTTTGAA ACCAAACCAG AGCCTGAGTG TTGCCTAATT TGTTTTCCCT TCTTACAATG CATTCTGAGG TAACCTCATT ATCAGTCCAA AGGGCATGGG TTTTATTATA TATATATATA TTTTTTTTTT AAAAAAAAAC GTATTGCATT TAATTTATTG AGGCTTTAAA ACTTATCCTC CATGAATATC AGTTATTTTT AAACTGTAAA GCTTTGTGCA GATTCTTTAC CCCCTGGGAG CCCCAATTCG ATCCCCTGTC ACGTGTGGGC AATGTTCCCC CTCTCCTCTC TTCCTCCCTG GAATCTTGTA AAGGTCCTGG CAAAGATGAT CAGTATGAAA ATGTCATTGT TCTTGTGAAC CCAAAGTGTG ACTCATTAAA TGGAAGTAAA TGTTGTTTTA GGAATAC ATGAAGGTCT CCGCAGCACT TCTGTGGCTG CTGCTCATAG CAGCTGCCTT CAGCCCCCAG GGGCTCGCTG GGCCAGCTTC TGTCCCAACC ACCTGCTGCT TTAACCTGGC CAATAGGAAG ATACCCCTTC AGCGACTAGA GAGCTACAGG AGAATCACCA GTGGCAAATG TCCCCAGAAA GCTGTGATCT TCAAGACCAA ACTGGCCAAG GATATCTGTG CCGACCCCAA GAAGAAGTGG GTGCAGGATT CCATGAAGTA TCTGGACCAA AAATCTCCAA CTCCAAAGCC ATAA CCACATATTC CCCTCCTTTT CCAAGGCAAG ATCCAGATGG ATTAAAAAAT GTACCAAGTC CCTCCTACTA GCTTGCCTCT CTTCTGTTCT GCTTGACTTC CTAGGATCTG GAATCTGGTC AGCAATCAGG AATCCCTTCA TCGTGACCCC CGCATGGGCA AAGGCTTCCC TGGAATCTCC CACACTGTCT GCTCCCTATA AAAGGCAGGC AGATGGGCCA GAGGAGCAGA GAGGCTGAGA CCAACCCAGA AACCACCACC TCTCACGCCA AAGCTCACAC CTTCAGCCTC CAACATGAAG GTCTCCGCAG CACTTCTGTG GCTGCTGCTC ATAGCAGCTG CCTTCAGCCC CCAGGGGCTC GCTGGGCCAG GTAAGCCCCC CAACTCCTTA CAGGAAAGGT AAGGTAACCA CCTCCAGGCT ACTAGGTCAG CAAGAATCTT TACAGACTCA CTGCAAATTC TCCATTTGAA AAATAGGGAA ACAGGTTTTG TGGGTGGACA AGAAATGCCT CAACCGTCAC ATCCAGTCAC TGGAAGAGCC AGAACTAGAA AGCTCCCGAG TCTTTTCCCC ACATTCAAGA GGGCCGCTGG GTGCATCCTT ACCCAGCTAT CCTTACAGTG TTTGGGAATG GGGAATGGCT CTGTCTTACT GTGGGCATGG TGGGCATTTT TGGCAGTGGG AGAGAAGGAA AATCTGTTGA TTAGAAGCTC AGTATGTTAA TTCGACTCCA GGACAGCTTT CAGAGACAGT GGCTAAGAGA AGAACGAGGT CCCAGGGGAT CTCTTGAGGT GACTTATTTT GACACTCTTT GGGAAAGTTA TCTAGGAGAT TTGTTCCATA ACTCATTTTC CCATACTCTG GTGACAAATT TACTGAGTGT ATCGGTCCCA CTGAGCCAGT GCATAGCATG GTAACAAACA GTTCTAAATT ATCAATGACT TAACAGAATT AACTAAATTA ACAAAAGTTA CTTTCTCACT TGTACTAAAT ATCTATAATG TATGGGCTCA GGCTTCTGCA TTTTATACTC AGGATTCTAG ACTGATGGAG AAGTTGCCAT GTGGGGGAAC ATTGATGGAT ACTGTGATAA AGCAGAAGAA AGCTCTCAGG AGTCTTGCAT AGGCAATGCA CTGTGGCTCA AAAATGACAC CCATCACTTT GTCTCCTTCT TTATTGATCA AAACTAATTA ATGCCTCCAA CCAAACAAAA GTGGCCAAGA AATGCAAGTC TACCTTGTGT CTCAAAACAG AGGATGGAGA ATATTTGGTG AAAATTACCA TGACCATCAC ATGGCCACGT AGGTCTTTAT AATGACAGAG CTAGCATTTG TCACATTGAC CAAGCTTTGT CCATACACTC TACAGTAATG ATGAGTCCTC AGTGCACAGG GGAGGATGCT GAAGACACAG GACAGCATCC TCCAGACACA TAAGACTTCA GAGCAGAGGG ATTCTCCCTC CACCTCTCGC AATTCCTTGC TTTCTCCTAA CTTCCTTTAC AAAGTCATGC TTGGAAATGT CTATGTATCA TCATGTGGCT CATTTTTTTC TCTGTTCATT TTTTTTCCCC AAAATTCAGC TTCTGTCCCA ACCACCTGCT GCTTTAACCT GGCCAATAGG AAGATACCCC TTCAGCGACT AGAGAGCTAC AGGAGAATCA CCAGTGGCAA ATGTCCCCAG AAAGCTGTGA TGTAAGTAAA TAAAGTTCAC CCTCCCCTAG ACAAAAAAAT AATGTCTAGG GCACAGAGTC AAGAACTGTG GGAGTCATAG ACTCTGATAG TTTGACCTCT ATGGTCCAAT TCATTAATTT TCACAAGTGA GTGTTCACTC CCAGCTCCCT GCCTGGGAGA

TTGCTGTAGT CATATCAATT TCTTCAAGTC AAGAGCAAAG ATGGTTTTAC TGGGCCTTTA AGAGCAGCAA CTAACCCAAG AGTCTCATCC TTCCTCCTCT CCGTAGCAAC CCTTTGTCCA GGGGCAGATG GTCCTTAAAT ATTTAGGGTC AAATGGGCAG AATTTTCAAA AACAATCCTT CCAATTGCAT CCTGATTCTC CCCACAGCTT CAAGACCAAA CTGGCCAAGG ATATCTGTGC CGACCCCAAG AAGAAGTGGG TGCAGGATTC CATGAAGTAT CTGGACCAAA AATCTCCAAC TCCAAAGCCA TAAATAATCA CCATTTTTGA AACCAAACCA GAGCCTGAGT GTTGCCTAAT TTGTTTTCCC TTCTTACAAT GCATTCTGAG GTAACCTCAT TATCAGTCCA AAGGGCATGG GTTTTATTAT ATATATATAT ATATATTTTT TTTTAAAAAA AAACGTATTG CATTTAATTT ATTGAGGCTT TAAAACTTAT CCTCCATGAA TATCAGTTAT TTTTAAACTG TAAAGCTTTG TGCAGATTCT TTACCCCCTG GGAGCCCCAA TTCGATCCCC TGTCACGTGT GGGCAATGTT CCCCCTCTCC TCTCTTCCTC CCTGGAATCT TGTAAAGGTC CTGGCAAAGA TGATCAGTAT GAAAATGTCA TTGTTCTTGT GAACCCAAAG TGTGACTCAT TAAATGGAAG TAATGTTGTT TTAGGAATAC ATAAAGTATG TGCATATTTT ATTATAGTCA CTAGTTGTAA TTTTTTTGTG GGAAATCCAC ACTGAGCTGA GGGGG-3- (FRAG. NO:_) (SEQ. ID NO:2494)

5'-GCATTTTTTC AAGTTTTATG ATTTATTTAA CTTGTGGAAC AAAAATAAAC CAGAAACCAC CACCTCTCAC GCCAAAGCTC ACACCTTCAG CCTCCAACAT GAAGGTCTCC GCAGCACTTC TGTGGCTGCT GCTCATAGCA GCTGCCTTCA GCCCCCAGGG GCTCGCTGGG CCAGCTTCTG TCCCAACCAC CTGCTGCTTT AACCTGGCCA ATAGGAAGAT ACCCCTTCAG CGACTAGAGA GCTACAGGAG AATCACCAGT GGCAAATGTC CCCAGAAAGC TGTGATCTTC AAGACCAAAC TGGCCAAGGA TATCTGTGCC GACCCCAAGA AGAAGTGGGT GCAGGATTCC ATGAAGTATC TGGACCAAAA ATCTCCAACT CCAAAGCCAT AAATAATCAC CATTTTTGAA ACCAAACCAG AGCCTGAGTG TTGCCTAATT TGTTTTCCCT TCTTACAATG CATTCTGAGG TAACCTCATT ATCAGTCCAA AGGGCATGGG TTTTATTATA TATATATATA TTTTTTTTTT AAAAAAAAAC GTATTGCATT TAATTTATTG AGGCTTTAAA ACTTATCCTC CATGAATATC AGTTATTTTT AAACTGTAAA GCTTTGTGCA GATTCTTTAC CCCCTGGGAG CCCCAATTCG ATCCCCTGTC ACGTGTGGGC AATGTTCCCC CTCTCCTCTC TTCCTCCCTG GAATCTTGTA AAGGTCCTGG CAAAGATGAT CAGTATGAAA ATGTCATTGT TCTTGTGAAC CCAAAGTGTG ACTCATTAAA TGGAAGTAAA TGTTGTTTTA GGAATAC-3' (FRAG.NO:_)(SEQ. ID NO:2491)

5'-ATGAAGGTCT CCGCAGCACT TCTGTGGCTG CTGCTCATAG CAGCTGCCTT CAGCCCCCAG GGGCTCGCTG GGCCAGCTTC TGTCCCAACC ACCTGCTGCT TTAACCTGGC CAATAGGAAG ATACCCCTTC AGCGACTAGA GAGCTACAGG AGAATCACCA GTGGCAAATG TCCCCAGAAA GCTGTGATCT TCAAGACCAA ACTGGCCAAG GATATCTGTG CCGACCCCAA GAAGAAGTGG GTGCAGGATT CCATGAAGTA TCTGGACCAA AAATCTCCAA CTCCAAAGCC ATAA-3' (FRAG. NO:_)(SEQ. ID NO:2492)

5'-CCACATATTC CCCTCCTTTT CCAAGGCAAG ATCCAGATGG ATTAAAAAAT GTACCAAGTC CCTCCTACTA GCTTGCCTCT CTTCTGTTCT GCTTGACTTC CTAGGATCTG GAATCTGGTC AGCAATCAGG AATCCCTTCA TCGTGACCCC CGCATGGGCA AAGGCTTCCC TGGAATCTCC CACACTGTCT GCTCCCTATA AAAGGCAGGC AGATGGGCCA GAGGAGCAGA GAGGCTGAGA CCAACCCAGA AACCACCACC TCTCACGCCA AAGCTCACAC CTTCAGCCTC CAACATGAAG GTCTCCGCAG CACTTCTGTG GCTGCTGCTC ATAGCAGCTG CCTTCAGCCC CCAGGGGCTC GCTGGGCCAG GTAAGCCCCC CAACTCCTTA CAGGAAAGGT AAGGTAACCA CCTCCAGGCT ACTAGGTCAG CAAGAATCTT TACAGACTCA CTGCAAATTC TCCATTTGAA AAATAGGGAA ACAGGTTTTG TGGGTGGACA AGAAATGCCT CAACCGTCAC ATCCAGTCAC TGGAAGAGCC AGAACTAGAA AGCTCCCGAG TCTTTTCCCC ACATTCAAGA GGGCCGCTGG GTGCATCCTT ACCCAGCTAT CCTTACAGTG TTTGGGAATG GGGAATGGCT CTGTCTTACT GTGGGCATGG TGGGCATTTT TGGCAGTGGG AGAGAAGGAA AATCTGTTGA TTAGAAGCTC AGTATGTTAA TTCGACTCCA GGACAGCTTT CAGAGACAGT GGCTAAGAGA AGAACGAGGT CCCAGGGGAT CTCTTGAGGT GACTTATTTT GACACTCTTT GGGAAAGTTA TCTAGGAGAT TTGTTCCATA ACTCATTTTC CCATACTCTG GTGACAAATT TACTGAGTGT ATCGGTCCCA CTGAGCCAGT GCATAGCATG GTAACAAACA GTTCTAAATT ATCAATGACT TAACAGAATT AACTAAATTA ACAAAAGTTA CTTTCTCACT TGTACTAAAT ATCTATAATG TATGGGCTCA GGCTTCTGCA TTTTATACTC AGGATTCTAG ACTGATGGAG AAGTTGCCAT GTGGGGGAAC ATTGATGGAT ACTGTGATAA AGCAGAAGAA AGCTCTCAGG AGTCTTGCAT AGGCAATGCA CTGTGGCTCA AAAATGACAC CCATCACTTT GTCTCCTTCT TTATTGATCA AAACTAATTA ATGCCTCCAA CCAAACAAAA GTGGCCAAGA AATGCAAGTC TACCTTGTGT CTCAAAACAG AGGATGGAGA ATATTTGGTG AAAATTACCA TGACCATCAC ATGGCCACGT AGGTCTTTAT AATGACAGAG CTAGCATTTG TCACATTGAC CAAGCTTTGT CCATACACTC TACAGTAATG ATGAGTCCTC AGTGCACAGG GGAGGATGCT GAAGACACAG GACAGCATCC TCCAGACACA TAAGACTTCA GAGCAGAGGG ATTCTCCCTC CACCTCTCGC AATTCCTTGC TTTCTCCTAA CTTCCTTTAC AAAGTCATGC TTGGAAATGT CTATGTATCA TCATGTGGCT CATTTTTTTC TCTGTTCATT TTTTTTCCCC AAAATTCAGC TTCTGTCCCA ACCACCTGCT GCTTTAACCT GGCCAATAGG AAGATACCCC TTCAGCGACT AGAGAGCTAC AGGAGAATCA CCAGTGGCAA ATGTCCCCAG AAAGCTGTGA TGTAAGTAAA TAAAGTTCAC CCTCCCCTAG ACAAAAAAAT AATGTCTAGG GCACAGAGTC AAGAACTGTG GGAGTCATAG ACTCTGATAG TTTGACCTCT ATGGTCCAAT TCATTAATTT TCACAAGTGA GTGTTCACTC CCAGCTCCCT GCCTGGGAGA TTGCTGTAGT CATATCAATT TCTTCAAGTC AAGAGCAAAG ATGGTTTTAC TGGGCCTTTA AGAGCAGCAA CTAACCCAAG AGTCTCATCC TTCCTCCTCT CCGTAGCAAC CCTTTGTCCA GGGGCAGATG GTCCTTAAAT ATTTAGGGTC AAATGGGCAG AATTTTCAAA AACAATCCTT CCAATTGCAT CCTGATTCTC CCCACAGCTT CAAGACCAAA CTGGCCAAGG ATATCTGTGC CGACCCCAAG AAGAAGTGGG TGCAGGATTC CATGAAGTAT CTGGACCAAA AATCTCCAAC TCCAAAGCCA TAAATAATCA CCATTTTTGA AACCAAACCA GAGCCTGAGT GTTGCCTAAT TTGTTTTCCC TTCTTACAAT GCATTCTGAG GTAACCTCAT TATCAGTCCA AAGGGCATGG GTTTTATTAT ATATATATAT ATATATTTTT TTTTAAAAAA AAACGTATTG CATTTAATTT ATTGAGGCTT TAAAACTTAT CCTCCATGAA TATCAGTTAT TTTTAAACTG TAAAGCTTTG TGCAGATTCT TTACCCCCTG GGAGCCCCAA TTCGATCCCC TGTCACGTGT GGGCAATGTT CCCCCTCTCC TCTCTTCCTC CCTGGAATCT TGTAAAGGTC CTGGCAAAGA TGATCAGTAT GAAAATGTCA TTGTTCTTGT GAACCCAAAG TGTGACTCAT TAAATGGAAG TAATGTTGTT TTAGGAATAC ATAAAGTATG TGCATATTTT ATTATAGTCA CTAGTTGTAA TTTTTTTGTG GGAAATCCAC ACTGAGCTGA GGGGG-3' (FRAG. NO:_)(SEQ. ID NO:2493)

FK-506 Binding Protein Nucleic Acids and Oligonucleotide Fragments

5'- GCCAGGTCGC TGTTGGTCCA CGCCGCCCGT CGCGCCGCCC GCCCGCTCAG CGTCCGCCGC CGCCATGGGA GGCCGGAGCC GAGCCGGGGT CGGGCAGCAG CAGGGACCCC CCAGAGGCGG GGCCTGTGGG ACCGCTATGG GCGTGGAGAT CGAGACCATC TCCCCCGGAG ACGGAAGGAC ATTCCCCAAG AAGGGCCAAA CGTGTGTGGT GCACTACACA GGAATGCTCC AAAATGGGAA GAAGTTTGAT TCATCCAGAG ACAGAAACAA ACCTTTCAAG TTCAGAATTG GCAAACAGGA AGTCATCAAA GGTTTTGAAG AGGGTGCAGC CCAGATGAGC TTGGGGCAGA GGGCGAAGCT GACCTGCACC CCTGATGTGG CATATGGAGC CACGGGCCAC CCCGGTGTCA TCCCTCCCAA TGCCACCCTC ATCTTTGACG TGGAGCTGCT CAACTTAGAG TGAAGGCAGG AAGGAACTCA AGGTGGCTGG AGATGGCTGC TGCTCACCCT CCTAGCCTGC TCTGCCACTG GGACGGCTCC TGCTTTTGGG GCTCTTGATC AGTGTGCTAA CCTCACTGCC TCATGGCATC ATCCATTCTC TCTGCCCAAG TTGCTCTGTA TGTGTTCGTC

AGTGTTCATG CGAATTCTTG CTTGAGGAAA CTTCGGTTGC AGATTGAAGC ATTTCAGGTT GTGCATTTTG TGTGATGCAT GTAGTAGCCT TTCCTGATGA CAGAACACAG ATCTCTTGTT CGCACAATCT ACACTGCCTT ACCTTCACTT AAACCACACA CACAAGGTGC TCAGACATGA AATGTACATG GCGTACCGTA CACAGAGGGA CTTGAGCCAG TTACCTTTGC TGTCACTTTC TCTCTTATAA ATTCTGTTAG CTGCTCACTT AAACAATGTC CTCTTTGAGA AAATGTAAAA TAAAGGCTCT GTGCTTGACA GAATTCGGGC CGCCGCCAGG TCGCTGTTGG TCCACGCCGC CCGTCGCGCC GCCCGCCCGC TCAGCGTCCG CCGCCGCCAT GGGAGTGCAG GTGGAAACCA TCTCCCCAGG AGACGGGCGC ACCTTCCCCA AGCGCGGCCA GACCTGCGTG GTGCACTACA CCGGGATGCT TGAAGATGGA AAGAAATTTG ATTCCTCCCG GGACAGAAAC AAGCCCTTTA AGTTTATGCT AGGCAAGCAG GAGGTGATCC GAGGCTGGGA AGAAGGGGTT GCCCAGATGA GTGTGGGTCA GAGAGCCAAA CTGACTATAT CTCCAGATTA TGCCTATGGT GCCACTGGGC ACCCAGGCAT CATCCCACCA CATGCCACTC TCGTCTTCGA TGTGGAGCTT CTAAAACTGG AATGACAGGA ATGGCCTCCT CCCTTAGCTC CCTGTTCTTG GATCTGCCAT GGAGGGATCT GGTGCCTCCA GACATGTGCA CATGAGTCCA TATGGAGCTT TTCCTGATGT TCCACTCCAC TTTGTATAGA CATCTGCCCT GACTGAATGT GTTCTGTCAC TCAGCTTTGC TTCCGACACC TCTGTTTCCT CTTCCCCTTT CTCCTCGTAT GTGTGTTTAC CTAAACTATA TGCCATAAAC CTCAAGTTAT TCATTTTATT TTGTTTTCAT TTTGGGGTGA AGATTCAGTT TCAGTCTTTT GGATATAGGT TTCCAATTAA GTACATGGTC AAGTATTAAC AGCACAAGTG GTAGGTTAAC ATTAGAATAG GAATTGGTGT TGGGGGGGGG GTTTGCAAGA ATATTTTATT TTAATTTTTT GGATGAAATT TTTATCTATT ATATATTAAA CATTCTTGCT GCTGCGCTGC AAAGCCATAG CAGATTTGAG GCGCTGTTGA GGACTGAATT ACTCTCCAAG TTGAGAGATG TCTTTGGGTT AAATTAAAAG CCCTACCTAA AACTGAGGTG GGGATGGGGA GAGCCTTTGC CTCCACCATT CCCACCCACC CTCCCCTTAA ACCCTCTGCC TTTGAAAGTA GATCATGTTC ACTGCAATGC TGGACACTAC AGGTATCTGT CCCTGGGCCA GCAGGGACCT CTGAAGCCTT CTTTGTGGCC TTTTTTTTTT TTCATCCTGT GGTTTTTCTA ATGGACTTTC AGGAATTTTG TAATCTCATA ACTTTCCAAG CTCCACCACT TCCTAAATCT TAAGAACTTT AATTGACAGT TTCAATTGAA GGTGCTGTTT GTAGACTTAA CACCCAGTGA AAGCCCAGCC ATCATGACAA ATCCTTGAAT GTTCTCTTAA GAAAATGATG CTGGTCATCG CAGCTTCAGC ATCTCCTGTT TTTTGATGCT TGGCTCCCTC TGCTGATCTC AGTTTCCTGG CTTTTCCTCC CTCAGCCCCT TCTCACCCCT TTGCTGTCCT GTGTAGTGAT TTGGTGAGAA ATCGTTGCTG CACCCTTCCC CCAGCACCAT TTATGAGTCT CAAGTTTTAT TATTGCAATA AAAGTGCTTT ATGCCCGAAT TC GCCGCCGCCA TGGGAGTGCA GGTGGAAACC ATCTCCCCAG GAGACGGGCG CACCTTCCCC AAGCGCGGCC AGACCTGCGT GGTGCACTAC ACCGGGATGC TTGAAGATGG AAAGAAATTT GATTCCTCCC GGGACAGAAA CAAGCCCTTT AAGTTTATGC TAGGCAAGCA GGAGGTGATC CGAGGCTGGG AAGAAGGGGT TGCCCAGATG AGTGTGGGTC AGAGAGCCAA ACTGACTATA TCTCCAGATT ATGCCTATGG TGCCACTGGG CACCCAGGCA TCATCCCACC ACATGCCACT CTCGTCTTCG ATGTGGAGCT TCTAAAACTG GAATGACAGG AATGGCCTCC TCCCTTAGCT CCCTGTTCTT GGATCTGCCR TGGAGGGATC TGGTGCCTCC AGACATGTGC ACATGARTCC ATATGGAGCT TTTCCTGATG TTCCACTCCA CTTTGTATAG ACATCTGCCC TGACTGAATG TGTTCTGTCA CTCAGCTTTG CTTCCGACAC CTCTGTTTCC TCTTCCCCTT TCTCCTCGTA TGTGTGTTTA CCTAAACTAT ATGCCATAAA CCTCAAGTTA TTCA-3' (FRAG. NO:_)(SEQ. ID NO:2499)

5'-GCCAGGTCGC TGTTGGTCCA CGCCGCCCGT CGCGCCGCCC GCCCGCTCAG CGTCCGCCGC CGCCATGGGA-3' (FRAG. No:_)(SEQ. ID NO: 2495)

5'-GGCCGGAGCC GAGCCGGGGT CGGGCAGCAG CAGGGACCCC CCAGAGGCGG GGCCTGTGGG ACCGCTATGG GCGTGGAGAT CGAGACCATC TCCCCCGGAG ACGGAAGGAC ATTCCCCAAG AAGGGCCAAA CGTGTGTGGT GCACTACACA GGAATGCTCC AAAATGGGAA GAAGTTTGAT TCATCCAGAG ACAGAAACAA ACCTTTCAAG TTCAGAATTG GCAAACAGGA AGTCATCAAA GGTTTTGAAG AGGGTGCAGC CCAGATGAGC TTGGGGCAGA GGGCGAAGCT GACCTGCACC CCTGATGTGG CATATGGAGC CACGGGCCAC CCCGGTGTCA TCCCTCCCAA TGCCACCCTC ATCTTTGACG TGGAGCTGCT CAACTTAGAG TGAAGGCAGG AAGGAACTCA AGGTGGCTGG AGATGGCTGC TGCTCACCCT CCTAGCCTGC TCTGCCACTG GGACGGCTCC TGCTTTTGGG GCTCTTGATC AGTGTGCTAA CCTCACTGCC TCATGGCATC ATCCATTCTC TCTGCCCAAG TTGCTCTGTA TGTGTTCGTC AGTGTTCATG CGAATTCTTG CTTGAGGAAA CTTCGGTTGC AGATTGAAGC ATTTCAGGTT GTGCATTTTG TGTGATGCAT GTAGTAGCCT TTCCTGATGA CAGAACACAG ATCTCTTGTT CGCACAATCT ACACTGCCTT ACCTTCACTT AAACCACACA CACAAGGTGC TCAGACATGA AATGTACATG GCGTACCGTA CACAGAGGGA CTTGAGCCAG TTACCTTTGC TGTCACTTTC TCTCTTATAA ATTCTGTTAG CTGCTCACTT AAACAATGTC CTCTTTGAGA AAATGTAAAA TAAAGGCTCT GTGCTTGACA-3' (FRAG. NO:_)(SEQ. ID NO:2496)

5'-GAATTCGGGC CGCCGCCAGG TCGCTGTTGG TCCACGCCGC CCGTCGCGCC GCCCGCCCGC TCAGCGTCCG CCGCCGCCAT GGGAGTGCAG GTGGAAACCA TCTCCCCAGG AGACGGGCGC ACCTTCCCCA AGCGCGGCCA GACCTGCGTG GTGCACTACA CCGGGATGCT TGAAGATGGA AAGAAATTTG ATTCCTCCCG GGACAGAAAC AAGCCCTTTA AGTTTATGCT AGGCAAGCAG GAGGTGATCC GAGGCTGGGA AGAAGGGGTT GCCCAGATGA GTGTGGGTCA GAGAGCCAAA CTGACTATAT CTCCAGATTA TGCCTATGGT GCCACTGGGC ACCCAGGCAT CATCCCACCA CATGCCACTC TCGTCTTCGA TGTGGAGCTT CTAAAACTGG AATGACAGGA ATGGCCTCCT CCCTTAGCTC CCTGTTCTTG GATCTGCCAT GGAGGGATCT GGTGCCTCCA GACATGTGCA CATGAGTCCA TATGGAGCTT TTCCTGATGT TCCACTCCAC TTTGTATAGA CATCTGCCCT GACTGAATGT GTTCTGTCAC TCAGCTTTGC TTCCGACACC TCTGTTTCCT CTTCCCCTTT CTCCTCGTAT GTGTGTTTAC CTAAACTATA TGCCATAAAC CTCAAGTTAT TCATTTTATT TTGTTTTCAT TTTGGGGTGA AGATTCAGTT TCAGTCTTTT GGATATAGGT TTCCAATTAA GTACATGGTC AAGTATTAAC AGCACAAGTG GTAGGTTAAC ATTAGAATAG GAATTGGTGT TGGGGGGGGG GTTTGCAAGA ATATTTTATT TTAATTTTTT GGATGAAATT TTTATCTATT ATATATTAAA CATTCTTGCT GCTGCGCTGC AAAGCCATAG CAGATTTGAG GCGCTGTTGA GGACTGAATT ACTCTCCAAG TTGAGAGATG TCTTTGGGTT AAATTAAAAG CCCTACCTAA AACTGAGGTG GGGATGGGGA GAGCCTTTGC CTCCACCATT CCCACCCACC CTCCCCTTAA ACCCTCTGCC TTTGAAAGTA GATCATGTTC ACTGCAATGC TGGACACTAC AGGTATCTGT CCCTGGGCCA GCAGGGACCT CTGAAGCCTT CTTTGTGGCC TTTTTTTTTT TTCATCCTGT GGTTTTTCTA ATGGACTTTC AGGAATTTTG TAATCTCATA ACTTTCCAAG CTCCACCACT TCCTAAATCT TAAGAACTTT AATTGACAGT TTCAATTGAA GGTGCTGTTT GTAGACTTAA CACCCAGTGA AAGCCCAGCC ATCATGACAA ATCCTTGAAT GTTCTCTTAA GAAAATGATG CTGGTCATCG CAGCTTCAGC ATCTCCTGTT TTTTGATGCT TGGCTCCCTC TGCTGATCTC AGTTTCCTGG CTTTTCCTCC CTCAGCCCCT TCTCACCCCT TTGCTGTCCT GTGTAGTGAT TTGGTGAGAA ATCGTTGCTG CACCCTTCCC CCAGCACCAT TTATGAGTCT CAAGTTTTAT TATTGCAATA AAAGTGCTTT ATGCCCGAAT TC-3' (FRAG. NO:_)(SEQ. ID NO:2497)

5' GCCGCCGCCA TGGGAGTGCA GGTGGAAACC ATCTCCCCAG GAGACGGGCG CACCTTCCCC AAGCGCGGCC AGACCTGCGT GGTGCACTAC ACCGGGATGC TTGAAGATGG AAAGAAATTT GATTCCTCCC GGGACAGAAA CAAGCCCTTT AAGTTTATGC TAGGCAAGCA GGAGGTGATC CGAGGCTGGG AAGAAGGGGT TGCCCAGATG AGTGTGGGTC AGAGAGCCAA ACTGACTATA TCTCCAGATT ATGCCTATGG TGCCACTGGG CACCCAGGCA TCATCCCACC ACATGCCACT CTCGTCTTCG

ATGTGGAGCT TCTAAAACTG GAATGACAGG AATGGCCTCC TCCCTTAGCT CCCTGTTCTT GGATCTGCCR TGGAGGGATC TGGTGCCTCC AGACATGTGC ACATGARTCC ATATGGAGCT TTTCCTGATG TTCCACTCCA CTTTGTATAG ACATCTGCCC TGACTGAATG TGTTCTGTCA CTCAGCTTTG CTTCCGACAC CTCTGTTTCC TCTTCCCCTT TCTCCTCGTA TGTGTGTTTA CCTAAACTAT ATGCCATAAA CCTCAAGTTA TTCA-3' (FRAG. NO:_)(SEQ. ID NO:2498)

The present agents are also pr vided as a pharmaceutical composition comprising an anti-sense oligonucleotide as given above in an amount effective to reduce expression of a target mRNA, by passing through a cell membrane and binding specifically with target mRNA in the cell so as to prevent its translation are another aspect of the present invention. Such compositions are pr vided in a suitable pharmaceutically acceptable carrier, e.g. sterile pyrogen-free saline solution. The agent of the invention may be formulated with a hydrophobic carrier capable of passing through a cell membrane, e.g. in a liposome, with the liposomes carried in a pharmaceutically acceptable aqueous carrier. The oligonucleotides may be coupled to an agent which inactivates mRNA, such as a ribozyme. Such oligonucleotides may be administered to a subject in need of such treatment to inhibit the activation of A_1, A_{2b} and/or A_3 adenosine receptors. The pharmaceutical formulation may also comprise chimeric molecules comprising anti-sense oligonucleotides attached to molecules which are known to be internalized by cells. These oligonucleotide conjugates utilize cellular up-take pathways to increase intracellular concentrations of the oligonucleotide. Examples of molecules used in this manner are macromolecules including transferrin, asialoglycoprotein (bound to oligonucleotides via polylysine) and streptavidin, among others.

The anti-sense compound may be contained in the pharmaceutical formulation within a lipid particle or vesicle, such as a liposome or microcrystal. The particles may be of any suitable structure, such as unilamellar or plurilamellar. The one preferred embodiment, the anti-sense oligonucleotide is comprised within the liposome. Positively charged lipids such as N-[1-(2, 3 -dioleoyloxi) propyl] -N, N, N-trimethylammoniumethylsulfate, or "DOTAP", are particularly preferred for such particles and vesicles. However, others are also suitable. The preparation of such lipid particles is well known. See, e.g., US Patent Nos. 4,880,635 to Janoff et al., 4,906,477 to Kurono et al., 4,911,928 to Wallach, 4,917,951 to Wallach, 4,920,016 to Allen et al., 4,921,757 to Wheatley et al., the relevant sections of all of which are herein incoporated in their entireties by reference. The composition of the invention may be administered by any means which transports the agent to the lung(s). The present agent(s) may be administered to the lungs of a patient by any suitable means, but are preferably administered through the respiratory system as a respirable formulation, more preferably in the form of an aerosol comprising respirable particles which, in turn, comprise the agent for respiration or inhalation by the subject. The respirable particles may be in gaseous, liquid or solid form, and they may, optionally, contain other therapeutic ingredients and formulation components. The particles of the present invention are preferably particles of respirable size, preferably of a size sufficiently small to pass, upon inhalation, through the mouth and larynx and into the bronchi and alveoli of the lungs. In general, particles ranging from about 0.5 to 10 microns in diameter are respirable. However, other sizes may also be suitable. Particles of non-respirable size, of considerably larger diameter, which are included in the respirable formulation tend to deposit in the throat and may be swallowed. Accordingly, it is desirable to minimize the quantity of non-respirable particles in the aerosol. For nasal administration, a particle size in the range of 10-500 :m is preferred to ensure their retention in the nasal cavity. Liquid pharmaceutical compositions of the agent of the invention for producing a respirable formulation, e.g. an aerosol may be prepared by combining the anti-sense oligo with a suitable vehicle or carrier, such as sterile pyrogen-free water and/or other known pharmaceutically or veterinarily acceptable carrier. Other therapeutic compounds may be included as well as other formulation ingredients as is known in the art. Solid particulate compositions comprising respirable dry particles of, e.g. the micronized agent of the invention may be prepared by grinding the dry anti-sense compound with a mortar and pestle, and then passing the thus ground, e.g. micronized composition through a screen, e.g. 400 mesh screen, to break up or separate large agglomerates of particles. A solid particulate composition comprising the anti-sense compound may optionally also comprise a dispersant and other known agents, which serve to facilitate the formation of a mist or aerosol. A suitable dispersant is lactose, which may be blended with the anti-sense compound in any suitable ratio, about 1:1 w/w. Other ratios may be utilized as well, and other therapeutic and formulation agents may also be included.

The dosage of the anti-sense comp und administered generally varies with the disease being treated, the c ndition of the subject, the particular formulation, the r ute of administration, the timing of administrati n to a subject, etc. In general, it is desirable to attain intracellular concentrations of the oligonucleotide of fr m 0.05 to 50 :M, or m re particularly 0.2 to 5 :M, although not critical. For administration to a subject such as a human, a dosage of from about .01, preferably about 0.01, more preferably about 1 mg/Kg, to about 150, preferably about

100, and still more preferably about 50 mg/Kg are typically employed. Higher and lower doses may als be administered as an artisan will see suitable for specific application. These amounts are preferably administered every 24 hrs, although other regimens are also suitable. Depending on the s lubility of the particular formulation of active c mpound administered, a daily dose may be divided among one or several unit dose administrations. Administration of the anti-sense compounds may be carried out therapeutically, i.e. as a rescue treatment, pr phylactically, or as a chronic maintenance regimen.

Aerosols of liquid particles comprising the agent may be produced by any suitable means, such as with an insufflator or nebulizer. See, e.g., US Patent No. 4,501,729. Nebulizers are commercially available devices which transform solutions or suspensions of an agent into a therapeutic aerosol mist either by means of acceleration of a compressed gas, typically air or oxygen, e.g. through a narrow venturi orifice or by means of ultrasonic agitation. Suitable formulations for use in insufflators and nebulizers comprise the present agent, the agent of this invention, in an amount of about 0.01 to about 40%, preferably less than 20% w/w in a liquid carrier which is typically water or a dilute aqueous alcoholic solution, preferably made isotonic with body fluids by the addition of, for example, sodium chloride. Other carriers are also suitable. Optional additives include preservatives if the formulation is n t prepared sterile, for example, methyl hydroxybenzoate, antioxidants, flavoring agents, volatile oils, buffering agents and surfactants, among others.

The pharmaceutical compositions provided herein comprise nucleic acid(s) comprising the anti-sense oligonucleotide(s) described above and one or more surfactants. Suitable surfactants or surfactant components for enhancing the uptake of the anti-sense oligonucleotides of the invention include synthetic and natural as well as full and truncated forms of surfactant protein A, surfactant protein B, surfactant protein C, surfactant protein D and surfactant Protein E, di-saturated phosphatidylcholine (other than dipalmitoyl), dipalmitoylphosphatidylcholine, phosphatidylcholine, phosphatidylglycerol, phosphatidylinositol, phosphatidylethanolamine, phosphatidylserine; phosphatidic acid, ubiquinones, lysophosphatidylethanolamine, lysophosphatidylcholine, palmitoyl-lysophosphatidylcholine, dehydroepiandrosterone, dolichols, sulfatidic acid, glycerol-3-phosphate, dihydroxyacetone phosphate, glycerol, glycero-3-phosphocholine, dihydroxyacetone, palmitate, cytidine diphosphate (CDP) diacylglycerol, CDP choline, choline, choline phosphate; as well as natural and artificial lamelar bodies which are the natural carrier vehicles for the components of surfactant, omega-3 fatty acids, polyenic acid, polyenoic acid, lecithin, palmitinic acid, non-ionic block copolymers of ethylene or propylene oxides, polyoxypropylene, monomeric and polymeric, polyoxyethylene, monomeric and polymeric, poly (vinyl amine) with dextran and/or alkanoyl side chains, Brij 35, Triton X-100 and synthetic surfactants ALEC, Exosurf, Survan and Atovaquone, among others. These surfactants may be useed either as single or part of a multiple component surfactant in a formulation, or as covalently bound additions to the 5' and/or 3' ends ofthe anti-sense oligonucleotides (oligos).

The composition of the invention may be administered by any means which transports the anti-sense nucleotide and the surfactant composition to the lung. The antisense compounds disclosed herein may be administered to the lungs of a patient by any suitable means, but are preferably administered by inhalation of an aerosol comprised of respirable particles which comprise the anti-sense compound. The respirable particles may be liquid or solid, and they may optionally contain other therapeutic or diagnostic ingredients as well as other typical ingredients for a particular formulation. Examples of other agents are analgesics such as acetominophen, anilerdine, aspirin, buprenorphine, butabital, butorpphanol, Choline Salicylate, Codeine, Dezocine, Diclofenac, Diflunisal, Dihydrocodeine, Elcatoninin, Etodolac, Fenoprofen, Hydrocodone, Hydromorphone, Ibuprofen, Ketoprofen, Ketorolac, Levorphanol, Magnesium Salicylate, Meclofenamate, Mefenamic Acid, Meperidine, Methadone, Methotrimeprazine, Morphine, Nalbuphine, Naproxen, Opium, Oxycodone, Oxymorphone, Pentazocine, Phenobarbital, Propoxyphene, Salsalate, Sodium Salicylate, Tramadol and Narcotic analgesics in addition to those listed above. See, Mosby's Physician's GenRx. Anti- anxiety agents are also useful including Alprazolam, Bromazepam, Buspirone, Chlordiazepoxide, Chlormezanone, Clorazepate, Diazepam, Halazepam, Hydroxyzine, Ketaszolam, Lorazepam, Meprobamate, Oxazepam and Prazepam, among others. Anti-anxiety agents associated with mental depression, such as Chlordiazepoxide, Amitriptyline, Loxapine Maprotiline and Perphenazine, among others. Anti-inflammatory agents such as non-rheumatic Aspirin, Choline Salicylate, Diclofenac, Diflunisal, Etodolac, Fenoprofen, Floctafenine, Flurbiprofen, Ibuprofen, Ind methacin, Ketoprofen, Magnesium Salicylate, Meclofenamate, Mefenamic Acid, Nabumetone, Naproxen, Oxaprozin, Phenylbutaz ne, Piroxicam, Salsalate, Sodium Salicylate, Sulindac, Tenoxicam, Tiaprofenic Acid, T lmetin, anti-inflammatories for

ocular treatment such as Diclofenac, Flurbiprofen, Indomethacin, Ketorolac, Rimexolone (generally for post-operative treatment), anti-inflammatories for, non-infectious nasal applications such as Beclomethaxone, Budes nide, Dexamethasone, Flunisolide, Triamcinolone, and the like. Soporifics (anti-insomnia/sleep inducing agents) such as those utilized for treatment of insomnia, including Alprazolam, Bromazepam, Diazepam, Diphenhydramine, Doxylamine, Estaz lam, Flurazepam, Halazepam, Ketazolam, Lorazepam, Nitrazepam, Prazepam Quazepam, Temazepam, Triazolam, Zolpidem and Sopiclone, among others. Sedatives including Diphenhydramine, Hydroxyzine, Methotrimeprazine, Promethazine, Propofol, Melatonin, Trimeprazine, and the like. Sedatives and agents used for treatment of petit mal and tremors, among other conditions, such as Amitriptyline HCl; Chlordiazepoxide, Amobarbital; Secobarbital, Aprobarbital, Butabarbital, Ethchiorvynol, Glutethimide, L-Tryptophan, Mephobarbital, MethoHexital Na, Midazolam Hcl, Oxazepam, Pentobarbital Na, Phenobarbital, Secobarbital Na, Thiamylal Na, and many others. Agents used in the treatment of head trauma (Brain Injury/Ischemia), such as Enadoline HCl (e.g. for treatment of severe head injury; orphan status, Warner Lambert), cytoprotective agents, and agents for the treatment of menopause, menopausal symptoms (treatment), e.g. Ergotamine, Belladonna Alkaloids and Phenobarbital, for the treatment of menopausal vasomotor sympt ms, e.g. Clonidine, Conjugated Estrogens and Medroxyprogesterone, Estradiol, Estradiol Cypionate, Estradiol Valerate, Estrogens, conjugated Estrogens, esterified Estrone, Estropipate, and Ethinyl Estradiol. Examples of agents for treatment of pre menstrual syndrome (PMS) are Progesterone, Progestin, Gonadotrophic Releasing Hormone, Oral contraceptives, Danazol, Luprolide Acetate, Vitamin B6. Examples of agents for treatment of emotional/psychiatric treatments such as Tricyclic Antidepressants, including Amitriptyline HCl (Elavil), Amitriptyline HCl, Perphenazine (Triavil) and Doxepin HCl (Sinequan). Examples of tranquilizers, anti-depressants and anti-anxiety agents are Diazepam (Valium), Lorazepam (Ativan), Alprazolam (Xanax), SSRI's (selective Ssrotonin reuptake inhibitors), Fluoxetine HCl (Prozac), Sertaline HCl (Zoloft), Paroxetine HCl (Paxil), Fluvoxamine Maleate (Luvox), Venlafaxine HCl (Effexor), Serotonin, Serotonin Agonists (Fenfluramine), and other over the counter (OTC) medications.

The composition of the present invention may be administered into the respiratory system as a formulation including particles of respirable size, e.g. particles of a size sufficiently small to pass through the nose, mouth and larynx upon inhalation and through the bronchi and alveoli of the lungs. In general, respirable particles range from about .5 to 10 microns in size. Particles of non-respirable size which are included in the aerosol tend to deposit in the throat and be swallowed, and the quantity of non-respirable particles in the aerosol is thus minimized. For nasal administration, a particle size in the range of 10-500 :m is preferred to ensure retention in the nasal cavity. Aerosols or mists of solid particles comprising the agent of the invention may likewise be produced with any device that generates solid particulate medicament aerosols or mists. Aerosol and mist generators are suitable for administering solid particulate medicaments. These devices produce respirable particles, as explained above., and generate a volume of aerosol or mist containing a predetermined metered dose of a medicament at a rate suitable for human or animal administration. One illustrative type of solid particulate aerosol generator is an insufflator. Suitable formulations for administration by insufflation include finely comminuted powders which may be delivered by means of an insufflator or taken into the nasal cavity in the manner of a snuff. In the insufflator, the powder, e.g. a metered dose of the agent effective to carry out the treatments described herein, is contained in a capsule r a cartridge. These capsules or cartridges are typically made of gelatin or plastic, and may be pierced or opened in situ, and the powder delivered by air drawn through the device upon inhalation or by means of a manually-operated pump. The powder employed in the insufflator may consist either solely of the agent or of a powder blend comprising the agent, a suitable powder diluent, such as lactose, and an optional surfactant as well as other agents. The agent typically comprises from 0.01 to 100 w/w of the formulation. A second type of illustrative aerosol generator comprises a metered dose inhaler. Metered dose inhalers are pressurized aerosol dispensers, typically comprising a suspension or solution formulation of the active ingredient in a liquified propellant. During use these devices discharge the formulation through a valve adapted to deliver a metered volume, typically about 10 to 150 :l, although other volumes are also suitable, to produce a fine particle spray containing the active ingredient. Suitable propellants include solvents such as certain chlorofluorocarbon compounds, for example, dichlorodifluoromethane, trichloroflu romethane, dichlorotetrafluoroethane and/or mixtures thereof. The formulation may additionally comprise one or more co-solvents, for example, ethanol, surfactants, such as oleic acid or sorbitan trioleate, antioxidants and suitable flavoring agents. The aerosol, whether f rmed from solid or liquid particles, may be produced by the aerosol generator at a rate of from about 10 to 150 liters per minute, more preferably from about

30 t 150 liters per minute, and most preferably about 60 liters per minute. Aerosols containing greater am unts f medicament may be administered more rapidly.

The foll wing examples are provided to illustrate the present invention, and should not be construed as limiting there n. In these examples, :M means micromolar, ml means milliliters, :M means micrometers, mm means millimeters, cm means centimeters, EC means degrees Celsius, :g means micr grams, mg means milligrams, g means grams, kg means kilograms, M means molar, and h means hours.

EXAMPLES

Example 1: Design and Synthesis of Anti-sense Oligonucleotides

The design of anti-sense oligonucleotides against the A_1 and A_3 adenosine receptors may require the solution of the complex secondary structure of the target A_1 receptor mRNA and the target A_3 receptor mRNA. After generating this structure, anti-sense nucleotide are designed which target regions of mRNA which might be construed to confer functional activity or stability to the mRNA and which optimally may overlap the initiation codon. Other target sites are readily usable. As a demonstration of specificity of the anti-sense effect, other oligonucleotides not totally complementary to the target mRNA, but containing identical nucleotide compositions on a w/w basis, are included as controls in anti-sense experiments. The mRNA secondary structure of the adenosine A_1 receptor was analyzed and used as described above. to design a phosphorothioate anti-sense oligonucle tide. The anti-sense oligonucleotide which was synthesized was designated HAdA$_1$AS and had the following sequence: **5' -GAT GGA GGG CGG CAT GGC GGG-3' (SEQ ID NO:1).** As a control, a mismatched phosphorothioate anti-sense nucleotide designated HAdAlMM1 was synthesized with the following sequence: **5' -GTA GCA GGC GGG GAT GGG GGC-3' (SEQ ID NO:2).** Each oligonucleotide had identical base content and general sequence structure. Homology searches in GENBANK (release 85.0) and EMBL (release 40.0) indicated that the anti-sense oligonucleotide was specific for the human and rabbit adenosine A_1 receptor genes, and that the mismatched control was not a candidate for hybridization with any known gene sequence.

The secondary structure of the adenosine A_3 receptor mRNA was similarly analyzed and used as described above to design two phosphorothioate anti-sense oligonucleotides. The first anti-sense oligonucleotide (HAdA3AS1) synthesized had the following sequence: **5'-GTT GTT GGG CAT CTT GCC-3' (SEQ ID NO:3).** As a control, a mismatched phosphorothioate anti-sense oligonucleotide (HAdA3MM1) was synthesized, having the following sequence: **5'-GTA CTT GCG GAT CTA GGC-3' (SEQ ID NO:4).** A second phosphorothi ate anti-sense oligonucleotide (HAdA3AS2) was also designed and synthesized, having the following sequence: **5'-GTG GGC CTA GCT CTC GCC-3' (SEQ ID NO:5).** Its control oligonucleotide (HAdA3MM2) had the sequence: **5'-GTC GGG GTA CCT GTC GGC-3' (SEQ ID NO:6).** Phosphorothioate oligonucleotides were synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (DuPont, MD).

Example 2: In Vivo Testing of Adenosine A_1 Receptor Anti-sense Oligos

The anti-sense oligonucleotide against the human A_1 receptor (**SEQ ID NO:1**) described above. was tested for efficacy in an in vitro model utilizing lung adenocarcinoma cells HTB-54. HTB-54 lung adenocarcinoma cells were demonstrated to express the A_1 adenosine receptor using standard northern blotting procedures and receptor probes designed and synthesized in the laboratory. HTB-54 human lung adenocarcinoma cells (106/100 mm tissue culture dish) were exposed to 5.0 :M HAdAlAS or HAdAlMM1 for 24 hours, with a fresh change of media and oligonucleotides after 12 hours of incubation. Following 24 hour exposure to the oligonucleotides, cells were harvested and their RNA extracted by standard procedures. A 21-mer probe corresponding to the region of mRNA targeted by the anti-sense (and therefore having the same sequence as the anti-sense, but not phosphorothioated) was synthesized and used to probe northern blots of RNA prepared from HAdAlAS-treated, HAdAlMM1-treated and non-treated HTB-54 cells. These blots showed clearly that HAdAlAS but not HAdAlMM1 effectively reduced human adenosine receptor mRNA by >50%. This result showed that HAdAlAS is a good candidate for an anti-asthma drug since it depletes intracellular mRNA for the adenosine A_1 receptor, which is involved in asthma.

Example 3: In Vivo Efficacy of Adenosine A_1 Receptor Anti-sense Olig s

A fortuit us homology between the rabbit and human DNA sequences within the adenosine A_1 gene overlapping the initiation codon permitted the use f the phosphorothioate anti-sense oligonucleotides initially designed for use against the human adenosine A_1 receptor in a rabbit model. Ne natal New Zealand white Pasteurella-free rabbits were immunized intraperitoneally within 24 hours of birth with 312 antigen units/ml house dustmite (D. farinae) extract (Berkeley Biologicals, Berkeley, CA), mixed with 10% kaolin. Immunizations were

repeated weekly for the first month and then biweekly for the next 2 months. At 3-4 months of age, eight sensitized rabbits were anesthetized and relaxed with a mixture of ketamine hydrochloride (44 mg/kg) and acepromazine maleate (0.4 mg/kg) administered intramuscularly. The rabbits were then laid supine in a comfortable position on a small molded, padded animal board and intubated with a 4.0-mm intratracheal tube (Mallinkrodt, Inc., Glens Falls, NY). A polyethylene catheter of external diameter 2.4 mm with an attached latex balloon was passed into the esophagus and maintained at the same distance (approximately 16 cm) from the mouth throughout the experiments. The intratracheal tube was attached to a heated Fleisch pneumotachograph (size 00; DOM Medical, Richmond, VA), and flow was measured using a Validyne differential pressure transducer (Model DP-45161927; Validyne Engineering Corp., Northridge, CA) driven by a Gould carrier amplifier (Model 11-4113; Gould Electronic, Cleveland, OH). The esophageal balloon was attached to one side of the differential pressure transducer, and the outflow of the intratracheal tube was connected to the opposite side of the pressure transducer to allow recording of transpulmonary pressure. Flow was integrated to give a continuous tidal volume, and measurements of total lung resistance (RL) and dynamic compliance (Cdyn) were calculated at isovolumetric and flow zero points, respectively, using an automated respiratory analyzer (Model 6; Buxco, Sharon, CT). Animals were randomized and on Day 1 pretreatment values for PC50 were obtained for aerosolized adenosine. Anti-sense (HAdAlAS) or mismatched control (HAdAlMM) oligonucleotides were dissolved in sterile physiological saline at a concentration of 5000 :g (5 mg) per 1.0 ml. Animals were subsequently administered the aerosolized anti-sense or mismatch oligonucleotide via the intratracheal tube (approximately 5000 :g in a volume of 1.0 ml), twice daily for two days. Aerosols of either saline, adenosine, or anti-sense or mismatch oligonucleotides were generated by an ultrasonic nebulizer (DeVilbiss, Somerset, PA), producing aerosol droplets 80% of which were smaller than 5 :m in diameter. In the first arm of the experiment, four randomly selected allergic rabbits were administered anti-sense oligonucleotide and four the mismatched control oligonucleotide. On the morning of the third day, PC50 values (the concentration of aerosolized adenosine in mg/ml required to reduce the dynamic compliance of the bronchial airway 50% from the baseline value) were obtained and compared to PC50 values obtained for these animals pri r to exposure to oligonucleotide. Following a 1 week interval, animals were crossed over, with those previously administered mismatch control oligonucleotide now administered anti-sense oligonucleotide, and those previously treated with anti-sense oligonucleotide now administered mismatch control oligonucleotide. Treatment methods and measurements were identical to those employed in the first arm of the experiment. It should be noted that in six of the eight animals treated with anti-sense oligonucleotide, adenosine-mediated bronchoconstriction could not be obtained up to the limit of solubility of adenosine, 20 mg/ml. For the purpose of calculation, PC50 values for these animals were set at 20 mg/ml. The values given therefore represent a minimum figure for anti-sense effectiveness. Actual effectiveness was higher. The results of this experiment are illustrated in Table 3 below.

Table 3: **Effect of Adenosine A_1 Receptor Anti-sense Oligo upon PC50 Values in Asthmatic Rabbits**

Mismatch Control		A_1 Receptor Anti-sense Oligo	
Pre Oligonucleotide	**Post Oligonucleotide**	**Pre Oligonucleotide**	**Post Oligonucleotide**
3.56 $\pm$ 1.02	5.16 $\pm$ 1.03	2.36 $\pm$ 0.68	>19.5 $\pm$ 0.34**

The results are presented as the mean (n=8) $\pm$ SEM.
The significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected test.
**Significantly different from all other groups, $p<0.01$.

In both arms of the experiment, animals receiving the anti-sense oligonucleotide showed an order of magnitude increase in the dose of aerosolized adenosine required to reduce dynamic compliance of the lung by 50%. No effect of the mismatched control oligonucleotide upon PC50 values was observed. No toxicity was observed in any animal receiving either anti-sense or control inhaled oligonucleotide. These results show clearly that the lung has exceptional potential as a target for anti-sense oligonucleotide-based therapeutic intervention in lung disease. They further show, in a model system which closely resembles human asthma, that downregulation of the adenosine A_1 receptor largely eliminates adenosine-mediated bronchoconstriction in asthmatic airways. Bronchial hyperresp nsiveness in the allergic rabbit model of human asthma is an excellent endpoint for anti-sense intervention since the tissues involved in this response lie near to the point of contact with aerosolized oligonucleotides, and the model closely simulates an important human disease.

Example 4: **Specificity of A_1-adenosine Receptor Anti-sense Oligonucleotide**

At the conclusion of the cross-over experiment of Example 3 above, airway smo th muscle from all rabbits was quantitatively analyzed for aden sine A_1 receptor number. As a control for the specificity of the anti-sense oligonucleotide, adenosine A_2 receptors, which sh uld n t have been affected, were also quantified. Airway smooth muscle tissue was dissected from each rabbit and a membrane fraction prepared according to the method of Kleinstein et al. (Kleinstein, J. and Glossmann, H., Naunyn-Schmiedeberg's Arch. Pharmac l. 305: 191-200 (1978)), the relevant portion of which is hereby incorporated in its entirety by r ference, with slight modifications. Crude plasma membrane preparations were stored at 70EC until the time of assay. Protein content was determined by the method of Bradford (M. Bradford, Anal. Biochem. 72, 240-254 (1976), the relevant portion of which is hereby incorporated in its entirety by reference). Frozen plasma membranes were thawed at room temperature and were incubated with 0.2 U/ml adenosine deaminase for 30 minutes at 37EC to remove endogenous adenosine. The binding of [^{3}H] DPCPX (A_1 receptor-specific) or [^{3}H] CGS-21680 (A_1 receptor-specific) was measured as previously described by Ali et al. (Ali, S. et al., J. Pharmacol. Exp. Ther. 268, Am. J. Physiol 266, L271-277 (1994), the relevant portion of which is hereby incorporated in its entirety by reference). The animals treated with adenosine A_1 anti-sense oligonucleotide in the cross-over experiment had a nearly 75% decrease in A_1 receptor number compared to controls, as assayed by specific binding of the A_1-specific antagonist DPCPX. There was no change in adenosine A_2 receptor number, as assayed by specific binding of the A_2 receptor-specific agonist 2- [p-(2-carboxyethyl)-phenethylamino] -5' - (N-ethylcarboxamido) adenosine (CGS-21680). This is illustrated in Table 4 below.

Table 4: Specificity of Action of Adenosine A_1 Receptor Anti-sense Oligonucleotide

	Mismatch Control Oligonucleotide	A_1 Anti-sense Oligonucleotide
A_1-Specific Binding	1105 ± 48**	293 ± 18
A_2-Specific Binding	302 ± 22	442 ± 171

The results are presented as the mean (n = 8) ± SEM.
The significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected test.
**Significantly different from mismatch control, p<0.01.

The above results illustrate the effectiveness of anti-sense oligonucleotides in treating airway disease. Since the anti-sense oligos described above. eliminate the receptor systems responsible for adenosine-mediated bronchoconstriction, it may be less imperative to eliminate adenosine from them. However, it would be preferable to eliminate adenosine from even these oligonucleotides to reduce the dose needed to attain a similar effect. Described above are other anti-sense oligonucleotides targeting mRNA of proteins involved in inflammation. Adenosine has been eliminated from their nucleotide content to prevent its liberation during degradation.

Example 5: Anti-sense Oligos directed to other Target Nucleic Acids

This work was conducted to demonstrate that the present invention is broadly applicable to anti-sense oligonucleotides ("oligos") specific to nucleic acid targets broadly. The following experimental studies were conducted to show that the method of the invention is broadly suitable for use with anti-sense oligos designed as taught by this application and targeted to any and all adenosine receptor mRNAs. For this purpose, various anti-sense oligos were porepared to adenosine receptor mRNAs exemplified by the adenosine A_1, A_{2b} and A_3 receptor mRNAs. Anti-sense Oligo I was disclosed above (**SEQ. ID NO:1**).Five additional anti-sense phosphorothioate oligos were designed asnd synthesized as indicated above.

1- Oligo II (**SEQ. ID NO: 7**) also targeted to the adenosine A_1 receptor, but to a different region than Oligo I.
2- Oligo V (**SEQ. ID NO: 10**) targeted to the adenosine A_{2b} receptor.
3- Oligos III (**SEQ. ID NO: 8**) and IV (**SEQ. ID NO: 9**) targeted to different regions of the adenosine A_3 receptor.
4- Oligo I-PD (**SEQ. ID NO: 1681**)(a phosphodiester oligo of the same sequence as Oligo I).

These anti-sense oligos were designed for therapy on a selected species as described above and are generally specific f r that species, unless the segment of the target mRNA of other species happens to contain a similar sequences. All anti-sense ligos were prepared as described below, and tested in vivo in a rabbit model for bronchoconstriction, inflammation and allergy, which have breathing difficulties and impeded lung airways, as is the case in ailments such as asthma, as described in the above-identified application.

Example 6: Design & Sequences of other Anti-sense Oligos

Six oligos and their effects in a rabbit model were studied and the results of these studies are reported and discussed below. Five of these oligos were selected f r this study to complement the data on Oligo I (**SEQ ID NO: 1**) provided in Examples 1 to 4 above. This oligo is anti-sense to one region f the aden sine A_1 receptor mRNA. The oligos tested are identified as anti-sense Oligos I (**SEQ ID NO: 1**) and II (**SEQ. ID No: 7**) targeted to a different region of the adenosine A_1 receptor mRNA, Oligo V (**SEQ. ID N :8**) targeted to the adenosine A_{2b} receptor mRNA, and anti-sense Oligos III and IV (**SEQ. ID NOS: 9 and 10**) targeted to two different regions of the adenosine A_3 receptor mRNA. The sixth ligo (Oligo I-PD) is a phosphodiester version of Oligo I (**SEQ. ID NO:1**). The design and synthesis of these anti-sense oligos was performed in accordance with Example 1 above.

(I) Anti-sense Oligo I: The anti-sense oligonucleotide I referred to in Examples 1 to 4 above is targeted to the human A_1 adenosine receptor mRNA (EPI 2010). Anti-sense oligo I is 21 nucleotide long, overlaps the initiation codon, and has the following sequence: 5'- GAT GGA GGG CGG CAT GGC GGG -3' (:**SEQ. ID No 1**). The oligo I was previously shown to abrogate the adenosine-induced bronchoconstriction in allergic rabbits, and to reduce allergen-induced airway obstruction and bronchial hyperresponsiveness (BHR), as discussed above and shown by Nyce, J. W. & Metzger, W. J., Nature, 385:721 (1977), the relevant portions of which reference are incorporated in their entireties herein by reference.

(II) Anti-sense Oligo II: A phosphorothioate anti-sense oligo (**SEQ. ID NO:7**) was designed in accordance with the invention to target the rabbit adenosine A_1 receptor mRNA region +936 to +956 relative to the initiation codon (start site). The anti-sense oligo II is 21 nucleotide long, and has the following sequence: **5'-CTC GTC GCC GTC GCC GGC GGG-3' (SEQ. ID NO:7).**

(III) Anti-sense Oligo III: A phosphorothioate anti-sense oligo other than that provided in Example 1 above (**SEQ. ID NO:8**) was designed in accordance with the invention to target the anti-sense A_3 receptor mRNA region +3 to + 22 relative to the initiation codon start site. The anti-sense oligo III is 20 nucleotide long, and has the following sequence: **5'-GGG TGG TGC TAT TGT CGG GC-3' (SEQ. ID NO:8).**

(IV) Anti-sense Oligo IV: Yet another phosphorothioate anti-sense oligo (**SEQ. ID NO:9**) was designed in accordance with the invention to target the adenosine A_3 receptor mRNA region + 386 to + 401 relative to the initiation codon (start site). The anti-sense oligo IV is 15 nucleotide long, and has the following sequence: **5'-GGC CCA GGG CCA GCC-3' (SEQ. ID NO:9).**

(V) Anti-sense Oligo V: A phosphorothioate anti-sense oligo (**SEQ. ID NO:10**) was designed in accordance with the invention to target the adenosine A_{2b} receptor mRNA region -21 to -1 relative to the initiation codon (start site). The anti-sense oligonucleotide V is 21 nucleotide long, and has the following sequence: **5'-GGC CGG GCC AGC CGG GCC CGG-3' (SEQ. ID NO:10).**

(VI) A_1 Mismatch Oligos: Two different mismatched oligonucleotides having the following sequences were used as controls for anti-sense oligo I (**SEQ. ID NO: 1**) described in Example 5 above.

A_1MM2 **5'-GTA GGT GGC GGG CAA GGC GGG-3' (SEQ. ID NO:1682)**

A_1MM3 **5'-GAT GGA GGC GGG CAT GGC GGG-3' (SEQ. ID NO:1683)**

Anti-sense oligo I and the two mismatch anti-sense oligos had identical base content and general sequence structure. Homology searches in GENBANK (release 85.0) and EMBL (release 40.0) indicated that the anti-sense oligo I was specific, not only for the human, but also for the rabbit, adenosine A_1 receptor genes, and that the mismatched controls were not candidates for hybridization with any known human or animal gene sequence.

(VII) Anti-sense Oligo A_1-PD (Oligo VI): A phosphodiester anti-sense oligo (**Oligo VI; SEQ. ID NO:1681**) having the same nucleotide sequence as Oligo I was designed as disclosed in the above-identified application. Anti-sense oligo I-PD is 21 nucleotide long, overlaps the initiation codon, and has the following sequence:

5'- GAT GGA GGG CGG CAT GGC GGG -3' **(SEQ. ID NO:1681)**

(VIII) Controls: Each rabbit was administered 5.0 ml aerosolized sterile saline following the same schedule as for the anti-sense oligos in (II), (III), and (IV) above.

<u>Example 7</u>: Synthesis of Anti-sense Oligos

Phosphorothioate anti-sense oligos having the sequences described in (a) above, were synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (DuPont, DE). TETD (tetraethylthiuram disulfide) was used as the sulfurizing agent during the synthesis. Anti-sense oligonucle tide II (**SEQ. ID NO:7**), anti-sense oligonucleotide III (**SEQ. ID NO: 8**) and anti-sense oligonucleotide IV (**SEQ. ID NO: 9**) were each synthesized and purified in this manner.

<u>Example 8</u>: Preparati n of Allergic Rabbits

Neonatal New Zealand white Pasturella-free rabbits were immunized intraperitoneally within 24 hours of birth with 0.5 ml of 312 antigen units/ml house dust mite (D. *farinae*) extract (Berkeley Bi logicals, Berkeley, CA) mixed with 10% kaolin as previ usly described (Metzger, W. J., in Late Phase Allergic Reactions, Dorsch, W., Ed., CRC Handbook, pp. 347-362, CRC Press, Boca Raton (1990); Ali, S., Metzger, W. J. and Mustafa, S. J., Am. J. Resp. Crit. Care Med. 149: 908 (1994)), the relevant porti ns of which are incorporated in their entireties here by reference. Immunizati ns were repeated weekly for the first month and then biweekly until the age of 4 months. These rabbits preferentially produce allergen-specific IgE antibody, typically respond to aeroallergen challenge with both an early and late-phase asthmatic response, and show bronchial hyper responsiveness (BHR). Monthly intraperitoneal administration of allergen (312 units dust mite allergen, as above) continues to stimulate and maintain allergen-specific IgE antibody and BHR. At 4 months of age, sensitized rabbits were prepared for aerosol administration as described by Ali et al. (Ali, S., Metzger, W. J. and Mustafa, S. J., Am. J. Resp. Crit. Care Med. 149 (1994)), the relevant section being incorporated in its entirety here by reference.

DOSE-RESPONSE STUDIES

Example 9: Experimental Setup

Aerosols of either adenosine (0-20 mg/ml), or anti-sense or one of two mismatch oligonucleotides (5 mg/ml) were separately prepared with an ultrasonic nebulizer (Model 646, DeVilbiss, Somerset, PA), which produced aerosol droplets, 80% of which were smaller than 5:m in diameter. Equal volumes of the aerosols were administered directly to the lungs *via* an intratracheal tube. The animals were randomized, and administered aerosolized adenosine. Day 1 pre-treatment values for sensitivity to adenosine were calculated as the dose of adenosine causing a 50% loss of compliance (PC_{50} Adenosine). The animals were then administered either the aerosolized anti-sense or one of the mismatch anti-sense oligos via the intratracheal tube (5 mg/1.0 ml), for 2 minutes, twice daily for 2 days (total dose, 20 mg). Post-treatment PC_{50} values were recorded (post-treatment challenge) on the morning of the third day. The results of these studies are provided in Example 21 below.

Example 10: Crossover Experiments

For some experiments utilizing anti-sense oligo I (**SEQ ID NO: 1**) and a corresponding mismatch contr l oligonucleotide A1MM2, following a 2 week interval, the animals were crossed over, with those previously administered the mismatch control A_1MM2, now receiving the anti-sense oligo I, and those previously treated with the anti-sense oligo I, now receiving the mismatch control A_1MM2 oligo. The number of animals per group was as follows. For mismatch A_1MM2 (Control 1), n=7, since one animal was lost in the second control arm of the experiment due to technical difficulties, for mismatch A_1MM3 n=4 (Control 2) and for A_1AS anti-sense olig I, n=8. The A_1MM3 oligo-treated animals were analyzed separately and were not part of the cross-over experiment. The treatment methods and measurements employed following the cross-over were identical to those employed in the first arm of the experiment. In 6 of the 8 animals treated with the anti-sense oligo I (**SEQ. ID NO: 1**), no PC_{50} value could be obtained for adenosine doses of up to 20 mg/ml, which is the limit of solubility of adenosine. Accordingly, the PC_{50} values for these animals were assumed to be 20 mg/ml for calculation purposes. The values given, therefore, represent a minimum figure for the effectiveness of the anti-sense oligonucleotides of the invention. Other groups of allergic rabbits (n=4 for each group) were administered 0.5 or 0.05 mg doses of the anti-sense oligo I (**SEQ ID NO: 1**), or the A_1MM2 oligo in the manner and according to the schedule described above (the total doses being 2.0 or 0.2 mg). The results of these studies are provided in Example 22 below.

Example 11: Anti-sense Oligo Formulation

Each one of anti-sense oligos were separately solubilized in an aqueous solution and administered as described for anti-sense oligo I (**SEQ. ID No:1**) in (e) above, in four 5 mg aliquots (20 mg total dose) by means f a nebulizer via endotracheal tube, as described above. The results obtained for anti-sense oligo I and its mismatch controls confirmed that the mismatch controls are equivalent to saline, as described in Example 19 below and in Table 1 of Nyce & Metzger, Nature 385, 721-725 (1997). Because of this finding, saline was used as a control for pulmonary function studies employing anti-sense oligos II, III and IV (**SEQ. ID NOS; 7, 8 and 9**).

Example 12: Specificity of Oligo I for Adenosine A_1 Recept r (Receptor Binding Studies)

Tissue from airway smooth muscle was dissected to primary, secondary and tertiary bronchi fr m rabbits which had been administered 20 mg ligo I (**SEQ ID NO: 1**) in 4 divided doses over a period of 48 hours as described above. A membrane fraction was prepared according to the method of Ali et al. (Ali, S., et al., Am. J. Resp. Crit. Care Med. 149: 908 (1994), the relevant section relating to the preparation of the membrane fraction is incorporated in its entirety hereby by reference). The protein content was determined by the method of Bradford

and plasma membranes were incubated with 0.2 U/ml adenosine deaminase for 30 minutes at 37EC to remove endogen us aden sine. See, Bradford, M. M. Anal. Biochem. 72, 240-254 (1976), the relevant portion of which is hereby incorporated in its entirety by reference. The binding of [^{3}H]DPCPX, [^{3}H]NPC17731, or [^{3}H]CGS-21680 was measured as described by Jarvis et al. See, Jarvis, M.F., et al., Pharmacol. Exptl. Ther. 251, 888-893 (1989), the relevant portion of which is fully incorporated herein by reference. The results of this study are shown in Table 8 and discussed in Example 20 below.

Example 13: Pulm nary Function Measurements (C mpliance c_{DYN} and Resistance)

At 4 months of age, the immunized animals were anesthetized and relaxed with 1.5 ml of a mixture of ketamine HCl (35 mg/kg) and acepromazine maleate (1.5 mg/kg) administered intramuscularly. After induction of anesthesia, allergic rabbits were comfortably positioned supine on a soft molded animal board. Salve was applied to the eyes to prevent drying, and they were closed. The animals were then intubated with a 4.0 mm intermediate high-low cuffed Murphy 1 endotracheal tube (Mallinckrodt, Glen Falls, NY), as previously described by Zavala and Rhodes. See, Zavala and Rhodes, Proc. Soc. Exp. Biol. Med. 144: 509-512 (1973), the relevant porti n of which is incorporated herein by reference in its entirety. A polyethylene catheter of OD 2.4 mm (Becton Dickinson, Clay Adams, Parsippany NJ) with an attached thin-walled latex balloon was passed into the esophagus and maintained at the same distance (approximately 16 cm) from the mouth throughout the experiment. The endotracheal tube was attached to a heated Fleisch pneumotach (size 00; DEM Medical, Richmond, VA), and the flow (v) measured using a Validyne differential pressure transducer (Model DP-45-16-1927, Validyne Engineering, Northridge, CA), driven by a Gould carrier amplifier (Model 11-4113, Gould Electronics, Cleveland, OH).
An esophageal balloon was attached to one side of the Validyne differential pressure transducer, and the other side was attached to the outflow of the endotracheal tube to obtain transpulmonary pressure (P_{tp}). The flow was integrated to yield a continuous tidal volume, and the measurements of total lung resistance (R_t) and dynamic compliance (C_{dyn}) were made at isovolumetric and zero flow points. The flow, volume and pressure were recorded on an eight channel Gould 2000 W high-frequency recorder and C_{dyn} was calculated using the total volume and the difference in P_{tp} at zero flow, and . R_t was calculated as the ratio of Ptp and V at midtidal lung volumes. These calculations were made automatically with the Buxco automated pulmonary mechanics respiratory analyzer (Model 6, Buxco Electronics, Sharon, CT), as previously described by Giles et al. See, Giles et al., Arch. Int. Pharmacodyn. Ther. 194: 213-232 (1971), the relevant portion of which describing these calculations is incorporated in toto hereby by reference. The results obtained upon administration of oligo II on allergic rabbits are shown and discussed in Example 26 below.

Example 14: Measurement of Bronchial Hyperresponsiveness (BHR)

Each allergic rabbit was administered histamine by aerosol to determine their baseline hyperresponsiveness. Aerosols of either saline or histamine were generated using a DeVilbiss nebulizer (DeVilbiss, Somerset, PA) for 30 seconds and then for 2 minutes at each dose employed. The ultrasonic nebulizer produced aerosol droplets of which 80% were <5 micron in diameter. The histamine aerosol was administered in increasing concentrations (0.156 to 80 mg/ml) and measurements of pulmonary function were made after each dose. The B4R was then determined by calculating the concentration of histamine (mg/ml) required to reduce the C_{dyn} 50% from baseline ($PC_{50\ Histamine}$).

Example 15: Cardiovascular Effect of Anti-sense Oligo I

The measurement of cardiac output and other cardiovascular parameters using CardiomaxJ utilizes the principal of thermal dilution in which the change in temperature of the blood exiting the heart after a venous injection of a known volume of cool saline is monitored. A single rapid injection of cool saline was made into the right atrium via cannulation of the right jugular vein, and the corresponding changes in temperature of the mixed injectate and blood in the aortic arch were recorded via cannulation of the carotid artery by a temperature-sensing miniprobe. Twelve hours after the allergic rabbits had been treated with aerosols of oligo I (EPI 2010; SEQ. ID NO: 1) as described in (d) above, the animals were anesthetized with 0.3 ml/kg of 80% Ketamine and 20% Xylazine. This time point coincides with previous data showing efficacy for SEQ. ID NO: 1, as is clearly shown by Nyce & Metzger, (1997), supra, the pertinent discl sure being inc rporated in its entirety here by reference. A thermoc uple was then inserted into the left carotid artery f each rabbit, and was then advanced 6.5 cm and secured with a silk ligature. The right jugular vein was then cannulated and a length of polyethylene tubing was inserted and secured. A thermodiluti n curve was then established on a CardiomaxJ II (Columbus Instruments, Ohio) by injecting sterile saline at 20EC to determine the c rrectness of positioning of the

thermocouple probe. After establishing the correctness of the position of the thermocouple, the femoral artery and vein were is lated. The fem ral vein was used as a portal for drug injecti ns, and the femoral artery for blo d pressure and heart rate measurements. Once constant baseline cardi vascular parameters were established, CardiomaxJ measurements of blood pr ssure, heart rate, cardiac output, total peripheral resistance, and cardiac c ntractility were made.

Example 16: Duration of Acti n f Oligo I (SEQ. ID NO: 1)

Eight allergic rabbits received initially increasing log doses of adenosine by means of a nebulizer via an intra-tracheal tube as described in (f) above, beginning with 0.156 mg/ml until compliance was reduced by 50% ($PC_{50\ Adenosine}$) to establish a baseline. Six of the rabbits then received four 5 mg aerosolized doses of (SEQ. ID NO: 1) as described above. Two rabbits received equivalent amounts of saline vehicle as controls. Beginning 18 hours after the last treatment, the $PC_{50\ Adenosine}$ values were tested again. After this point, the measurements were continued for all animals each day, for up to 10 days. The results of this study are discussed in Example 25 below.

Example 17: Reduction of Adenosine A_{2b} Receptor Number by Anti-sense Oligo V

Sprague Dawley rats were administered 2.0 mg respirable anti-sense oligo V (SEQ ID NO:10) three times over two days using an inhalation chamber as described above. Twelve hours after the last administration, lung parenchymal tissue was dissected and assayed for adenosine A_{2b} receptor binding using [311]-NECA as described by Nyce & Metzger (1997), supra. Controls were conducted by administration of equal volumes of saline. The results are significant at $p<0.05$ using Student's paired t test, and are discussed in Example 28 below.

Example 18: Comparison of Oligo I & Corresponding Phosphodiester Oligo VI (SEQ. ID NO:1681)

Oligo I (SEQ ID NO:1) countered the effects of adenosine and eliminated sensitivity to it for aden sine amounte up to 20 mg adenosine/5.0 ml (the limit of solubility of adenosine). Oligo VI (SEQ ID NO:1681), the phosphodiester version of the oligonucleotide sequence, was completely ineffective when tested in the same manner. Both compounds have identical sequence, differing only in the presence of phosphorothioate residues in Oligo I (SEQ ID NO:1), and were delivered as an aerosol as described above and in Nyce & Metzger (1997), supra. Significantly different at $p<0.001$, Student's paired t test. The results are discussed in Example 29 below..

RESULTS OBTAINED FOR ANTI-SENSE OLIGO I (SEQ. ID NO: 1)

Example 19: Results of Prior Work

The nucleotide sequence and other data for anti-sense oligo I (SEQ. ID NO: 1), which is specific for the adenosine A_1 receptor, were provided above. The experimental data showing the effectiveness of oligo I in down regulating the receptor number and activity were also provided above. Further information on the characteristics and activities of anti-sense oligo I is provided in Nyce, J. W. and Metzger, W. J., Nature 385:721 (1997), the relevant parts of which relating to the following results are incorporated in their entireties herein by reference. The Nyce & Metzger (1997) publication provided data showing that the anti-sense oligo I (SEQ. ID NO: 1):

(1) The anti-sense oligo I reduces the number of adenosine A_1 receptors in the bronchial smooth muscle of allergic rabbits in a dose-dependent manner as may be seen in Table 5.

(2) Anti-sense Oligo I attenuates adenosine-induced bronchoconstriction and allergen-induced bronchoconstriction.

(3) The Oligo I attenuates bronchial hyperresponsiveness as measured by PC_{50} histamine, a standard measurement to assess bronchial hyperresponsiveness. This result clearly demonstrates anti-inflammatory activity of the anti-sense oligo I as is shown in Table 5.

(4) As expected, because it was designed to target it, the anti-sense oligo I is totally specific for the adenosine A_1 receptor, and has no effect at all at any dose on either the very closely related adenosine A_2 receptor or the related bradykinin B_2 receptor. This is seen in Table 5.

(5) In contradistinction to the above effects of the Oligo I, the mismatch control molecules MM2 and MM3 (SEQ. ID NO:1682 and SEQ. ID NO:1683) which have identical base composition and molecular weight but differed from the anti-sense oligo I (SEQ ID NO: 1) by 6 and 2 mismatches, respectively. These mismatches, which are the minimum possible while still retaining identical base composition, produced absolutely no effect upon any of the targeted receptors (A_1, A_2 or B_2).

These results, along with a complete lack of prior art on the use of anti-sense oligonucleotides, such as oligo I, targeted to the adenosine A_1 receptor, are unexpected results. The sh wings presented in this patent clearly enable and demonstrate the effectiveness, for their intended use, of the claimed agents and method for treating a disease or condition associated with lung airway, such as bronchoconstriction, inflammation, allergy(ies), and the like.

Example 20: **Olig I Significantly Reduces Resp nse to Adenosine Challenge**

The receptor binding experiment is described in Example 12 above, and the results shown in Table 5 below which shows the binding characteristics of the adenosine A_1-selective ligand $[_3H]$DPCPX and the bradykinin B_2-selective ligand $[^3H]$NPC 17731 in membranes isolated from airway smooth muscle of A_1 adenosine recept r and B_2 bradykinin receptor anti-sense- and mismatch-treated allergic rabbits.

Table 5: Binding Characteristics of Three Anti-Sense Oligos

Treatment[1]	A_1 receptor		B_2 receptor	
	Kd	B_{max}	Kd	Bmax
Adenosine A_1	Receptor			
20 mg	0.36±0.029 nM	19±1.52 fmoles*	0.39±0.031 nM	14.8±0.99fmoles
2 mg	0.38±0.030 nM	32±2.56 fmoles*	0.41±0.028 nM	15.5±1.08 fmoles
0.2 mg	0.37±0.030 nM	49±3.43 fmoles	0.34±0.024 nM	15.0±1.06 fmoles
A_1MM1	(Control)			
20 mg	0.34±0.027 nM	52.0±3.64 fmoles	0.35±0.024 nM	14.0±1.0 fmoles
2 mg	0.37±0.033 nM	51.8±3.88 fmoles	0.38±0.028 nM	14.6±1.02 fmoles
B_2A (Bradykinin	Receptor)			
20 mg	0.36±0.028 nM	45.0±o.15 fmoles	0.38±0.027 nM	8.7±0.62 fmoles*
2 mg	0.39±0.035 nM	44.3±2.90 fmoles	0.34±0.024 nM	11.9±0.76 fmoles**
0.2 mg	0.40±0.028 nM	47.0±3.76 fmoles	0.35±0.028 nM	15.1±1.05 fmoles
B_2MM (Control)				±
20 mg	0.39±0.031 nM	42.0±2.94 fmoles	0.41±0.029 nM	14.0±0.98 fmoles
2 mg	0.41±0.035 nM	40.0±3.20 fmoles	0.37±0.030 nM	14.8±0.99 fmoles
0.2 mg	0.37±0.029 nM	43.0±3.14 fmoles	0.36±0.025 nM	15.1±1.35 fmoles
Saline Control	0.37±0.041	46.0±5.21	0.39±0.047 nM	14.2±1.35 fmoles

[1] Refers to total oligo administered in four equivalently divided doses over a 48 hour period. Treatments and analyses were performed as described in methods. Significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected t test. n = 4-6 for all groups.
* Significantly different from mismatch control- and saline-treated groups, $p<0.001$;
** Significantly different from mismatch control- and saline-treated groups, $p<0.05$.

Example 21: **Dose-response Effect of Oligo I**

Anti-sense oligo I (SEQ ID NO:1) was found to reduce the effect of adenosine administration to the animal in a dose-dependent manner over the dose range tested as shown in Table 6 below.

Table 6: D se-Resp nse Effect to Anti-sense Oligo I

T tal Dose (mg)	$PC_{50\ Adenosine}$ (mg Adenosine)
Anti-sense Oligo I	
0.2	8.32±7.2
2.0	14.0±7.2
20	19.5±0.34
A_1MM2 oligo (control)	
0.2	2.51±0.46
2.0	3.13±0.71
20	3.25±0.34

The above results were found by the Student's paired t test statistically different, p=0.05

The oligo I (**SEQ. ID NO:1**), an anti-adenosine A_1 receptor oligo, acts specifically on the adenosine A_1 receptor, but not on the adenosine A_2 receptors. These results stem from the treatment of rabbits with anti-sense oligo I (**SEQ. ID NO.1**) or mismatch control oligo (**SEQ. ID NO:1682**; A_1MM2) as described in Example 9 above and in Nyce & Metzger (1997), supra (four doses of 5 mg spaced 8 to 12 hours apart via nebulizer via endotracheal tube), bronchial smooth muscle tissue excised and the number of adenosine A_1 and adenosine A_2 receptors determined as reported in Nyce & Metzger (1997), supra.

Example 22: Specificity of Oligo I (SEQ. ID NO:1) for Target Gene Product

Oligo I (SEQ. ID No:1) is specific for the adenosine A_1 receptor whereas its mismatch controls had n activity. Figure 1 depicts the results obtained from the cross-over experiment described in Example 10 above and in Nyce & Metzger (1997), supra. The two mismatch controls (**SEQ. ID NO:1682** and **SEQ. ID NO:1683**) evidenced no effect on the $PC_{50\ Adenosine}$ value. On the contrary, the administration of anti-sense oligo I (**SEQ. ID NO:1**) showed a seven-fold increase in the $PC_{50\ Adenosine}$ value. The results clearly indicate that the anti-sense oligo I (**SEQ. ID NO: 1**) reduces the response (attenuates the sensitivity) to exogenously administered adenosine when compared with a saline control. The results provided in Table 2 above clearly establish that the effect of the anti-sense oligo I is dose dependent (see, column 3 of Table 1). The Oligo I was also shown to be totally specific for the adenosine A_1 receptor, (see, top 3 rows of Table), inducing no activity at either the closely related adenosine A_2 receptor or the bradykinin B_2 receptor (see, lines 8-10 of Table 2 above). In addition, the results shown in Table 2 establish that the anti-sense oligo I (**SEQ. ID NO:1**) decreases sensitivity to adenosine in a dose dependent manner, and that it does this in an anti-sense oligo-dependent manner since neither of two mismatch control oligonucleotides (A_1MM2; **SEQ. ID NO:1682** and A_1MM3; **SEQ. ID NO:1683**) show any effect on $PC_{50\ Adenosine}$ values or on attenuating the number of adenosine A_1 receptors.

Example 23: Effect on Aeroallergen-induced Bronchoconstriction & Inflammation

The Oligo I (**SEQ. ID NO:1**) was shown to significantly reduce the histamine-induced effect in the rabbit model when compared to the mismatch oligos. The effect of the anti-sense Oligo I (SEQ. ID No:1) and the mismatch oligos (A_1MM2, **SEQ. ID NO:1682** and A_1MM3, **SEQ. ID NO:1682**) on allergen-induced airway obstruction and bronchial hyperresponsiveness was assessed in allergic rabbits. The effect of the anti-sense oligo I (**SEQ. ID NO:1**) on allergen-induced airway obstruction was assessed. As calculated from the area under the plotted curve, the anti-sense oligo I significantly inhibited allergen-induced airway obstruction when compared with the mismatched control (55%, p<0.05; repeated measures ANOVA, and Tukey's t test). A complete lack of effect was induced by the mismatch oligo A_1MM2 (Control) on allergen induced airway obstruction. The effect of the anti-sense oligo I (**SEQ. ID NO:1**) on allergen-induced BHR was determined as above. As calculated from the $PC_{50\ Histamine}$ value, the anti-sense oligo I (**SEQ. ID NO:1**) significantly inhibited allergen-induced BHR in allergic rabbits when compared to the mismatched contr l (61%, p<0.05; repeated measures ANOVA, Tukey's t test). A complete lack of effect of the A_1MM mismatch control n allergen-induced BHR was observed. The results indicated that anti-sense oligo I (**SEQ. ID NO: 1**) is effective to protect against aeroallergen-induced bronchoconstriction (house dust mite). In addition, the anti-sense oligo I (**SEQ. ID NO:1**) was also found to be a

potent inhibitor of dust mite-induced bronchial hyper responsiveness, as shown by its effects upon histamine sensitivity which indicates anti- inflammatory activity f r anti-sense oligo I (**SEQ. ID NO:1**).

Example 24: Anti-sense Oligo I is Free of Deleteri us Side Effects

The Oligo I (**SEQ. ID NO:1**) was shown to be free of side effects that might be toxic to the recipient. No changes in arterial blood pressure, cardiac output, str ke volume, heart rate, total peripheral resistance or heart contractility (dPdT) were observed following administration of 2.0 or 20 mg ligo I (**SEQ. ID NO:1**). The addition, the results of the measurement of cardiac output (CO), stroke volume (SV), mean arterial pressure (MAP), heart rate (HR), total peripheral resistance (TPR), and contractility (dPdT) with a CardiomaxJ apparatus (Columbus Instruments, Ohio) were assessed. These results evidenced that oligo I (**SEQ. ID NO:1**) has no detrimental effect upon critical cardiovascular parameters. More particularly, this oligo does not cause hypotension. This finding is of particular importance because other phosphorothioate anti-sense oligonucleotides have been shown in the past to induce hypotension in some model systems. Furthermore, the adenosine A_1 receptor plays an important role in sinoatrial conduction within the heart. Attenuation of the adenosine A_1 receptor by anti-sense oligo I (**SEQ. ID NO:1**) might be expected to result, therefore, in deleterious extrapulmonary activity in response to the downregulation of the receptor. This is not the case. The anti-sense oligo I (**SEQ. ID NO:1**) does not produce any deleterious intrapulmonary effects and renders the administration of the low doses of the present anti-sense oligo free of unexpected, undesirable side effects. This demonstrates that when oligo I (**SEQ. ID NO:1**) is administered directly to the lung, it does not reach the heart in significant quantities to cause deleterious effects. This is in contrast to traditional adenosine receptor antagonists like theophylline which do escape the lung and can cause deleterious, even life-threatening effects outside the lung.

Example 25: Long Lasting Effect of Oligo I

The Oligo I (**SEQ. ID NO:1**) evidenced a long lasting effect as evidenced by the PC_{50} and Resistance values obtained upon its administration prior to adenosine challenge. The duration of the effect was measured for with respect to the PC_{50} of adenosine anti-sense oligo I when administered in four equal doses of 5 mg each by means of a nebulizer via an endotracheal tube, as described above. The effect of the agent is significant over days 1 to 8 after administration. When the effect of the anti-sense oligo I (**SEQ. ID NO:1**) had disappeared, the animals were administered saline aerosols (controls), and the $PC_{50\ Adenosine}$ values for all animals were measured again. Saline-treated animals showed base line PC_{50} adenosine values (n=6). The duration of the effect (with respect to Resistance) was measured for six allergic rabbits which were administered 20 mg of anti-sense oligo I (**SEQ. ID NO: 1**) as described above, upon airway resistance measured as also described above. The mean calculated duration of effect was 8.3 days for both PC_{50} adenosine ($p<0.05$) and resistance ($p<0.05$). These results show that anti-sense oligo I (**SEQ. ID NO:1**) has an extremely long duration of action, which is completely unexpected.

Example 26: Anti-sense Oligo II

Anti-sense oligo II, targeted to a different region of the adenosine A_1 receptor mRNA, was found to be highly active against the adenosine A_1-mediated effects. The experiment measured the effect of the administration of anti-sense oligo II (**SEQ. ID NO:7**) upon compliance and resistance values when 20 mg anti-sense oligo II or saline (control) were administered to two groups of allergic rabbits as described above. Compliance and resistance values were measured following an administration of adenosine or saline as described above in Example 13. The effect of the anti-sense oligo of the invention was different from the control in a statistically significant manner, $p<0.05$ using paired t-test, compliance; $p<0.01$ for resistance. The results showed that anti-sense oligo II (**SEQ. ID NO:7**), which targets the adenosine A_1 receptor, effectively maintains compliance and reduces resistance upon adenosine challenge.

Example 27: Antisense Oligos III and IV

Oligos III (**SEQ. ID NO:8**) and IV (**SEQ. ID NO:9**) were shown to be in fact specifically targeted to the adenosine A_3 receptor by their effect on reducing inflammation and the number of inflammatory cells present upon separate administration of 20 mg of the anti-sense oligos III (**SEQ. ID NO:8**) and IV (**SEQ. ID NO:9**) to allergic rabbits as described above. The number of inflammatory cells was determined in their bronchial lavage fluid 3 hours later by counting at least 100 viable cells per lavage. The effect of anti-sense oligos III (**SEQ. ID NO:8**) and IV (**SEQ. ID NO:9**) upon granulocytes, and upon total cells in bronchial lavage were assessed following exposure to dust mite allergen. The results showed that the anti-sense oligo IV (**SEQ. ID NO:9**) and anti-sense oligo III (**SEQ. ID NO:8**) are very potent anti-inflammatory agents in the asthmatic lung following exposure to dust mite allergen. As is known in the art, granulocytes, especially eosinophils. are the primary inflammatory cells of

asthma, and the administration of anti-sense oligos III (SEQ. ID NO:8) and IV (SEQ. ID NO:9) reduced their numbers by 40% and 66%, respectively. Furthermore, anti-sense oligos IV (SEQ. ID NO:9) and III (SEQ. ID NO:8) also reduced the total number of cells in the bronchial lavage fluid by 40% and 80%, respectively. This is also an important indicator of anti-inflammatory activity by the present anti-adenosine A_3 agents of the invention. Inflammati n is kn wn to underlie bronchial hyperresponsiveness and allergen-induced bronchoconstriction in asthma. Both anti-sense oligonucleotides III (SEQ. ID NO:8) and IV (SEQ. ID NO:9), which are targeted t the adenosine A_3 receptor, are representative of an important new class of anti-inflammatory agents which may be designed to specifically target the lung receptors of each species.

Example 28: Anti-sense Oligo V

The anti-sense oligo V (SEQ. ID NO:10), targeted to the adenosine A_{2b} adenosine receptor mRNA was shown to be highly effective at countering adenosine A_{2b}-mediated effects and at reducing the number of adenosine A_{2b} receptors present to less than half.

Example 29: Unexpected Superiority of Substituted over Phosphodiester-residue Oligo I-DS(SEQ.ID NO:1681)

Oligos I (SEQ. ID NO:1) and I-DS (SEQ. ID NO:1681) were separately administered to allergic rabbits as described above, and the rabbits were then challenged with adenosine. The phosphodiester oligo I-DS (SEQ. ID NO:1681) was statistically significantly less effective in countering the effect of adenosine whereas oligo I (SEQ. ID NO:1) showed high effectiveness, evidencing a $PC_{50\ Adenosine}$ of 20 mg.

Example 30: Anti-sense Oligo VI

For the present work, I designed an additional anti-sense phosphorothioate oligo targeted to the adenosine A_1 receptor (Oligo VI). This anti-sense oligo was designed for therapy on a selected species as described in the above patent application and is generally specific for that species, unless the segment of the adenosine receptor mRNA of other species elected happens to have a similar sequence. The anti-sense oligos were prepared as described below, and tested in vivo in a rabbit model for bronchoconstriction, inflammation and lung allergy, which have breathing difficulties and impeded lung airways, as is the case in ailments such as asthma, as described in the above-identified application. One additional oligo and its effect in a rabbit model was studied and the results of the study are reported and discussed below. The present oligo (anti-sense oligo VI) was selected for this study to complement the data on SEQ ID NO: 1 (Oligo I), which is anti-sense to the adenosine A_1 receptor mRNA provided in the above-identified patent application. This additional oligo is identified as anti-sense Oligo VI, and is targeted to a different region of the adenosine A_1 receptor mRNA than Oligo I. The design and synthesis of this anti-sense oligo was performed in accordance with the teaching, particularly Example 1, of the above-identified patent application. The anti-sense Oligo VI is a phosphorothioate designed to target the coding region of the rabbit adenosine A_1 receptor mRNA region +964 to +984 relative to the initiation codon (start site). The Oligo VI was prepared as described in the above-indicated application, and is 20 nucleotides long. The OligoVI is directed to the adenosine A_1 receptor gene, and has the following sequence: 5'-CGC CGG CGG GTG CGG GCC GG-3' (SEQ. ID NO:_). The phosphorothioate anti-sense Oligo VI having the sequence described in (5) above, was synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (DuPont, DE). TETD (tetraethylthiuram disulfide) was used as the sulfurizing agent during the synthesis.

Example 31: Preparation of Allergic Rabbits

Neonatal New Zealand white Pasturella-free rabbits were immunized intraperitoneally within 24 hours of birth with 0.5 ml of 312 antigen units/ml house dust mite (D. farinae) extract (Berkeley Biologicals, Berkeley, CA) mixed with 10% kaolin as previously described (Metzger, W. J., in Late Phase Allergic Reactions, Dorsch, W., Ed., CRC Handbook, pp 347-362, CRC Press, Boca Raton, 1990; Ali, S. Et al., Am. J. Resp. Crit. Care Med. 149: 908 (1994)). The immunizations were repeated weekly for the first month and then bi-weekly until the animals were 4 months old. These rabbits preferentially produce allergen-specific IgE antibody, typically respond to aeroallergen challenge with both an early and late-phase asthmatic response, and show bronchial hyper responsiveness (BHR). Monthly intraperitoneal administration of allergen (312 units dust mite allergen, as above) continues to stimulate and maintain allergen-specific IgE antibody and BHR. At 4 months of age, sensitized rabbits were prepared for aerosol administration as described by Ali et al. (1994), supra.

Example 32: Adenosine Aerosol Preparation

An adenosine aerosol (20 mg/ml) was prepared with an ultrasonic nebulizer (Model 646, DeVilbiss, Somerset, PA), which produced aerosol droplets, 80% of which were smaller than 5:m in diameter. Equal volumes of the aerosols were administered directly to the lungs via an intratracheal tube to all three rabbits. The animals

were then administered the aerosolized adenosine and Day 1 pre-treatment values for sensitivity to adenosine were calculated as the dose of adenosine causing a 50% loss of compliance (PC_{50} Adenosine). The animals were then administered the aerosolized anti-sense via the intratracheal tube (5 mg/1.0 ml), for 2 minutes, twice daily for 2 days (total dose, 20 mg). Post-treatment PC_{50} values were rec rded (post-treatment challenge) on the morning of the third day. The results of these studies are provided in (9) bel w.

Example 33: Anti-sense Oligo F rmulation

Each one of anti-sense oligos were separately solubilized in an aqueous solution and administered as described for anti-sense oligo I in (e) above, in four 5 mg aliquots (20 mg total dose) by means of a nebulizer via endotracheal tube, as described above.

Example 34: Oligo VI Reduces Response to Adenosine Challenge as well or Better than Oligo I

Oligo VI was tested in three allergic rabbits of the characteristics and readied as described in (7) above and in the above-indicated patent application. Oligo VI targets a section of the coding region of the A_1 receptor which is different from Oligo I. Both these target sequences were selected randomly from many possible coding region target sequences. The three rabbits were treated identically as previously indicated for Oligo I. Briefly, 5 mg of Oligo VI were nebulized to the rabbits twice per day at 8 hour intervals, for two days. Thereafter, PC_{50} aden sine studies were performed on the morning of the third day and compared to pre-treatment PC_{50} values. This protocol is described in more detail in Nyce and Metzger (Nyce & Metzger, Nature 385: 721-725 (1997)). The results obtained for the three rabbits are shown in Table 1 below.

Table 1: PC_{50} Adenosine before & after Aerosolized Adenosine Treatment

Treatment Time (mg)	PC_{50} Adenosine
Pre-treatment	3.0±2.1
Post-treatment	>20.0*

* maximum achievable dose due to adenosine insolubility in saline

All three animals treated with Oligo VI completely eliminated sensitivity to adenosine up to the measurable level of the agent shown in Table 1 above. That is, the administration of the Oligo VI abrogated the adenosine-induced bronchoconstriction in the three allergic rabbits. The actual efficacy of Oligo VI is, therefore, greater than could be measured in the experimental system used. By comparing with the previously submitted results for the Oligo I, it may be seen that the Oligo VI was found to be as effective, or more, than Oligo I.

Example 34: Conclusions

The work described and results discussed in the examples clearly indicates that all anti-sense oligonucleotides designed in accordance with the teachings of the above-identified application were found to be highly effective at countering or reducing effects mediated by the receptors they are targeted to. That is, each and all of the two anti-sense oligos targeting an adenosine A_1 receptor mRNA, 1 anti-sense oligo targeting an adenosine A_{2b} receptor mRNA, and the 2 anti-sense oligos targeting an A_3 receptor mRNA were shown capable of countering the effect of exogenously administered adenosine which is mediated by the specific receptor they are targeted to. The activity of the anti-sense oligos of this invention, moreover, is specific to the target and substitutively fails to inhibit another target. In addition, the results presented also show that the administration of the present agents results in extremely low or non-existent deleterious side effects or toxicity. This represents 100% success in providing agents that are highly effective and specific in the treatment of bronchoconstriction and/or inflammation. This invention is broadly applicable in the same manner to all gene(s) and corresponding mRNAs encoding proteins involved in or associated with airway diseases. A comparison of the phosphodiester and a version of the same oligonucleotide wherein the phosphodiester bonds are substituted with phosphorothioate bonds evidenced an unexpected superiority for the phosphothiorate oligonucleotide over the phosphodiester anti-sense oligo. The foregoing examples are illustrative of the present invention, and are not to be construed as limiting thereof. The invention is defined by the following claims, with equivalents of the claims to be included therein.

SEQUENCE LISTING

(1) GENERAL INFORMATION
(i) APPLICANT: East Carolina University et al.
(ii) TITLE OF THE INVENTION: LOW ADENOSINE OLIGONUCLEOTIDE AGENT, COMPOSITION, KIT & TREATMENTS
(iii) NUMBER OF SEQUENCES:
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: ARTER & HADDEN
(B) STREET: 725 South Figueroa St, # 2400
(C) CITY: Los Angeles
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 90071
(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US99/
(B) FILING DATE: 3-AUG-1999
(C) CLASSIFICATION: UNKNOWN
(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/095,212
(B) FILING DATE: 03-AUG-1998
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(2) INFORMATION FOR SEQ ID NO:1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
GATGGAGGGC GGCATGGCGG G 21

(2) INFORMATION FOR SEQ ID NO:2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
GTAGCAGGCG GGGATGGGGG C 21

(2) INFORMATION FOR SEQ ID NO:3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
GTTGTTGGGC ATCTTGCC 18

(2) INFORMATION FOR SEQ ID NO:4:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
GTACTTGCGG ATCTAGGC 18

(2) INFORMATION FOR SEQ ID NO:5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
GTGGGCCTAG CTCTCGCC 18

(2) INFORMATION FOR SEQ ID NO:6:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
GTCGGGGTAC CTGTCGGC 18

(2) INFORMATION FOR SEQ ID NO:7:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
CTCGTCGCCG TCGCCGGCGG G 21

(2) INFORMATION FOR SEQ ID NO:8:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
GGGTGGTGCT ATTGTCGGGC 20

(2) INFORMATION FOR SEQ ID NO:9:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
GGCCCAGGGC CAGCC 15

(2) INFORMATION FOR SEQ ID NO:10:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
GGCCGGGCCA GCCGGGCCCG G 21

(2) INFORMATION FOR SEQ ID NO:11:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTGGGC 50

(2) INFORMATION FOR SEQ ID NO:12:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTGGGC 49

(2) INFORMATION FOR SEQ ID NO:13:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGCTGGGC 48

(2) INFORMATION FOR SEQ ID NO:14:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTGGGC 47

(2) INFORMATION FOR SEQ ID NO:15:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG CGGGCACAGG CTGGGC 46

(2) INFORMATION FOR SEQ ID NO:16:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAGGC TGGGC 45

(2) INFORMATION FOR SEQ ID NO:17:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAGGCT GGGC 44

(2) INFORMATION FOR SEQ ID NO:18:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACAGGCTG GGC 43

(2) INFORMATION FOR SEQ ID NO:19:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAGGCTGG GC 42

(2) INFORMATION FOR SEQ ID NO:20:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGGG C 41

(2) INFORMATION FOR SEQ ID NO:21:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTGGGC 40

(2) INFORMATION FOR SEQ ID NO:22:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTGGGC 39

(2) INFORMATION FOR SEQ ID NO:23:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGCTGGGC 38

(2) INFORMATION FOR SEQ ID NO:24:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTGGGC 37

(2) INFORMATION FOR SEQ ID NO:25:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
TGAGATGGAG GGCGGCATGG CGGGCACAGG CTGGGC 36

(2) INFORMATION FOR SEQ ID NO:26:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
GAGATGGAGG GCGGCATGGC GGGCACAGGC TGGGC 35

(2) INFORMATION FOR SEQ ID NO:27:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
AGATGGAGGG CGGCATGGCG GGCACAGGCT GGGC 34

(2) INFORMATION FOR SEQ ID NO:28:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
GATGGAGGGC GGCATGGCGG GCACAGGCTG GGC 33

(2) INFORMATION FOR SEQ ID NO:29:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
ATGGAGGGCG GCATGGCGGG CACAGGCTGG GC 32

(2) INFORMATION FOR SEQ ID NO:30:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
TGGAGGGCGG CATGGCGGGC ACAGGCTGGG C 31

(2) INFORMATION FOR SEQ ID NO:31:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
GGAGGGCGGC ATGGCGGGCA CAGGCTGGGC 30

(2) INFORMATION FOR SEQ ID NO:32:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
GAGGGCGGCA TGGCGGGCAC AGGCTGGGC 29

(2) INFORMATION FOR SEQ ID NO:33:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGGGCGGCAT GGCGGGCACA GGCTGGGC 28

(2) INFORMATION FOR SEQ ID NO:34:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
GGGCGGCATG GCGGGCACAG GCTGGGC 27

(2) INFORMATION FOR SEQ ID NO:35:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucl ic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
GGCGGCATGG CGGGCACAGG CTGGGC 26

(2) INFORMATION FOR SEQ ID NO:36:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
GCGGCATGGC GGGCACAGGC TGGGC 25

(2) INFORMATION FOR SEQ ID NO:37:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
CGGCATGGCG GGCACAGGCT GGGC 24

(2) INFORMATION FOR SEQ ID NO:38:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
GGCATGGCGG GCACAGGCTG GGC 23

(2) INFORMATION FOR SEQ ID NO:39:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
GCATGGCGGG CACAGGCTGG GC 22

(2) INFORMATION FOR SEQ ID NO:40:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
CATGGCGGGC ACAGGCTGGG C 21

(2) INFORMATION FOR SEQ ID NO:41:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:
ATGGCGGGCA CAGGCTGGGC 20

(2) INFORMATION FOR SEQ ID NO:42:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:
TGGCGGGCAC AGGCTGGGC 19

(2) INFORMATION FOR SEQ ID NO:43:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
GGCGGGCACA GGCTGGGC 18

(2) INFORMATION FOR SEQ ID NO:44:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:
GCGGGCACAG GCTGGGC 17

(2) INFORMATION FOR SEQ ID NO:45:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
CGGGCACAGG CTGGGC 16

(2) INFORMATION FOR SEQ ID NO:46:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
GGGCACAGGC TGGGC 15

(2) INFORMATION FOR SEQ ID NO:47:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
GGCACAGGCT GGGC 14

(2) INFORMATION FOR SEQ ID NO:48:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:
GCACAGGCTG GGC 13

(2) INFORMATION FOR SEQ ID NO:49:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
CACAGGCTGG GC 12

(2) INFORMATION FOR SEQ ID NO:50:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:
ACAGGCTGGG C 11

(2) INFORMATION FOR SEQ ID NO:51:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:
CAGGCTGGGC 10

(2) INFORMATION FOR SEQ ID NO:52:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:
AGGCTGGGC 9

(2) INFORMATION FOR SEQ ID NO:53:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGGG C 51

(2) INFORMATION FOR SEQ ID NO:54:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGGG 50

(2) INFORMATION FOR SEQ ID NO:55:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGG 49

(2) INFORMATION FOR SEQ ID NO:56:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTG 48

(2) INFORMATION FOR SEQ ID NO:57:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCT 47

(2) INFORMATION FOR SEQ ID NO:58:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGC 46

(2) INFORMATION FOR SEQ ID NO:59:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGG 45

(2) INFORMATION FOR SEQ ID NO:60:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAG 44

(2) INFORMATION FOR SEQ ID NO:61:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACA 43

(2) INFORMATION FOR SEQ ID NO:62:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC AC 42

(2) INFORMATION FOR SEQ ID NO:63:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC A 41

(2) INFORMATION FOR SEQ ID NO:64:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC 40

(2) INFORMATION FOR SEQ ID NO:65:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGG 39

(2) INFORMATION FOR SEQ ID NO:66:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGG 38

(2) INFORMATION FOR SEQ ID NO:67:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCG 37

(2) INFORMATION FOR SEQ ID NO:68:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGC 36

(2) INFORMATION FOR SEQ ID NO:69:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGG 35

(2) INFORMATION FOR SEQ ID NO:70:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATG 34

(2) INFORMATION FOR SEQ ID NO:71:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CAT 33

(2) INFORMATION FOR SEQ ID NO:72:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CA 32

(2) INFORMATION FOR SEQ ID NO:73:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG C 31

(2) INFORMATION FOR SEQ ID NO:74:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:
GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG 30

(2) INFORMATION FOR SEQ ID NO:75:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:
GGCGGCCTGG AAAGCTGAGA TGGAGGGCG 29

(2) INFORMATION FOR SEQ ID NO:76:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:
GGCGGCCTGG AAAGCTGAGA TGGAGGGC 28

(2) INFORMATION FOR SEQ ID NO:77:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:
GGCGGCCTGG AAAGCTGAGA TGGAGGG 27

(2) INFORMATION FOR SEQ ID NO:78:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:
GGCGGCCTGG AAAGCTGAGA TGGAGG 26

(2) INFORMATION FOR SEQ ID NO:79:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:
GGCGGCCTGG AAAGCTGAGA TGGAG 25

(2) INFORMATION FOR SEQ ID NO:80:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:
GGCGGCCTGG AAAGCTGAGA TGGA 24

(2) INFORMATION FOR SEQ ID NO:81:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:
GGCGGCCTGG AAAGCTGAGA TGG 23

(2) INFORMATION FOR SEQ ID NO:82:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:
GGCGGCCTGG AAAGCTGAGA TG 22

(2) INFORMATION FOR SEQ ID NO:83:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:
GGCGGCCTGG AAAGCTGAGA T 21

(2) INFORMATION FOR SEQ ID NO:84:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:
GGCGGCCTGG AAAGCTGAGA 20

(2) INFORMATION FOR SEQ ID NO:85:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:
GGCGGCCTGG AAAGCTGAG 19

(2) INFORMATION FOR SEQ ID NO:86:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:
GGCGGCCTGG AAAGCTGA 18

(2) INFORMATION FOR SEQ ID NO:87:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:
GGCGGCCTGG AAAGCTG 17

(2) INFORMATION FOR SEQ ID NO:88:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:
GGCGGCCTGG AAAGCT 16

(2) INFORMATION FOR SEQ ID NO:89:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:
GGCGGCCTGG AAAGC 15

(2) INFORMATION FOR SEQ ID NO:90:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:
GGCGGCCTGG AAAG 14

(2) INFORMATION FOR SEQ ID NO:91:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:
GGCGGCCTGG AAA 13

(2) INFORMATION FOR SEQ ID NO:92:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:
GGCGGCCTGG AA 12

(2) INFORMATION FOR SEQ ID NO:93:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:
GGCGGCCTGG A 11

(2) INFORMATION FOR SEQ ID NO:94:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:
GGCGGCCTGG 10

(2) INFORMATION FOR SEQ ID NO:95:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTGGGC 50

(2) INFORMATION FOR SEQ ID NO:96:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTGGG 49

(2) INFORMATION FOR SEQ ID NO:97:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTGG 48

(2) INFORMATION FOR SEQ ID NO:98:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTG 47

(2) INFORMATION FOR SEQ ID NO:99:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCT 46

(2) INFORMATION FOR SEQ ID NO:100:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGC 45

(2) INFORMATION FOR SEQ ID NO:101:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGG 44

(2) INFORMATION FOR SEQ ID NO:102:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAG 43

(2) INFORMATION FOR SEQ ID NO:103:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CA 42

(2) INFORMATION FOR SEQ ID NO:104:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA C 41

(2) INFORMATION FOR SEQ ID NO:105:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA 40

(2) INFORMATION FOR SEQ ID NO:106:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGC 39

(2) INFORMATION FOR SEQ ID NO:107:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGG 38

(2) INFORMATION FOR SEQ ID NO:108:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGG 37

(2) INFORMATION FOR SEQ ID NO:109:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCG 36

(2) INFORMATION FOR SEQ ID NO:110:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGC 35

(2) INFORMATION FOR SEQ ID NO:111:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGG 34

(2) INFORMATION FOR SEQ ID NO:112:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATG 33

(2) INFORMATION FOR SEQ ID NO:113:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC AT 32

(2) INFORMATION FOR SEQ ID NO:114:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC A 31

(2) INFORMATION FOR SEQ ID NO:115:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC 30

(2) INFORMATION FOR SEQ ID NO:116:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:
GCGGCCTGGA AAGCTGAGAT GGAGGGCGG 29

(2) INFORMATION FOR SEQ ID NO:117:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCGGCCTGGA AAGCTGAGAT GGAGGGCG 28

(2) INFORMATION FOR SEQ ID NO:118:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GCGGCCTGGA AAGCTGAGAT GGAGGGC 27

(2) INFORMATION FOR SEQ ID NO:119:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GCGGCCTGGA AAGCTGAGAT GGAGGG 26

(2) INFORMATION FOR SEQ ID NO:120:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GCGGCCTGGA AAGCTGAGAT GGAGG 25

(2) INFORMATION FOR SEQ ID NO:121:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCGGCCTGGA AAGCTGAGAT GGAG 24

(2) INFORMATION FOR SEQ ID NO:122:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCGGCCTGGA AAGCTGAGAT GGA 23

(2) INFORMATION FOR SEQ ID NO:123:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GCGGCCTGGA AAGCTGAGAT GG 22

(2) INFORMATION FOR SEQ ID NO:124:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GCGGCCTGGA AAGCTGAGAT G 21

(2) INFORMATION FOR SEQ ID NO:125:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:
GCGGCCTGGA AAGCTGAGAT 20

(2) INFORMATION FOR SEQ ID NO:126:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:
GCGGCCTGGA AAGCTGAGA 19

(2) INFORMATION FOR SEQ ID NO:127:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:
GCGGCCTGGA AAGCTGAG 18

(2) INFORMATION FOR SEQ ID NO:128:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:
GCGGCCTGGA AAGCTGA 17

(2) INFORMATION FOR SEQ ID NO:129:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:
GCGGCCTGGA AAGCTG 16

(2) INFORMATION FOR SEQ ID NO:130:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:
GCGGCCTGGA AAGCT 15

(2) INFORMATION FOR SEQ ID NO:131:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:
GCGGCCTGGA AAGC 14

(2) INFORMATION FOR SEQ ID NO:132:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:
GCGGCCTGGA AAG 13

(2) INFORMATION FOR SEQ ID NO:133:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:
GCGGCCTGGA AA 12

(2) INFORMATION FOR SEQ ID NO:134:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:
GCGGCCTGGA A 11

(2) INFORMATION FOR SEQ ID NO:135:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:
GCGGCCTGGA 10

(2) INFORMATION FOR SEQ ID NO:136:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTGGGC 49

(2) INFORMATION FOR SEQ ID NO:137:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTGGG 48

(2) INFORMATION FOR SEQ ID NO:138:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTGG 47

(2) INFORMATION FOR SEQ ID NO:139:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTG 46

(2) INFORMATION FOR SEQ ID NO:140:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCT 45

(2) INFORMATION FOR SEQ ID NO:141:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGC 44

(2) INFORMATION FOR SEQ ID NO:142:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGG 43

(2) INFORMATION FOR SEQ ID NO:143:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AG 42

(2) INFORMATION FOR SEQ ID NO:144:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC A 41

(2) INFORMATION FOR SEQ ID NO:145:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC 40

(2) INFORMATION FOR SEQ ID NO:146:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCA 39

(2) INFORMATION FOR SEQ ID NO:147:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGC 38

(2) INFORMATION FOR SEQ ID NO:148:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGG 37

(2) INFORMATION FOR SEQ ID NO:149:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGG 36

(2) INFORMATION FOR SEQ ID NO:150:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCG 35

(2) INFORMATION FOR SEQ ID NO:151:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGC 34

(2) INFORMATION FOR SEQ ID NO:152:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGG 33

(2) INFORMATION FOR SEQ ID NO:153:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TG 32

(2) INFORMATION FOR SEQ ID NO:154:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA T 31

(2) INFORMATION FOR SEQ ID NO:155:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:
CGGCCTGGAA AGCTGAGATG GAGGGCGGCA 30

(2) INFORMATION FOR SEQ ID NO:156:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:
CGGCCTGGAA AGCTGAGATG GAGGGCGGC 29

(2) INFORMATION FOR SEQ ID NO:157:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:
CGGCCTGGAA AGCTGAGATG GAGGGCGG 28

(2) INFORMATION FOR SEQ ID NO:158:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:
CGGCCTGGAA AGCTGAGATG GAGGGCG 27

(2) INFORMATION FOR SEQ ID NO:159:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:
CGGCCTGGAA AGCTGAGATG GAGGGC 26

(2) INFORMATION FOR SEQ ID NO:160:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:
CGGCCTGGAA AGCTGAGATG GAGGG 25

(2) INFORMATION FOR SEQ ID NO:161:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:
CGGCCTGGAA AGCTGAGATG GAGG 24

(2) INFORMATION FOR SEQ ID NO:162:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:
CGGCCTGGAA AGCTGAGATG GAG 23

(2) INFORMATION FOR SEQ ID NO:163:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:
CGGCCTGGAA AGCTGAGATG GA 22

(2) INFORMATION FOR SEQ ID NO:164:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:
CGGCCTGGAA AGCTGAGATG G 21

(2) INFORMATION FOR SEQ ID NO:165:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:
CGGCCTGGAA AGCTGAGATG 20

(2) INFORMATION FOR SEQ ID NO:166:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:
CGGCCTGGAA AGCTGAGAT 19

(2) INFORMATION FOR SEQ ID NO:167:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:
CGGCCTGGAA AGCTGAGA 18

(2) INFORMATION FOR SEQ ID NO:168:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:
CGGCCTGGAA AGCTGAG 17

(2) INFORMATION FOR SEQ ID NO:169:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:
CGGCCTGGAA AGCTGA 16

(2) INFORMATION FOR SEQ ID NO:170:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:
CGGCCTGGAA AGCTG 15

(2) INFORMATION FOR SEQ ID NO:171:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:
CGGCCTGGAA AGCT 14

(2) INFORMATION FOR SEQ ID NO:172:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:
CGGCCTGGAA AGC 13

(2) INFORMATION FOR SEQ ID NO:173:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:
CGGCCTGGAA AG 12

(2) INFORMATION FOR SEQ ID NO:174:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:
CGGCCTGGAA A 11

(2) INFORMATION FOR SEQ ID NO:175:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:
CGGCCTGGAA 10

(2) INFORMATION FOR SEQ ID NO:176:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGCTGGGC 48

(2) INFORMATION FOR SEQ ID NO:177:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGCTGGG 47

(2) INFORMATION FOR SEQ ID NO:178:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGCTGG 46

(2) INFORMATION FOR SEQ ID NO:179:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGCTG 45

(2) INFORMATION FOR SEQ ID NO:180:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGCT 44

(2) INFORMATION FOR SEQ ID NO:181:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGC 43

(2) INFORMATION FOR SEQ ID NO:182:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGGGCACA GG 42

(2) INFORMATION FOR SEQ ID NO:183:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGGGCACA G 41

(2) INFORMATION FOR SEQ ID NO:184:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGGGCACA 40

(2) INFORMATION FOR SEQ ID NO:185:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGGGCAC 39

(2) INFORMATION FOR SEQ ID NO:186:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGGGCA 38

(2) INFORMATION FOR SEQ ID NO:187:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGGGC 37

(2) INFORMATION FOR SEQ ID NO:188:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGGG 36

(2) INFORMATION FOR SEQ ID NO:189:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGG 35

(2) INFORMATION FOR SEQ ID NO:190:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCG 34

(2) INFORMATION FOR SEQ ID NO:191:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGC 33

(2) INFORMATION FOR SEQ ID NO:192:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GG 32

(2) INFORMATION FOR SEQ ID NO:193:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT G 31

(2) INFORMATION FOR SEQ ID NO:194:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:
GGCCTGGAAA GCTGAGATGG AGGGCGGCAT 30

(2) INFORMATION FOR SEQ ID NO:195:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:
GGCCTGGAAA GCTGAGATGG AGGGCGGCA 29

(2) INFORMATION FOR SEQ ID NO:196:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:
GGCCTGGAAA GCTGAGATGG AGGGCGGC 28

(2) INFORMATION FOR SEQ ID NO:197:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:
GGCCTGGAAA GCTGAGATGG AGGGCGG 27

(2) INFORMATION FOR SEQ ID NO:198:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:
GGCCTGGAAA GCTGAGATGG AGGGCG 26

(2) INFORMATION FOR SEQ ID NO:199:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:
GGCCTGGAAA GCTGAGATGG AGGGC 25

(2) INFORMATION FOR SEQ ID NO:200:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:
GGCCTGGAAA GCTGAGATGG AGGG 24

(2) INFORMATION FOR SEQ ID NO:201:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:
GGCCTGGAAA GCTGAGATGG AGG 23

(2) INFORMATION FOR SEQ ID NO:202:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:
GGCCTGGAAA GCTGAGATGG AG 22

(2) INFORMATION FOR SEQ ID NO:203:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:
GGCCTGGAAA GCTGAGATGG A 21

(2) INFORMATION FOR SEQ ID NO:204:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:
GGCCTGGAAA GCTGAGATGG 20

(2) INFORMATION FOR SEQ ID NO:205:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:
GGCCTGGAAA GCTGAGATG 19

(2) INFORMATION FOR SEQ ID NO:206:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:
GGCCTGGAAA GCTGAGAT 18

(2) INFORMATION FOR SEQ ID NO:207:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:
GGCCTGGAAA GCTGAGA 17

(2) INFORMATION FOR SEQ ID NO:208:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:
GGCCTGGAAA GCTGAG 16

(2) INFORMATION FOR SEQ ID NO:209:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:
GGCCTGGAAA GCTGA 15

(2) INFORMATION FOR SEQ ID NO:210:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:
GGCCTGGAAA GCTG 14

(2) INFORMATION FOR SEQ ID NO:211:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:
GGCCTGGAAA GCT 13

(2) INFORMATION FOR SEQ ID NO:212:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:
GGCCTGGAAA GC 12

(2) INFORMATION FOR SEQ ID NO:213:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:
GGCCTGGAAA G 11

(2) INFORMATION FOR SEQ ID NO:214:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:
GGCCTGGAAA 10

(2) INFORMATION FOR SEQ ID NO:215:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTGGGC 47

(2) INFORMATION FOR SEQ ID NO:216:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTGGG 46

(2) INFORMATION FOR SEQ ID NO:217:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTGG 45

(2) INFORMATION FOR SEQ ID NO:218:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTG 44

(2) INFORMATION FOR SEQ ID NO:219:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG GCT 43

(2) INFORMATION FOR SEQ ID NO:220:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG GC 42

(2) INFORMATION FOR SEQ ID NO:221:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG G 41

(2) INFORMATION FOR SEQ ID NO:222:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG 40

(2) INFORMATION FOR SEQ ID NO:223:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGCACA 39

(2) INFORMATION FOR SEQ ID NO:224:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGCAC 38

(2) INFORMATION FOR SEQ ID NO:225:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGCA 37

(2) INFORMATION FOR SEQ ID NO:226:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGGC 36

(2) INFORMATION FOR SEQ ID NO:227:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGGG 35

(2) INFORMATION FOR SEQ ID NO:228:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCGG 34

(2) INFORMATION FOR SEQ ID NO:229:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GCG 33

(2) INFORMATION FOR SEQ ID NO:230:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG GC 32

(2) INFORMATION FOR SEQ ID NO:231:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG G 31

(2) INFORMATION FOR SEQ ID NO:232:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:
GCCTGGAAAG CTGAGATGGA GGGCGGCATG 30

(2) INFORMATION FOR SEQ ID NO:233:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:
GCCTGGAAAG CTGAGATGGA GGGCGGCAT 29

(2) INFORMATION FOR SEQ ID NO:234:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:
GCCTGGAAAG CTGAGATGGA GGGCGGCA 28

(2) INFORMATION FOR SEQ ID NO:235:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:
GCCTGGAAAG CTGAGATGGA GGGCGGC 27

(2) INFORMATION FOR SEQ ID NO:236:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:
GCCTGGAAAG CTGAGATGGA GGGCGG 26

(2) INFORMATION FOR SEQ ID NO:237:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:
GCCTGGAAAG CTGAGATGGA GGGCG 25

(2) INFORMATION FOR SEQ ID NO:238:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:
GCCTGGAAAG CTGAGATGGA GGGC 24

(2) INFORMATION FOR SEQ ID NO:239:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:
GCCTGGAAAG CTGAGATGGA GGG 23

(2) INFORMATION FOR SEQ ID NO:240:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:
GCCTGGAAAG CTGAGATGGA GG 22

(2) INFORMATION FOR SEQ ID NO:241:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:
GCCTGGAAAG CTGAGATGGA G 21

(2) INFORMATION FOR SEQ ID NO:242:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:
GCCTGGAAAG CTGAGATGGA 20

(2) INFORMATION FOR SEQ ID NO:243:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:
GCCTGGAAAG CTGAGATGG 19

(2) INFORMATION FOR SEQ ID NO:244:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:
GCCTGGAAAG CTGAGATG 18

(2) INFORMATION FOR SEQ ID NO:245:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:
GCCTGGAAAG CTGAGAT 17

(2) INFORMATION FOR SEQ ID NO:246:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:
GCCTGGAAAG CTGAGA 16

(2) INFORMATION FOR SEQ ID NO:247:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:
GCCTGGAAAG CTGAG 15

(2) INFORMATION FOR SEQ ID NO:248:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:
GCCTGGAAAG CTGA 14

(2) INFORMATION FOR SEQ ID NO:249:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:
GCCTGGAAAG CTG 13

(2) INFORMATION FOR SEQ ID NO:250:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:
GCCTGGAAAG CT 12

(2) INFORMATION FOR SEQ ID NO:251:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:
GCCTGGAAAG C 11

(2) INFORMATION FOR SEQ ID NO:252:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:
GCCTGGAAAG 10

(2) INFORMATION FOR SEQ ID NO:253:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG CGGGCACAGG CTGGGC 46

(2) INFORMATION FOR SEQ ID NO:254:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG CGGGCACAGG CTGGG 45

(2) INFORMATION FOR SEQ ID NO:255:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG CGGGCACAGG CTGG 44

(2) INFORMATION FOR SEQ ID NO:256:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG CGGGCACAGG CTG 43

(2) INFORMATION FOR SEQ ID NO:257:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG CGGGCACAGG CT 42

(2) INFORMATION FOR SEQ ID NO:258:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG CGGGCACAGG C 41

(2) INFORMATION FOR SEQ ID NO:259:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG CGGGCACAGG 40

(2) INFORMATION FOR SEQ ID NO:260:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG CGGGCACAG 39

(2) INFORMATION FOR SEQ ID NO:261:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG CGGGCACA 38

(2) INFORMATION FOR SEQ ID NO:262:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG CGGGCAC 37

(2) INFORMATION FOR SEQ ID NO:263:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG CGGGCA 36

(2) INFORMATION FOR SEQ ID NO:264:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG CGGGC 35

(2) INFORMATION FOR SEQ ID NO:265:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG CGGG 34

(2) INFORMATION FOR SEQ ID NO:266:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG CGG 33

(2) INFORMATION FOR SEQ ID NO:267:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG CG 32

(2) INFORMATION FOR SEQ ID NO:268:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG C 31

(2) INFORMATION FOR SEQ ID NO:269:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:
CCTGGAAAGC TGAGATGGAG GGCGGCATGG 30

(2) INFORMATION FOR SEQ ID NO:270:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:
CCTGGAAAGC TGAGATGGAG GGCGGCATG 29

(2) INFORMATION FOR SEQ ID NO:271:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:
CCTGGAAAGC TGAGATGGAG GGCGGCAT 28

(2) INFORMATION FOR SEQ ID NO:272:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:
CCTGGAAAGC TGAGATGGAG GGCGGCA 27

(2) INFORMATION FOR SEQ ID NO:273:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:
CCTGGAAAGC TGAGATGGAG GGCGGC 26

(2) INFORMATION FOR SEQ ID NO:274:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:
CCTGGAAAGC TGAGATGGAG GGCGG 25

(2) INFORMATION FOR SEQ ID NO:275:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:
CCTGGAAAGC TGAGATGGAG GGCG 24

(2) INFORMATION FOR SEQ ID NO:276:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:
CCTGGAAAGC TGAGATGGAG GGC 23

(2) INFORMATION FOR SEQ ID NO:277:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:
CCTGGAAAGC TGAGATGGAG GG 22

(2) INFORMATION FOR SEQ ID NO:278:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:
CCTGGAAAGC TGAGATGGAG G 21

(2) INFORMATION FOR SEQ ID NO:279:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:
CCTGGAAAGC TGAGATGGAG 20

(2) INFORMATION FOR SEQ ID NO:280:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:
CCTGGAAAGC TGAGATGGA 19

(2) INFORMATION FOR SEQ ID NO:281:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:
CCTGGAAAGC TGAGATGG 18

(2) INFORMATION FOR SEQ ID NO:282:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:
CCTGGAAAGC TGAGATG 17

(2) INFORMATION FOR SEQ ID NO:283:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:
CCTGGAAAGC TGAGAT 16

(2) INFORMATION FOR SEQ ID NO:284:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:
CCTGGAAAGC TGAGA 15

(2) INFORMATION FOR SEQ ID NO:285:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:
CCTGGAAAGC TGAG 14

(2) INFORMATION FOR SEQ ID NO:286:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:
CCTGGAAAGC TGA 13

(2) INFORMATION FOR SEQ ID NO:287:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:
CCTGGAAAGC TG 12

(2) INFORMATION FOR SEQ ID NO:288:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:
CCTGGAAAGC T 11

(2) INFORMATION FOR SEQ ID NO:289:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:
CCTGGAAAGC 10

(2) INFORMATION FOR SEQ ID NO:290:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAGGC TGGGC 45

(2) INFORMATION FOR SEQ ID NO:291:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAGGC TGGG 44

(2) INFORMATION FOR SEQ ID NO:292:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAGGC TGG 43

(2) INFORMATION FOR SEQ ID NO:293:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAGGC TG 42

(2) INFORMATION FOR SEQ ID NO:294:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAGGC T 41

(2) INFORMATION FOR SEQ ID NO:295:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAGGC 40

(2) INFORMATION FOR SEQ ID NO:296:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAGG 39

(2) INFORMATION FOR SEQ ID NO:297:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACAG 38

(2) INFORMATION FOR SEQ ID NO:298:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCACA 37

(2) INFORMATION FOR SEQ ID NO:299:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCAC 36

(2) INFORMATION FOR SEQ ID NO:300:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGCA 35

(2) INFORMATION FOR SEQ ID NO:301:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGGC 34

(2) INFORMATION FOR SEQ ID NO:302:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GGG 33

(2) INFORMATION FOR SEQ ID NO:303:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC GG 32

(2) INFORMATION FOR SEQ ID NO:304:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC G 31

(2) INFORMATION FOR SEQ ID NO:305:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:
CTGGAAAGCT GAGATGGAGG GCGGCATGGC 30

(2) INFORMATION FOR SEQ ID NO:306:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:
CTGGAAAGCT GAGATGGAGG GCGGCATGG 29

(2) INFORMATION FOR SEQ ID NO:307:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:
CTGGAAAGCT GAGATGGAGG GCGGCATG 28

(2) INFORMATION FOR SEQ ID NO:308:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:
CTGGAAAGCT GAGATGGAGG GCGGCAT 27

(2) INFORMATION FOR SEQ ID NO:309:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:
CTGGAAAGCT GAGATGGAGG GCGGCA 26

(2) INFORMATION FOR SEQ ID NO:310:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:
CTGGAAAGCT GAGATGGAGG GCGGC 25

(2) INFORMATION FOR SEQ ID NO:311:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:
CTGGAAAGCT GAGATGGAGG GCGG 24

(2) INFORMATION FOR SEQ ID NO:312:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:
CTGGAAAGCT GAGATGGAGG GCG 23

(2) INFORMATION FOR SEQ ID NO:313:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

CTGGAAAGCT GAGATGGAGG GC 22

(2) INFORMATION FOR SEQ ID NO:314:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:
CTGGAAAGCT GAGATGGAGG G 21

(2) INFORMATION FOR SEQ ID NO:315:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:
CTGGAAAGCT GAGATGGAGG 20

(2) INFORMATION FOR SEQ ID NO:316:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:
CTGGAAAGCT GAGATGGAG 19

(2) INFORMATION FOR SEQ ID NO:317:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:
CTGGAAAGCT GAGATGGA 18

(2) INFORMATION FOR SEQ ID NO:318:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:
CTGGAAAGCT GAGATGG 17

(2) INFORMATION FOR SEQ ID NO:319:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:
CTGGAAAGCT GAGATG 16

(2) INFORMATION FOR SEQ ID NO:320:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:
CTGGAAAGCT GAGAT 15

(2) INFORMATION FOR SEQ ID NO:321:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:
CTGGAAAGCT GAGA 14

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:
CTGGAAAGCT GAG 13

(2) INFORMATION FOR SEQ ID NO:323:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:
CTGGAAAGCT GA 12

(2) INFORMATION FOR SEQ ID NO:324:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:
CTGGAAAGCT G 11

(2) INFORMATION FOR SEQ ID NO:325:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:
CTGGAAAGCT 10

(2) INFORMATION FOR SEQ ID NO:326:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAGGCT GGGC 44

(2) INFORMATION FOR SEQ ID NO:327:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAGGCT GGG 43

(2) INFORMATION FOR SEQ ID NO:328:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAGGCT GG 42

(2) INFORMATION FOR SEQ ID NO:329:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAGGCT G 41

(2) INFORMATION FOR SEQ ID NO:330:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAGGCT 40

(2) INFORMATION FOR SEQ ID NO:331:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAGGC 39

(2) INFORMATION FOR SEQ ID NO:332:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAGG 38

(2) INFORMATION FOR SEQ ID NO:333:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAG 37

(2) INFORMATION FOR SEQ ID NO:334:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACA 36

(2) INFORMATION FOR SEQ ID NO:335:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCAC 35

(2) INFORMATION FOR SEQ ID NO:336:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCA 34

(2) INFORMATION FOR SEQ ID NO:337:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:
TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGC 33

(2) INFORMATION FOR SEQ ID NO:338:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

TGGAAAGCTG AGATGGAGGG CGGCATGGCG GG 32

(2) INFORMATION FOR SEQ ID NO:339:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:
TGGAAAGCTG AGATGGAGGG CGGCATGGCG G 31

(2) INFORMATION FOR SEQ ID NO:340:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:
TGGAAAGCTG AGATGGAGGG CGGCATGGCG 30

(2) INFORMATION FOR SEQ ID NO:341:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:
TGGAAAGCTG AGATGGAGGG CGGCATGGC 29

(2) INFORMATION FOR SEQ ID NO:342:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:
TGGAAAGCTG AGATGGAGGG CGGCATGG 28

(2) INFORMATION FOR SEQ ID NO:343:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:
TGGAAAGCTG AGATGGAGGG CGGCATG 27

(2) INFORMATION FOR SEQ ID NO:344:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:
TGGAAAGCTG AGATGGAGGG CGGCAT 26

(2) INFORMATION FOR SEQ ID NO:345:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:
TGGAAAGCTG AGATGGAGGG CGGCA 25

(2) INFORMATION FOR SEQ ID NO:346:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:
TGGAAAGCTG AGATGGAGGG CGGC 24

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:
TGGAAAGCTG AGATGGAGGG CGG 23

(2) INFORMATION FOR SEQ ID NO:348:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:
TGGAAAGCTG AGATGGAGGG CG 22

(2) INFORMATION FOR SEQ ID NO:349:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:
TGGAAAGCTG AGATGGAGGG C 21

(2) INFORMATION FOR SEQ ID NO:350:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:
TGGAAAGCTG AGATGGAGGG 20

(2) INFORMATION FOR SEQ ID NO:351:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:
TGGAAAGCTG AGATGGAGG 19

(2) INFORMATION FOR SEQ ID NO:352:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:
TGGAAAGCTG AGATGGAG 18

(2) INFORMATION FOR SEQ ID NO:353:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:
TGGAAAGCTG AGATGGA 17

(2) INFORMATION FOR SEQ ID NO:354:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:
TGGAAAGCTG AGATGG 16

(2) INFORMATION FOR SEQ ID NO:355:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:
TGGAAAGCTG AGATG 15

(2) INFORMATION FOR SEQ ID NO:356:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:
TGGAAAGCTG AGAT 14

(2) INFORMATION FOR SEQ ID NO:357:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:
TGGAAAGCTG AGA 13

(2) INFORMATION FOR SEQ ID NO:358:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:
TGGAAAGCTG AG 12

(2) INFORMATION FOR SEQ ID NO:359:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:
TGGAAAGCTG A 11

(2) INFORMATION FOR SEQ ID NO:360:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:
TGGAAAGCTG 10

(2) INFORMATION FOR SEQ ID NO:361:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:
GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACAGGCTG GGC 43

(2) INFORMATION FOR SEQ ID NO:362:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:
GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACAGGCTG GG 42

(2) INFORMATION FOR SEQ ID NO:363:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACAGGCTG G 41

(2) INFORMATION FOR SEQ ID NO:364:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:
GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACAGGCTG 40

(2) INFORMATION FOR SEQ ID NO:365:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:
GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACAGGCT 39

(2) INFORMATION FOR SEQ ID NO:366:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:
GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACAGGC 38

(2) INFORMATION FOR SEQ ID NO:367:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 0 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

(2) INFORMATION FOR SEQ ID NO:368:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:
GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACAG 36

(2) INFORMATION FOR SEQ ID NO:369:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:
GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCACA 35

(2) INFORMATION FOR SEQ ID NO:370:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:
GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCAC 34

(2) INFORMATION FOR SEQ ID NO:371:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:
GGAAAGCTGA GATGGAGGGC GGCATGGCGG GCA 33

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:
GGAAAGCTGA GATGGAGGGC GGCATGGCGG GC 32

(2) INFORMATION FOR SEQ ID NO:373:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:
GGAAAGCTGA GATGGAGGGC GGCATGGCGG G 31

(2) INFORMATION FOR SEQ ID NO:374:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:
GGAAAGCTGA GATGGAGGGC GGCATGGCGG 30

(2) INFORMATION FOR SEQ ID NO:375:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:
GGAAAGCTGA GATGGAGGGC GGCATGGCG 29

(2) INFORMATION FOR SEQ ID NO:376:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:
GGAAAGCTGA GATGGAGGGC GGCATGGC 28

(2) INFORMATION FOR SEQ ID NO:377:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:
GGAAAGCTGA GATGGAGGGC GGCATGG 27

(2) INFORMATION FOR SEQ ID NO:378:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:
GGAAAGCTGA GATGGAGGGC GGCATG 26

(2) INFORMATION FOR SEQ ID NO:379:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:
GGAAAGCTGA GATGGAGGGC GGCAT 25

(2) INFORMATION FOR SEQ ID NO:380:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:
GGAAAGCTGA GATGGAGGGC GGCA 24

(2) INFORMATION FOR SEQ ID NO:381:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:
GGAAAGCTGA GATGGAGGGC GGC 23

(2) INFORMATION FOR SEQ ID NO:382:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:
GGAAAGCTGA GATGGAGGGC GG 22

(2) INFORMATION FOR SEQ ID NO:383:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:
GGAAAGCTGA GATGGAGGGC G 21

(2) INFORMATION FOR SEQ ID NO:384:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:
GGAAAGCTGA GATGGAGGGC 20

(2) INFORMATION FOR SEQ ID NO:385:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:
GGAAAGCTGA GATGGAGGG 19

(2) INFORMATION FOR SEQ ID NO:386:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:
GGAAAGCTGA GATGGAGG 18

(2) INFORMATION FOR SEQ ID NO:387:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:
GGAAAGCTGA GATGGAGG 18

(2) INFORMATION FOR SEQ ID NO:388:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

GGAAAGCTGA GATGGA 16

(2) INFORMATION FOR SEQ ID NO:389:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:
GGAAAGCTGA GATGG 15

(2) INFORMATION FOR SEQ ID NO:390:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:
GGAAAGCTGA GATG 14

(2) INFORMATION FOR SEQ ID NO:391:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:
GGAAAGCTGA GAT 13

(2) INFORMATION FOR SEQ ID NO:392:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:
GGAAAGCTGA GA 12

(2) INFORMATION FOR SEQ ID NO:393:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:
GGAAAGCTGA G 11

(2) INFORMATION FOR SEQ ID NO:394:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:
GGAAAGCTGA 10

(2) INFORMATION FOR SEQ ID NO:395:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAGGCTGG GC 42

(2) INFORMATION FOR SEQ ID NO:396:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAGGCTGG G 41

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAGGCTGG 40

(2) INFORMATION FOR SEQ ID NO:398:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAGGCTG 39

(2) INFORMATION FOR SEQ ID NO:399:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAGGCT 38

(2) INFORMATION FOR SEQ ID NO:400:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAGGC 37

(2) INFORMATION FOR SEQ ID NO:401:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAGG 36

(2) INFORMATION FOR SEQ ID NO:402:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACAG 35

(2) INFORMATION FOR SEQ ID NO:403:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACA 34

(2) INFORMATION FOR SEQ ID NO:404:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CACA 34

(2) INFORMATION FOR SEQ ID NO:405:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG CA 32

(2) INFORMATION FOR SEQ ID NO:406:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG C 31

(2) INFORMATION FOR SEQ ID NO:407:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:
GAAAGCTGAG ATGGAGGGCG GCATGGCGGG 30

(2) INFORMATION FOR SEQ ID NO:408:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:
GAAAGCTGAG ATGGAGGGCG GCATGGCGG 29

(2) INFORMATION FOR SEQ ID NO:409:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:
GAAAGCTGAG ATGGAGGGCG GCATGGCG 28

(2) INFORMATION FOR SEQ ID NO:410:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:
GAAAGCTGAG ATGGAGGGCG GCATGGC 27

(2) INFORMATION FOR SEQ ID NO:411:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:
GAAAGCTGAG ATGGAGGGCG GCATGG 26

(2) INFORMATION FOR SEQ ID NO:412:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:
GAAAGCTGAG ATGGAGGGCG GCATG 25

(2) INFORMATION FOR SEQ ID NO:413:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GAAAGCTGAG ATGGAGGGCG GCAT 24

(2) INFORMATION FOR SEQ ID NO:414:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:
GAAAGCTGAG ATGGAGGGCG GCA 23

(2) INFORMATION FOR SEQ ID NO:415:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:
GAAAGCTGAG ATGGAGGGCG GC 22

(2) INFORMATION FOR SEQ ID NO:416:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:
GAAAGCTGAG ATGGAGGGCG G 21

(2) INFORMATION FOR SEQ ID NO:417:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:
GAAAGCTGAG ATGGAGGGCG 20

(2) INFORMATION FOR SEQ ID NO:418:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:
GAAAGCTGAG ATGGAGGGC 19

(2) INFORMATION FOR SEQ ID NO:419:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:
GAAAGCTGAG ATGGAGGG 18

(2) INFORMATION FOR SEQ ID NO:420:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:
GAAAGCTGAG ATGGAGG 17

(2) INFORMATION FOR SEQ ID NO:421:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:
GAAAGCTGAG ATGGAG 16

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:
GAAAGCTGAG ATGGA 15

(2) INFORMATION FOR SEQ ID NO:423:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:
GAAAGCTGAG ATGG 14

(2) INFORMATION FOR SEQ ID NO:424:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:
GAAAGCTGAG ATG 13

(2) INFORMATION FOR SEQ ID NO:425:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:
GAAAGCTGAG AT 12

(2) INFORMATION FOR SEQ ID NO:426:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:
GAAAGCTGAG A 11

(2) INFORMATION FOR SEQ ID NO:427:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:
GAAAGCTGAG 10

(2) INFORMATION FOR SEQ ID NO:428:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGGG C 41

(2) INFORMATION FOR SEQ ID NO:429:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGGG 40

(2) INFORMATION FOR SEQ ID NO:430:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGG 39

(2) INFORMATION FOR SEQ ID NO:431:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTG 38

(2) INFORMATION FOR SEQ ID NO:432:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCT 37

(2) INFORMATION FOR SEQ ID NO:433:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGC 36

(2) INFORMATION FOR SEQ ID NO:434:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGG 35

(2) INFORMATION FOR SEQ ID NO:435:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAG 34

(2) INFORMATION FOR SEQ ID NO:436:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACA 33

(2) INFORMATION FOR SEQ ID NO:437:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC AC 32

(2) INFORMATION FOR SEQ ID NO:438:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

AAAGCTGAGA TGGAGGGCGG CATGGCGGGC A 31

(2) INFORMATION FOR SEQ ID NO:439:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:
AAAGCTGAGA TGGAGGGCGG CATGGCGGGC 30

(2) INFORMATION FOR SEQ ID NO:440:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:
AAAGCTGAGA TGGAGGGCGG CATGGCGGG 29

(2) INFORMATION FOR SEQ ID NO:441:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:
AAAGCTGAGA TGGAGGGCGG CATGGCGG 28

(2) INFORMATION FOR SEQ ID NO:442:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:
AAAGCTGAGA TGGAGGGCGG CATGGCG 27

(2) INFORMATION FOR SEQ ID NO:443:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:
AAAGCTGAGA TGGAGGGCGG CATGGC 26

(2) INFORMATION FOR SEQ ID NO:444:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:
AAAGCTGAGA TGGAGGGCGG CATGG 25

(2) INFORMATION FOR SEQ ID NO:445:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:
AAAGCTGAGA TGGAGGGCGG CATG 24

(2) INFORMATION FOR SEQ ID NO:446:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:
AAAGCTGAGA TGGAGGGCGG CAT 23

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:
AAAGCTGAGA TGGAGGGCGG CA 22

(2) INFORMATION FOR SEQ ID NO:448:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:
AAAGCTGAGA TGGAGGGCGG C 21

(2) INFORMATION FOR SEQ ID NO:449:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:
AAAGCTGAGA TGGAGGGCGG 20

(2) INFORMATION FOR SEQ ID NO:450:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:
AAAGCTGAGA TGGAGGGCG 19

(2) INFORMATION FOR SEQ ID NO:451:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:
AAAGCTGAGA TGGAGGGC 18

(2) INFORMATION FOR SEQ ID NO:452:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:
AAAGCTGAGA TGGAGGG 17

(2) INFORMATION FOR SEQ ID NO:453:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:
AAAGCTGAGA TGGAGG 16

(2) INFORMATION FOR SEQ ID NO:454:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:
AAAGCTGAGA TGGAG 15

(2) INFORMATION FOR SEQ ID NO:455:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:
AAAGCTGAGA TGGA 14

(2) INFORMATION FOR SEQ ID NO:456:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:
AAAGCTGAGA TGG 13

(2) INFORMATION FOR SEQ ID NO:457:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:
AAAGCTGAGA TG 12

(2) INFORMATION FOR SEQ ID NO:458:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:
AAAGCTGAGA T 11

(2) INFORMATION FOR SEQ ID NO:459:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:
AAAGCTGAGA 10

(2) INFORMATION FOR SEQ ID NO:460:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:
AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTGGGC 40

(2) INFORMATION FOR SEQ ID NO:461:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:
AAAGCTGAGA T 11

(2) INFORMATION FOR SEQ ID NO:462:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:
AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTGG 38

(2) INFORMATION FOR SEQ ID NO:463:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTG 37

(2) INFORMATION FOR SEQ ID NO:464:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: lin ar
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:
AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCT 36

(2) INFORMATION FOR SEQ ID NO:465:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:
AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGC 35

(2) INFORMATION FOR SEQ ID NO:466:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:
AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGG 34

(2) INFORMATION FOR SEQ ID NO:467:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:
AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAG 33

(2) INFORMATION FOR SEQ ID NO:468:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:
AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CA 32

(2) INFORMATION FOR SEQ ID NO:469:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:
AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA C 31

(2) INFORMATION FOR SEQ ID NO:470:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:
AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA 30

(2) INFORMATION FOR SEQ ID NO:471:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:
AAGCTGAGAT GGAGGGCGGC ATGGCGGGC 29

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:
AAGCTGAGAT GGAGGGCGGC ATGGCGGG 28

(2) INFORMATION FOR SEQ ID NO:473:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:
AAGCTGAGAT GGAGGGCGGC ATGGCGG 27

(2) INFORMATION FOR SEQ ID NO:474:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:
AAGCTGAGAT GGAGGGCGGC ATGGCG 26

(2) INFORMATION FOR SEQ ID NO:475:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:
AAGCTGAGAT GGAGGGCGGC ATGGC 25

(2) INFORMATION FOR SEQ ID NO:476:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:
AAGCTGAGAT GGAGGGCGGC ATGG 24

(2) INFORMATION FOR SEQ ID NO:477:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:
AAGCTGAGAT GGAGGGCGGC ATG 23

(2) INFORMATION FOR SEQ ID NO:478:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:
AAGCTGAGAT GGAGGGCGGC AT 22

(2) INFORMATION FOR SEQ ID NO:479:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:
AAGCTGAGAT GGAGGGCGGC A 21

(2) INFORMATION FOR SEQ ID NO:480:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:
AAGCTGAGAT GGAGGGCGGC 20

(2) INFORMATION FOR SEQ ID NO:481:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:
AAGCTGAGAT GGAGGGCGG 19

(2) INFORMATION FOR SEQ ID NO:482:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:
AAGCTGAGAT GGAGGGCG 18

(2) INFORMATION FOR SEQ ID NO:483:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:
AAGCTGAGAT GGAGGGC 17

(2) INFORMATION FOR SEQ ID NO:484:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:
AAGCTGAGAT GGAGGG 16

(2) INFORMATION FOR SEQ ID NO:485:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:
AAGCTGAGAT GGAGG 15

(2) INFORMATION FOR SEQ ID NO:486:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:
AAGCTGAGAT GGAG 14

(2) INFORMATION FOR SEQ ID NO:487:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:
AAGCTGAGAT GGA 13

(2) INFORMATION FOR SEQ ID NO:488:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

AAGCTGAGAT GG 12

(2) INFORMATION FOR SEQ ID NO:489:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:
AAGCTGAGAT G 11

(2) INFORMATION FOR SEQ ID NO:490:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:
AAGCTGAGAT 10

(2) INFORMATION FOR SEQ ID NO:491:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:
AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTGGGC 39

(2) INFORMATION FOR SEQ ID NO:492:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:
AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTGGG 38

(2) INFORMATION FOR SEQ ID NO:493:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:
AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTGG 37

(2) INFORMATION FOR SEQ ID NO:494:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:
AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTG 36

(2) INFORMATION FOR SEQ ID NO:495:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:
AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCT 35

(2) INFORMATION FOR SEQ ID NO:496:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:
AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGC 34

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:
AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGG 33

(2) INFORMATION FOR SEQ ID NO:498:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:
AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AG 32

(2) INFORMATION FOR SEQ ID NO:499:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:
AGCTGAGATG GAGGGCGGCA TGGCGGGCAC A 31

(2) INFORMATION FOR SEQ ID NO:500:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:
AGCTGAGATG GAGGGCGGCA TGGCGGGCAC 30

(2) INFORMATION FOR SEQ ID NO:501:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:
AGCTGAGATG GAGGGCGGCA TGGCGGGCA 29

(2) INFORMATION FOR SEQ ID NO:502:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:
AGCTGAGATG GAGGGCGGCA TGGCGGGC 28

(2) INFORMATION FOR SEQ ID NO:503:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:
AGCTGAGATG GAGGGCGGCA TGGCGGG 27

(2) INFORMATION FOR SEQ ID NO:504:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:
AGCTGAGATG GAGGGCGGCA TGGCGG 26

(2) INFORMATION FOR SEQ ID NO:505:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:
AGCTGAGATG GAGGGCGGCA TGGCG 25

(2) INFORMATION FOR SEQ ID NO:506:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:
AGCTGAGATG GAGGGCGGCA TGGC 24

(2) INFORMATION FOR SEQ ID NO:507:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:
AGCTGAGATG GAGGGCGGCA TGG 23

(2) INFORMATION FOR SEQ ID NO:508:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:
AGCTGAGATG GAGGGCGGCA TG 22

(2) INFORMATION FOR SEQ ID NO:509:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:
AGCTGAGATG GAGGGCGGCA T 21

(2) INFORMATION FOR SEQ ID NO:510:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:
AGCTGAGATG GAGGGCGGCA 20

(2) INFORMATION FOR SEQ ID NO:511:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:
AGCTGAGATG GAGGGCGGC 19

(2) INFORMATION FOR SEQ ID NO:512:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:
AGCTGAGATG GAGGGCGG 18

(2) INFORMATION FOR SEQ ID NO:513:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

AGCTGAGATG GAGGGCG 17

(2) INFORMATION FOR SEQ ID NO:514:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:
AGCTGAGATG GAGGGC 16

(2) INFORMATION FOR SEQ ID NO:515:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:
AGCTGAGATG GAGGG 15

(2) INFORMATION FOR SEQ ID NO:516:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:
AGCTGAGATG GAGG 14

(2) INFORMATION FOR SEQ ID NO:517:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:
AGCTGAGATG GAG 13

(2) INFORMATION FOR SEQ ID NO:518:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:
AGCTGAGATG GA 12

(2) INFORMATION FOR SEQ ID NO:519:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:
AGCTGAGATG G 11

(2) INFORMATION FOR SEQ ID NO:520:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:
AGCTGAGATG 10

(2) INFORMATION FOR SEQ ID NO:521:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:
GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGCTGGGC 38

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:
GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGCTGGG 37

(2) INFORMATION FOR SEQ ID NO:523:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:
GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGCTGG 36

(2) INFORMATION FOR SEQ ID NO:524:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:
GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGCTG 35

(2) INFORMATION FOR SEQ ID NO:525:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:
GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGCT 34

(2) INFORMATION FOR SEQ ID NO:526:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:
GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGC 33

(2) INFORMATION FOR SEQ ID NO:527:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:
GCTGAGATGG AGGGCGGCAT GGCGGGCACA GG 32

(2) INFORMATION FOR SEQ ID NO:528:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:
GCTGAGATGG AGGGCGGCAT GGCGGGCACA G 31

(2) INFORMATION FOR SEQ ID NO:529:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:
GCTGAGATGG AGGGCGGCAT GGCGGGCACA 30

(2) INFORMATION FOR SEQ ID NO:530:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:
GCTGAGATGG AGGGCGGCAT GGCGGGCAC 29

(2) INFORMATION FOR SEQ ID NO:531:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:
GCTGAGATGG AGGGCGGCAT GGCGGGCA 28

(2) INFORMATION FOR SEQ ID NO:532:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:
GCTGAGATGG AGGGCGGCAT GGCGGGC 27

(2) INFORMATION FOR SEQ ID NO:533:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:
GCTGAGATGG AGGGCGGCAT GGCGGG 26

(2) INFORMATION FOR SEQ ID NO:534:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:
GCTGAGATGG AGGGCGGCAT GGCGG 25

(2) INFORMATION FOR SEQ ID NO:535:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:
GCTGAGATGG AGGGCGGCAT GGCG 24

(2) INFORMATION FOR SEQ ID NO:536:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:
GCTGAGATGG AGGGCGGCAT GGC 23

(2) INFORMATION FOR SEQ ID NO:537:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:
GCTGAGATGG AGGGCGGCAT GG 22

(2) INFORMATION FOR SEQ ID NO:538:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

GCTGAGATGG AGGGCGGCAT G 21

(2) INFORMATION FOR SEQ ID NO:539:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:
GCTGAGATGG AGGGCGGCAT 20

(2) INFORMATION FOR SEQ ID NO:540:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:
GCTGAGATGG AGGGCGGCA 19

(2) INFORMATION FOR SEQ ID NO:541:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:
GCTGAGATGG AGGGCGGC 18

(2) INFORMATION FOR SEQ ID NO:542:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:
GCTGAGATGG AGGGCGG 17

(2) INFORMATION FOR SEQ ID NO:543:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:
GCTGAGATGG AGGGCG 16

(2) INFORMATION FOR SEQ ID NO:544:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:
GCTGAGATGG AGGGC 15

(2) INFORMATION FOR SEQ ID NO:545:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:
GCTGAGATGG AGGG 14

(2) INFORMATION FOR SEQ ID NO:546:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:
GCTGAGATGG AGG 13

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:
GCTGAGATGG AG 12

(2) INFORMATION FOR SEQ ID NO:548:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:
GCTGAGATGG A 11

(2) INFORMATION FOR SEQ ID NO:549:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:
GCTGAGATGG 10

(2) INFORMATION FOR SEQ ID NO:550:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:
CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTGGGC 37

(2) INFORMATION FOR SEQ ID NO:551:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:
CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTGGG 36

(2) INFORMATION FOR SEQ ID NO:552:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:
CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTGG 35

(2) INFORMATION FOR SEQ ID NO:553:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:
CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTG 34

(2) INFORMATION FOR SEQ ID NO:554:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:
CTGAGATGGA GGGCGGCATG GCGGGCACAG GCT 33

(2) INFORMATION FOR SEQ ID NO:555:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:
CTGAGATGGA GGGCGGCATG GCGGGCACAG GC 32

(2) INFORMATION FOR SEQ ID NO:556:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:
CTGAGATGGA GGGCGGCATG GCGGGCACAG G 31

(2) INFORMATION FOR SEQ ID NO:557:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:
CTGAGATGGA GGGCGGCATG GCGGGCACAG 30

(2) INFORMATION FOR SEQ ID NO:558:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:
CTGAGATGGA GGGCGGCATG GCGGGCACA 29

(2) INFORMATION FOR SEQ ID NO:559:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:
CTGAGATGGA GGGCGGCATG GCGGGCAC 28

(2) INFORMATION FOR SEQ ID NO:560:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:
CTGAGATGGA GGGCGGCATG GCGGGCA 27

(2) INFORMATION FOR SEQ ID NO:561:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:
CTGAGATGGA GGGCGGCATG GCGGGC 26

(2) INFORMATION FOR SEQ ID NO:562:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:
CTGAGATGGA GGGCGGCATG GCGGG 25

(2) INFORMATION FOR SEQ ID NO:563:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

CTGAGATGGA GGGCGGCATG GCGG 24

(2) INFORMATION FOR SEQ ID NO:564:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:
CTGAGATGGA GGGCGGCATG GCG 23

(2) INFORMATION FOR SEQ ID NO:565:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:
CTGAGATGGA GGGCGGCATG GC 22

(2) INFORMATION FOR SEQ ID NO:566:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:
CTGAGATGGA GGGCGGCATG G 21

(2) INFORMATION FOR SEQ ID NO:567:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:
CTGAGATGGA GGGCGGCATG 20

(2) INFORMATION FOR SEQ ID NO:568:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:
CTGAGATGGA GGGCGGCAT 19

(2) INFORMATION FOR SEQ ID NO:569:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:
CTGAGATGGA GGGCGGCA 18

(2) INFORMATION FOR SEQ ID NO:570:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:
CTGAGATGGA GGGCGGC 17

(2) INFORMATION FOR SEQ ID NO:571:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:
CTGAGATGGA GGGCGG 16

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:
CTGAGATGGA GGGCG 15

(2) INFORMATION FOR SEQ ID NO:573:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:
CTGAGATGGA GGGC 14

(2) INFORMATION FOR SEQ ID NO:574:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:
CTGAGATGGA GGG 13

(2) INFORMATION FOR SEQ ID NO:575:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:
CTGAGATGGA GG 12

(2) INFORMATION FOR SEQ ID NO:576:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:
CTGAGATGGA G 11

(2) INFORMATION FOR SEQ ID NO:577:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:
CTGAGATGGA 10

(2) INFORMATION FOR SEQ ID NO:578:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:
TGAGATGGAG GGCGGCATGG CGGGCACAGG CTGGGC 36

(2) INFORMATION FOR SEQ ID NO:579:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:
TGAGATGGAG GGCGGCATGG CGGGCACAGG CTGGG 35

(2) INFORMATION FOR SEQ ID NO:580:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:
TGAGATGGAG GGCGGCATGG CGGGCACAGG CTGG 34

(2) INFORMATION FOR SEQ ID NO:581:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:
TGAGATGGAG GGCGGCATGG CGGGCACAGG CTG 33

(2) INFORMATION FOR SEQ ID NO:582:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:
TGAGATGGAG GGCGGCATGG CGGGCACAGG CT 32

(2) INFORMATION FOR SEQ ID NO:583:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:
TGAGATGGAG GGCGGCATGG CGGGCACAGG C 31

(2) INFORMATION FOR SEQ ID NO:584:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:
TGAGATGGAG GGCGGCATGG CGGGCACAGG 30

(2) INFORMATION FOR SEQ ID NO:585:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:
TGAGATGGAG GGCGGCATGG CGGGCACAG 29

(2) INFORMATION FOR SEQ ID NO:586:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:
TGAGATGGAG GGCGGCATGG CGGGCACA 28

(2) INFORMATION FOR SEQ ID NO:587:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:
TGAGATGGAG GGCGGCATGG CGGGCAC 27

(2) INFORMATION FOR SEQ ID NO:588:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

TGAGATGGAG GGCGGCATGG CGGGCA 26

(2) INFORMATION FOR SEQ ID NO:589:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:
TGAGATGGAG GGCGGCATGG CGGGC 25

(2) INFORMATION FOR SEQ ID NO:590:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:
TGAGATGGAG GGCGGCATGG CGGG 24

(2) INFORMATION FOR SEQ ID NO:591:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:
TGAGATGGAG GGCGGCATGG CGG 23

(2) INFORMATION FOR SEQ ID NO:592:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:
TGAGATGGAG GGCGGCATGG CG 22

(2) INFORMATION FOR SEQ ID NO:593:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:
TGAGATGGAG GGCGGCATGG C 21

(2) INFORMATION FOR SEQ ID NO:594:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:
TGAGATGGAG GGCGGCATGG 20

(2) INFORMATION FOR SEQ ID NO:595:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:
TGAGATGGAG GGCGGCATG 19

(2) INFORMATION FOR SEQ ID NO:596:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:
TGAGATGGAG GGCGGCAT 18

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:
TGAGATGGAG GGCGGCA 17

(2) INFORMATION FOR SEQ ID NO:598:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:
TGAGATGGAG GGCGGC 16

(2) INFORMATION FOR SEQ ID NO:599:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:
TGAGATGGAG GGCGG 15

(2) INFORMATION FOR SEQ ID NO:600:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:
TGAGATGGAG GGCG 14

(2) INFORMATION FOR SEQ ID NO:601:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:
TGAGATGGAG GGC 13

(2) INFORMATION FOR SEQ ID NO:602:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:
TGAGATGGAG GG 12

(2) INFORMATION FOR SEQ ID NO:603:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:
TGAGATGGAG G 11

(2) INFORMATION FOR SEQ ID NO:604:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:
TGAGATGGAG 10

(2) INFORMATION FOR SEQ ID NO:605:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:
GAGATGGAGG GCGGCATGGC GGGCACAGGC TGGGC 35

(2) INFORMATION FOR SEQ ID NO:606:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:
GAGATGGAGG GCGGCATGGC GGGCACAGGC TGGG 34

(2) INFORMATION FOR SEQ ID NO:607:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:
GAGATGGAGG GCGGCATGGC GGGCACAGGC TGG 33

(2) INFORMATION FOR SEQ ID NO:608:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:
GAGATGGAGG GCGGCATGGC GGGCACAGGC TG 32

(2) INFORMATION FOR SEQ ID NO:609:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:
GAGATGGAGG GCGGCATGGC GGGCACAGGC T 31

(2) INFORMATION FOR SEQ ID NO:610:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:
GAGATGGAGG GCGGCATGGC GGGCACAGG 29

(2) INFORMATION FOR SEQ ID NO:611:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:
GAGATGGAGG GCGGCATGGC GGGCACAGG 29

(2) INFORMATION FOR SEQ ID NO:612:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:
GAGATGGAGG GCGGCATGGC GGGCACAG 28

(2) INFORMATION FOR SEQ ID NO:613:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

GAGATGGAGG GCGGCATGGC GGGCACA 27

(2) INFORMATION FOR SEQ ID NO:614:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:
GAGATGGAGG GCGGCATGGC GGGCAC 26

(2) INFORMATION FOR SEQ ID NO:615:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:
GAGATGGAGG GCGGCATGGC GGGCA 25

(2) INFORMATION FOR SEQ ID NO:616:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:
GAGATGGAGG GCGGCATGGC GGGC 24

(2) INFORMATION FOR SEQ ID NO:617:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:
GAGATGGAGG GCGGCATGGC GGG 23

(2) INFORMATION FOR SEQ ID NO:618:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:
GAGATGGAGG GCGGCATGGC GG 22

(2) INFORMATION FOR SEQ ID NO:619:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:
GAGATGGAGG GCGGCATGGC G 21

(2) INFORMATION FOR SEQ ID NO:620:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:
GAGATGGAGG GCGGCATGGC 20

(2) INFORMATION FOR SEQ ID NO:621:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:
GAGATGGAGG GCGGCATGG 19

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:
GAGATGGAGG GCGGCATG 18

(2) INFORMATION FOR SEQ ID NO:623:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:
GAGATGGAGG GCGGCAT 17

(2) INFORMATION FOR SEQ ID NO:624:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:
GAGATGGAGG GCGGCA 16

(2) INFORMATION FOR SEQ ID NO:625:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:
GAGATGGAGG GCGGC 15

(2) INFORMATION FOR SEQ ID NO:626:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:
GAGATGGAGG GCGG 14

(2) INFORMATION FOR SEQ ID NO:627:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:
GAGATGGAGG GCG 13

(2) INFORMATION FOR SEQ ID NO:628:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:
GAGATGGAGG GC 12

(2) INFORMATION FOR SEQ ID NO:629:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:
GAGATGGAGG G 11

(2) INFORMATION FOR SEQ ID NO:630:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:
GAGATGGAGG 10

(2) INFORMATION FOR SEQ ID NO:631:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:
AGATGGAGGG CGGCATGGCG GGCACAGGCT GGGC 34

(2) INFORMATION FOR SEQ ID NO:632:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:
AGATGGAGGG CGGCATGGCG GGCACAGGCT GGG 33

(2) INFORMATION FOR SEQ ID NO:633:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:
AGATGGAGGG CGGCATGGCG GGCACAGGCT GG 32

(2) INFORMATION FOR SEQ ID NO:634:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:
AGATGGAGGG CGGCATGGCG GGCACAGGCT G 31

(2) INFORMATION FOR SEQ ID NO:635:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:
AGATGGAGGG CGGCATGGCG GGCACAGGCT 30

(2) INFORMATION FOR SEQ ID NO:636:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:
AGATGGAGGG CGGCATGGCG GGCACAGGC 29

(2) INFORMATION FOR SEQ ID NO:637:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:
AGATGGAGGG CGGCATGGCG GGCACAGG 28

(2) INFORMATION FOR SEQ ID NO:638:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

AGATGGAGGG CGGCATGGCG GGCACAG 27

(2) INFORMATION FOR SEQ ID NO:639:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:
AGATGGAGGG CGGCATGGCG GGCACA 26

(2) INFORMATION FOR SEQ ID NO:640:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:
AGATGGAGGG CGGCATGGCG GGCAC 25

(2) INFORMATION FOR SEQ ID NO:641:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:
AGATGGAGGG CGGCATGGCG GGCA 24

(2) INFORMATION FOR SEQ ID NO:642:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:
AGATGGAGGG CGGCATGGCG GGC 23

(2) INFORMATION FOR SEQ ID NO:643:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:
AGATGGAGGG CGGCATGGCG GG 22

(2) INFORMATION FOR SEQ ID NO:644:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:
AGATGGAGGG CGGCATGGCG G 21

(2) INFORMATION FOR SEQ ID NO:645:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:
AGATGGAGGG CGGCATGGCG 20

(2) INFORMATION FOR SEQ ID NO:646:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:
AGATGGAGGG CGGCATGGC 19

(2) INFORMATION FOR SEQ ID NO:647:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:
AGATGGAGGG CGGCATGG 18

(2) INFORMATION FOR SEQ ID NO:648:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:
AGATGGAGGG CGGCATG 17

(2) INFORMATION FOR SEQ ID NO:649:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:
AGATGGAGGG CGGCAT 16

(2) INFORMATION FOR SEQ ID NO:650:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:
AGATGGAGGG CGGCA 15

(2) INFORMATION FOR SEQ ID NO:651:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:
AGATGGAGGG CGGC 14

(2) INFORMATION FOR SEQ ID NO:652:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:
AGATGGAGGG CGG 13

(2) INFORMATION FOR SEQ ID NO:653:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:
AGATGGAGGG CG 12

(2) INFORMATION FOR SEQ ID NO:654:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:
AGATGGAGGG C 11

(2) INFORMATION FOR SEQ ID NO:655:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:
AGATGGAGGG 10

(2) INFORMATION FOR SEQ ID NO:656:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:
GATGGAGGGC GGCATGGCGG GCACAGGCTG GGC 33

(2) INFORMATION FOR SEQ ID NO:657:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:
GATGGAGGGC GGCATGGCGG GCACAGGCTG GG 32

(2) INFORMATION FOR SEQ ID NO:658:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:
GATGGAGGGC GGCATGGCGG GCACAGGCTG G 31

(2) INFORMATION FOR SEQ ID NO:659:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:
GATGGAGGGC GGCATGGCGG GCACAGGCTG 30

(2) INFORMATION FOR SEQ ID NO:660:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:
GATGGAGGGC GGCATGGCGG GCACAGGCT 29

(2) INFORMATION FOR SEQ ID NO:661:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:
GATGGAGGGC GGCATGGCGG GCACAGGC 28

(2) INFORMATION FOR SEQ ID NO:662:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:
GATGGAGGGC GGCATGGCGG GCACAGG 27

(2) INFORMATION FOR SEQ ID NO:663:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

GATGGAGGGC GGCATGGCGG GCACAG 26

(2) INFORMATION FOR SEQ ID NO:664:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:
GATGGAGGGC GGCATGGCGG GCACA 25

(2) INFORMATION FOR SEQ ID NO:665:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:
GATGGAGGGC GGCATGGCGG GCAC 24

(2) INFORMATION FOR SEQ ID NO:666:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:
GATGGAGGGC GGCATGGCGG GCA 23

(2) INFORMATION FOR SEQ ID NQ:667:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:
GATGGAGGGC GGCATGGCGG GC 22

(2) INFORMATION FOR SEQ ID NO:668:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:
GATGGAGGGC GGCATGGCGG G 21

(2) INFORMATION FOR SEQ ID NO:669:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:
GATGGAGGGC GGCATGGCGG 20

(2) INFORMATION FOR SEQ ID NO:670:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:
GATGGAGGGC GGCATGGCG 19

(2) INFORMATION FOR SEQ ID NO:671:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:
GATGGAGGGC GGCATGGC 18

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:
GATGGAGGGC GGCATGG 17

(2) INFORMATION FOR SEQ ID NO:673:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:
GATGGAGGGC GGCATG 16

(2) INFORMATION FOR SEQ ID NO:674:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:
GATGGAGGGC GGCAT 15

(2) INFORMATION FOR SEQ ID NO:675:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:
GATGGAGGGC GGCA 14

(2) INFORMATION FOR SEQ ID NO:676:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:
GATGGAGGGC GGC 13

(2) INFORMATION FOR SEQ ID NO:677:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:
GATGGAGGGC GG 12

(2) INFORMATION FOR SEQ ID NO:678:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:
GATGGAGGGC G 11

(2) INFORMATION FOR SEQ ID NO:679:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:
GATGGAGGGC 10

(2) INFORMATION FOR SEQ ID NO:680:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:
ATGGAGGGCG GCATGGCGGG CACAGGCTGG GC 32

(2) INFORMATION FOR SEQ ID NO:681:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:
ATGGAGGGCG GCATGGCGGG CACAGGCTGG G 31

(2) INFORMATION FOR SEQ ID NO:682:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:
ATGGAGGGCG GCATGGCGGG CACAGGCTGG 30

(2) INFORMATION FOR SEQ ID NO:683:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:
ATGGAGGGCG GCATGGCGGG CACAGGCTG 29

(2) INFORMATION FOR SEQ ID NO:684:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:
ATGGAGGGCG GCATGGCGGG CACAGGCT 28

(2) INFORMATION FOR SEQ ID NO:685:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:
ATGGAGGGCG GCATGGCGGG CACAGGC 27

(2) INFORMATION FOR SEQ ID NO:686:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:
ATGGAGGGCG GCATGGCGGG CACAGG 26

(2) INFORMATION FOR SEQ ID NO:687:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:
ATGGAGGGCG GCATGGCGGG CACAG 25

(2) INFORMATION FOR SEQ ID NO:688:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

ATGGAGGGCG GCATGGCGGG CACA 24

(2) INFORMATION FOR SEQ ID NO:689:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:
ATGGAGGGCG GCATGGCGGG CAC 23

(2) INFORMATION FOR SEQ ID NO:690:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:
ATGGAGGGCG GCATGGCGGG CA 22

(2) INFORMATION FOR SEQ ID NO:691:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:
ATGGAGGGCG GCATGGCGGG C 21

(2) INFORMATION FOR SEQ ID NO:692:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:
ATGGAGGGCG GCATGGCGGG 20

(2) INFORMATION FOR SEQ ID NO:693:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:
ATGGAGGGCG GCATGGCGG 19

(2) INFORMATION FOR SEQ ID NO:694:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:
ATGGAGGGCG GCATGGCG 18

(2) INFORMATION FOR SEQ ID NO:695:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:
ATGGAGGGCG GCATGGC 17

(2) INFORMATION FOR SEQ ID NO:696:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:
ATGGAGGGCG GCATGG 16

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:
ATGGAGGGCG GCATG 15

(2) INFORMATION FOR SEQ ID NO:698:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:
ATGGAGGGCG GCAT 14

(2) INFORMATION FOR SEQ ID NO:699:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:
ATGGAGGGCG GCA 13

(2) INFORMATION FOR SEQ ID NO:700:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:
ATGGAGGGCG GC 12

(2) INFORMATION FOR SEQ ID NO:701:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:
ATGGAGGGCG G 11

(2) INFORMATION FOR SEQ ID NO:702:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:
ATGGAGGGCG 10

(2) INFORMATION FOR SEQ ID NO:703:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:
TGGAGGGCGG CATGGCGGGC ACAGGCTGGG C 31

(2) INFORMATION FOR SEQ ID NO:704:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:
TGGAGGGCGG CATGGCGGGC ACAGGCTGGG 30

(2) INFORMATION FOR SEQ ID NO:705:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:
TGGAGGGCGG CATGGCGGGC ACAGGCTGG 29

(2) INFORMATION FOR SEQ ID NO:706:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:
TGGAGGGCGG CATGGCGGGC ACAGGCTG 28

(2) INFORMATION FOR SEQ ID NO:707:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:
TGGAGGGCGG CATGGCGGGC ACAGGCT 27

(2) INFORMATION FOR SEQ ID NO:708:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:
TGGAGGGCGG CATGGCGGGC ACAGGC 26

(2) INFORMATION FOR SEQ ID NO:709:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:
TGGAGGGCGG CATGGCGGGC ACAGG 25

(2) INFORMATION FOR SEQ ID NO:710:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:
TGGAGGGCGG CATGGCGGGC ACAG 24

(2) INFORMATION FOR SEQ ID NO:711:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:
TGGAGGGCGG CATGGCGGGC ACA 23

(2) INFORMATION FOR SEQ ID NO:712:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:
TGGAGGGCGG CATGGCGGGC AC 22

(2) INFORMATION FOR SEQ ID NO:713:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

TGGAGGGCGG CATGGCGGGC A 21

(2) INFORMATION FOR SEQ ID NO:714:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:
TGGAGGGCGG CATGGCGGGC 20

(2) INFORMATION FOR SEQ ID NO:715:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:
TGGAGGGCGG CATGGCGGG 19

(2) INFORMATION FOR SEQ ID NO:716:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:
TGGAGGGCGG CATGGCGG 18

(2) INFORMATION FOR SEQ ID NO:717:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:
TGGAGGGCGG CATGGCG 17

(2) INFORMATION FOR SEQ ID NO:718:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:
TGGAGGGCGG CATGGC 16

(2) INFORMATION FOR SEQ ID NO:719:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:
TGGAGGGCGG CATGG 15

(2) INFORMATION FOR SEQ ID NO:720:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:
TGGAGGGCGG CATG 14

(2) INFORMATION FOR SEQ ID NO:721:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:
TGGAGGGCGG CAT 13

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:
TGGAGGGCGG CA 12

(2) INFORMATION FOR SEQ ID NO:723:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:
TGGAGGGCGG C 11

(2) INFORMATION FOR SEQ ID NO:724:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:
TGGAGGGCGG 10

(2) INFORMATION FOR SEQ ID NO:725:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:
GGAGGGCGGC ATGGCGGGCA CAGGCTGGGC 30

(2) INFORMATION FOR SEQ ID NO:726:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:
GGAGGGCGGC ATGGCGGGCA CAGGCTGGG 29

(2) INFORMATION FOR SEQ ID NO:727:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:
GGAGGGCGGC ATGGCGGGCA CAGGCTGG 28

(2) INFORMATION FOR SEQ ID NO:728:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:
GGAGGGCGGC ATGGCGGGCA CAGGCTG 27

(2) INFORMATION FOR SEQ ID NO:729:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:
GGAGGGCGGC ATGGCGGGCA CAGGCT 26

(2) INFORMATION FOR SEQ ID NO:730:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:
GGAGGGCGGC ATGGCGGGCA CAGGC 25

(2) INFORMATION FOR SEQ ID NO:731:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:
GGAGGGCGGC ATGGCGGGCA CAGG 24

(2) INFORMATION FOR SEQ ID NO:732:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:
GGAGGGCGGC ATGGCGGGCA CAG 23

(2) INFORMATION FOR SEQ ID NO:733:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:
GGAGGGCGGC ATGGCGGGCA CA 22

(2) INFORMATION FOR SEQ ID NO:734:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:
GGAGGGCGGC ATGGCGGGCA C 21

(2) INFORMATION FOR SEQ ID NO:735:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:
GGAGGGCGGC ATGGCGGGCA 20

(2) INFORMATION FOR SEQ ID NO:736:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:
GGAGGGCGGC ATGGCGGGC 19

(2) INFORMATION FOR SEQ ID NO:737:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:
GGAGGGCGGC ATGGCGGG 18

(2) INFORMATION FOR SEQ ID NO:738:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

GGAGGGCGGC ATGGCGG 17

(2) INFORMATION FOR SEQ ID NO:739:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:
GGAGGGCGGC ATGGCG 16

(2) INFORMATION FOR SEQ ID NO:740:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:
GGAGGGCGGC ATGGC 15

(2) INFORMATION FOR SEQ ID NO:741:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:
GGAGGGCGGC ATGG 14

(2) INFORMATION FOR SEQ ID NO:742:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:
GGAGGGCGGC ATG 13

(2) INFORMATION FOR SEQ ID NO:743:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:
GGAGGGCGGC AT 12

(2) INFORMATION FOR SEQ ID NO:744:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:
GGAGGGCGGC A 11

(2) INFORMATION FOR SEQ ID NO:745:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:
GGAGGGCGGC 10

(2) INFORMATION FOR SEQ ID NO:746:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:
GAGGGCGGCA TGGCGGGCAC AGGCTGGGC 29

(2) INFORMATION FOR SEQ ID NO:747:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:
GAGGGCGGCA TGGCGGGCAC AGGCTGGG 28

(2) INFORMATION FOR SEQ ID NO:748:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:
GAGGGCGGCA TGGCGGGCAC AGGCTGG 27

(2) INFORMATION FOR SEQ ID NO:749:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:
GAGGGCGGCA TGGCGGGCAC AGGCTG 26

(2) INFORMATION FOR SEQ ID NO:750:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:
GAGGGCGGCA TGGCGGGCAC AGGCT 25

(2) INFORMATION FOR SEQ ID NO:751:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:
GAGGGCGGCA TGGCGGGCAC AGGC 24

(2) INFORMATION FOR SEQ ID NO:752:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:
GAGGGCGGCA TGGCGGGCAC AGG 23

(2) INFORMATION FOR SEQ ID NO:753:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:
GAGGGCGGCA TGGCGGGCAC AG 22

(2) INFORMATION FOR SEQ ID NO:754:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:
GAGGGCGGCA TGGCGGGCAC A 21

(2) INFORMATION FOR SEQ ID NO:755:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

GAGGGCGGCA TGGCGGGCAC 20

(2) INFORMATION FOR SEQ ID NO:756:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

GAGGGCGGCA TGGCGGGCA 19

(2) INFORMATION FOR SEQ ID NO:757:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

GAGGGCGGCA TGGCGGGC 18

(2) INFORMATION FOR SEQ ID NO:758:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

GAGGGCGGCA TGGCGGG 17

(2) INFORMATION FOR SEQ ID NO:759:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

GAGGGCGGCA TGGCGG 16

(2) INFORMATION FOR SEQ ID NO:760:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

GAGGGCGGCA TGGCG 15

(2) INFORMATION FOR SEQ ID NO:761:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

GAGGGCGGCA TGGC 14

(2) INFORMATION FOR SEQ ID NO:762:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

GAGGGCGGCA TGG 13

(2) INFORMATION FOR SEQ ID NO:763:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

GAGGGCGGCA TG 12

(2) INFORMATION FOR SEQ ID NO:764:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

GAGGGCGGCA T 11

(2) INFORMATION FOR SEQ ID NO:765:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:
GAGGGCGGCA 10

(2) INFORMATION FOR SEQ ID NO:766:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:
AGGGCGGCAT GGCGGGCACA GGCTGGGC 28

(2) INFORMATION FOR SEQ ID NO:767:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:
AGGGCGGCAT GGCGGGCACA GGCTGGG 27

(2) INFORMATION FOR SEQ ID NO:768:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:
AGGGCGGCAT GGCGGGCACA GGCTGG 26

(2) INFORMATION FOR SEQ ID NO:769:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:
AGGGCGGCAT GGCGGGCACA GGCTG 25

(2) INFORMATION FOR SEQ ID NO:770:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:
AGGGCGGCAT GGCGGGCACA GGCT 24

(2) INFORMATION FOR SEQ ID NO:771:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:
AGGGCGGCAT GGCGGGCACA GGC 23

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:
AGGGCGGCAT GGCGGGCACA GG 22

(2) INFORMATION FOR SEQ ID NO:773:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:
AGGGCGGCAT GGCGGGCACA G 21

(2) INFORMATION FOR SEQ ID NO:774:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:
AGGGCGGCAT GGCGGGCACA 20

(2) INFORMATION FOR SEQ ID NO:775:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:
AGGGCGGCAT GGCGGGCAC 19

(2) INFORMATION FOR SEQ ID NO:776:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:
AGGGCGGCAT GGCGGGCA 18

(2) INFORMATION FOR SEQ ID NO:777:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:
AGGGCGGCAT GGCGGGC 17

(2) INFORMATION FOR SEQ ID NO:778:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:
AGGGCGGCAT GGCGGG 16

(2) INFORMATION FOR SEQ ID NO:779:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:
AGGGCGGCAT GGCGG 15

(2) INFORMATION FOR SEQ ID NO:780:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:
AGGGCGGCAT GGCG 14

(2) INFORMATION FOR SEQ ID NO:781:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:
AGGGCGGCAT GGC 13

(2) INFORMATION FOR SEQ ID NO:782:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:
AGGGCGGCAT GG 12

(2) INFORMATION FOR SEQ ID NO:783:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:
AGGGCGGCAT G 11

(2) INFORMATION FOR SEQ ID NO:784:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:
AGGGCGGCAT 10

(2) INFORMATION FOR SEQ ID NO:785:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:
GGGCGGCATG GCGGGCACAG GCTGGGC 27

(2) INFORMATION FOR SEQ ID NO:786:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:
GGGCGGCATG GCGGGCACAG GCTGGG 26

(2) INFORMATION FOR SEQ ID NO:787:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:
GGGCGGCATG GCGGGCACAG GCTGG 25

(2) INFORMATION FOR SEQ ID NO:788:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

GGGCGGCATG GCGGGCACAG GCTG 24

(2) INFORMATION FOR SEQ ID NO:789:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:
GGGCGGCATG GCGGGCACAG GCT 23

(2) INFORMATION FOR SEQ ID NO:790:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:
GGGCGGCATG GCGGGCACAG GC 22

(2) INFORMATION FOR SEQ ID NO:791:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:
GGGCGGCATG GCGGGCACAG G 21

(2) INFORMATION FOR SEQ ID NO:792:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:
GGGCGGCATG GCGGGCACAG 20

(2) INFORMATION FOR SEQ ID NO:793:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:
GGGCGGCATG GCGGGCACA 19

(2) INFORMATION FOR SEQ ID NO:794:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:
GGGCGGCATG GCGGGCAC 18

(2) INFORMATION FOR SEQ ID NO:795:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:
GGGCGGCATG GCGGGCA 17

(2) INFORMATION FOR SEQ ID NO:796:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:
GGGCGGCATG GCGGGC 16

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:
GGGCGGCATG GCGGG 15

(2) INFORMATION FOR SEQ ID NO:798:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:
GGGCGGCATG GCGG 14

(2) INFORMATION FOR SEQ ID NO:799:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:
GGGCGGCATG GCG 13

(2) INFORMATION FOR SEQ ID NO:800:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:
GGGCGGCATG GC 12

(2) INFORMATION FOR SEQ ID NO:801:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:
GGGCGGCATG G 11

(2) INFORMATION FOR SEQ ID NO:802:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:
GGGCGGCATG 10

(2) INFORMATION FOR SEQ ID NO:803:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:
GGCGGCATGG CGGGCACAGG CTGGGC 26

(2) INFORMATION FOR SEQ ID NO:804:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:
GGCGGCATGG CGGGCACAGG CTGGG 25

(2) INFORMATION FOR SEQ ID NO:805:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:
GGCGGCATGG CGGGCACAGG CTGG 24

(2) INFORMATION FOR SEQ ID NO:806:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:
GGCGGCATGG CGGGCACAGG CTG 23

(2) INFORMATION FOR SEQ ID NO:807:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:
GGCGGCATGG CGGGCACAGG CT 22

(2) INFORMATION FOR SEQ ID NO:808:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:
GGCGGCATGG CGGGCACAGG C 21

(2) INFORMATION FOR SEQ ID NO:809:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:
GGCGGCATGG CGGGCACAGG 20

(2) INFORMATION FOR SEQ ID NO:810:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:
GGCGGCATGG CGGGCACAG 19

(2) INFORMATION FOR SEQ ID NO:811:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:
GGCGGCATGG CGGGCACA 18

(2) INFORMATION FOR SEQ ID NO:812:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:
GGCGGCATGG CGGGCAC 17

(2) INFORMATION FOR SEQ ID NO:813:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

GGCGGCATGG CGGGCA 16

(2) INFORMATION FOR SEQ ID NO:814:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: singl
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:
GGCGGCATGG CGGGC 15

(2) INFORMATION FOR SEQ ID NO:815:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:
GGCGGCATGG CGGG 14

(2) INFORMATION FOR SEQ ID NO:816:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:
GGCGGCATGG CGG 13

(2) INFORMATION FOR SEQ ID NO:817:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:
GGCGGCATGG CG 12

(2) INFORMATION FOR SEQ ID NO:818:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:
GGCGGCATGG C 11

(2) INFORMATION FOR SEQ ID NO:819:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:
GGCGGCATGG 10

(2) INFORMATION FOR SEQ ID NO:820:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:
GCGGCATGGC GGGCACAGGC TGGGC 25

(2) INFORMATION FOR SEQ ID NO:821:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:
GCGGCATGGC GGGCACAGGC TGGG 24

(2) INFORMATION FOR SEQ ID NO:822:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:
GCGGCATGGC GGGCACAGGC TGG 23

(2) INFORMATION FOR SEQ ID NO:823:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:
GCGGCATGGC GGGCACAGGC TG 22

(2) INFORMATION FOR SEQ ID NO:824:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:
GCGGCATGGC GGGCACAGGC T 21

(2) INFORMATION FOR SEQ ID NO:825:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:
GCGGCATGGC GGGCACAGGC 20

(2) INFORMATION FOR SEQ ID NO:826:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:
GCGGCATGGC GGGCACAGG 19

(2) INFORMATION FOR SEQ ID NO:827:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:
GCGGCATGGC GGGCACAG 18

(2) INFORMATION FOR SEQ ID NO:828:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:
GCGGCATGGC GGGCACA 17

(2) INFORMATION FOR SEQ ID NO:829:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:
GCGGCATGGC GGGCAC 16

(2) INFORMATION FOR SEQ ID NO:830:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:
GCGGCATGGC GGGCA 15

(2) INFORMATION FOR SEQ ID NO:831:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:
GCGGCATGGC GGGC 14

(2) INFORMATION FOR SEQ ID NO:832:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:
GCGGCATGGC GGG 13

(2) INFORMATION FOR SEQ ID NO:833:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:
GCGGCATGGC GG 12

(2) INFORMATION FOR SEQ ID NO:834:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:
GCGGCATGGC G 11

(2) INFORMATION FOR SEQ ID NO:835:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:
GCGGCATGGC 10

(2) INFORMATION FOR SEQ ID NO:836:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:
CGGCATGGCG GGCACAGGCT GGGC 24

(2) INFORMATION FOR SEQ ID NO:837:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:
CGGCATGGCG GGCACAGGCT GGG 23

(2) INFORMATION FOR SEQ ID NO:838:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

CGGCATGGCG GGCACAGGCT GG 22

(2) INFORMATION FOR SEQ ID NO:839:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:
CGGCATGGCG GGCACAGGCT G 21

(2) INFORMATION FOR SEQ ID NO:840:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:
CGGCATGGCG GGCACAGGCT 20

(2) INFORMATION FOR SEQ ID NO:841:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:
CGGCATGGCG GGCACAGGC 19

(2) INFORMATION FOR SEQ ID NO:842:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:
CGGCATGGCG GGCACAGG 18

(2) INFORMATION FOR SEQ ID NO:843:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:
CGGCATGGCG GGCACAG 17

(2) INFORMATION FOR SEQ ID NO:844:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:
CGGCATGGCG GGCACA 16

(2) INFORMATION FOR SEQ ID NO:845:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:
CGGCATGGCG GGCAC 15

(2) INFORMATION FOR SEQ ID NO:846:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:
CGGCATGGCG GGCA 14

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:
CGGCATGGCG GGC 13

(2) INFORMATION FOR SEQ ID NO:848:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:
CGGCATGGCG GG 12

(2) INFORMATION FOR SEQ ID NO:849:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:
CGGCATGGCG G 11

(2) INFORMATION FOR SEQ ID NO:850:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:
CGGCATGGCG 10

(2) INFORMATION FOR SEQ ID NO:851:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:
GGCATGGCGG GCACAGGCTG GGC 23

(2) INFORMATION FOR SEQ ID NO:852:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:
GGCATGGCGG GCACAGGCTG GG 22

(2) INFORMATION FOR SEQ ID NO:853:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:
GGCATGGCGG GCACAGGCTG G 21

(2) INFORMATION FOR SEQ ID NO:854:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:
GGCATGGCGG GCACAGGCTG 20

(2) INFORMATION FOR SEQ ID NO:855:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:
GGCATGGCGG GCACAGGCT 19

(2) INFORMATION FOR SEQ ID NO:856:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucl ic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:
GGCATGGCGG GCACAGGC 18

(2) INFORMATION FOR SEQ ID NO:857:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:
GGCATGGCGG GCACAGG 17

(2) INFORMATION FOR SEQ ID NO:858:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:
GGCATGGCGG GCACAG 16

(2) INFORMATION FOR SEQ ID NO:859:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:
GGCATGGCGG GCACA 15

(2) INFORMATION FOR SEQ ID NO:860:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:
GGCATGGCGG GCAC 14

(2) INFORMATION FOR SEQ ID NO:861:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:
GGCATGGCGG GCA 13

(2) INFORMATION FOR SEQ ID NO:862:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:
GGCATGGCGG GC 12

(2) INFORMATION FOR SEQ ID NO:863:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

GGCATGGCGG G 11

(2) INFORMATION FOR SEQ ID NO:864:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:
GGCATGGCGG 10

(2) INFORMATION FOR SEQ ID NO:865:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:
GCATGGCGGG CACAGGCTGG GC 22

(2) INFORMATION FOR SEQ ID NO:866:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:
GCATGGCGGG CACAGGCTGG G 21

(2) INFORMATION FOR SEQ ID NO:867:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:
GCATGGCGGG CACAGGCTGG 20

(2) INFORMATION FOR SEQ ID NO:868:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:
GCATGGCGGG CACAGGCTG 19

(2) INFORMATION FOR SEQ ID NO:869:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:
GCATGGCGGG CACAGGCT 18

(2) INFORMATION FOR SEQ ID NO:870:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:
GCATGGCGGG CACAGGC 17

(2) INFORMATION FOR SEQ ID NO:871:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:
GCATGGCGGG CACAGG 16

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:
GCATGGCGGG CACAG 15

(2) INFORMATION FOR SEQ ID NO:873:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:
GCATGGCGGG CACA 14

(2) INFORMATION FOR SEQ ID NO:874:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:
GCATGGCGGG CAC 13

(2) INFORMATION FOR SEQ ID NO:875:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:
GCATGGCGGG CA 12

(2) INFORMATION FOR SEQ ID NO:876:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:
GCATGGCGGG C 11

(2) INFORMATION FOR SEQ ID NO:877:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:
GCATGGCGGG 10

(2) INFORMATION FOR SEQ ID NO:878:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:
CATGGCGGGC ACAGGCTGGG C 21

(2) INFORMATION FOR SEQ ID NO:879:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:
CATGGCGGGC ACAGGCTGGG 20

(2) INFORMATION FOR SEQ ID NO:880:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:
CATGGCGGGC ACAGGCTGG 19

(2) INFORMATION FOR SEQ ID NO:881:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:
CATGGCGGGC ACAGGCTG 18

(2) INFORMATION FOR SEQ ID NO:882:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:
CATGGCGGGC ACAGGCT 17

(2) INFORMATION FOR SEQ ID NO:883:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:
CATGGCGGGC ACAGGC 16

(2) INFORMATION FOR SEQ ID NO:884:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:
CATGGCGGGC ACAGG 15

(2) INFORMATION FOR SEQ ID NO:885:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:
CATGGCGGGC ACAG 14

(2) INFORMATION FOR SEQ ID NO:886:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:
CATGGCGGGC ACA 13

(2) INFORMATION FOR SEQ ID NO:887:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:
CATGGCGGGC AC 12

(2) INFORMATION FOR SEQ ID NO:888:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

CATGGCGGGC A 11

(2) INFORMATION FOR SEQ ID NO:889:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:
CATGGCGGGC 10

(2) INFORMATION FOR SEQ ID NO:890:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:
ATGGCGGGCA CAGGCTGGGC 20

(2) INFORMATION FOR SEQ ID NO:891:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:
ATGGCGGGCA CAGGCTGGG 19

(2) INFORMATION FOR SEQ ID NO:892:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:
ATGGCGGGCA CAGGCTGG 18

(2) INFORMATION FOR SEQ ID NO:893:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:
ATGGCGGGCA CAGGCTG 17

(2) INFORMATION FOR SEQ ID NO:894:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:
ATGGCGGGCA CAGGCT 16

(2) INFORMATION FOR SEQ ID NO:895:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:
ATGGCGGGCA CAGGC 15

(2) INFORMATION FOR SEQ ID NO:896:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:
ATGGCGGGCA CAGG 14

(2) INFORMATION FOR SEQ ID NO:897:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:
ATGGCGGGCA CAG 13

(2) INFORMATION FOR SEQ ID NO:898:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:
ATGGCGGGCA CA 12

(2) INFORMATION FOR SEQ ID NO:899:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:
ATGGCGGGCA C 11

(2) INFORMATION FOR SEQ ID NO:900:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:
ATGGCGGGCA 10

(2) INFORMATION FOR SEQ ID NO:901:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:
TGGCGGGCAC AGGCTGGGC 19

(2) INFORMATION FOR SEQ ID NO:902:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:
TGGCGGGCAC AGGCTGGG 18

(2) INFORMATION FOR SEQ ID NO:903:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:
TGGCGGGCAC AGGCTGG 17

(2) INFORMATION FOR SEQ ID NO:904:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:
TGGCGGGCAC AGGCTG 16

(2) INFORMATION FOR SEQ ID NO:905:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:
TGGCGGGCAC AGGCT 15

(2) INFORMATION FOR SEQ ID NO:906:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:
TGGCGGGCAC AGGC 14

(2) INFORMATION FOR SEQ ID NO:907:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:
TGGCGGGCAC AGG 13

(2) INFORMATION FOR SEQ ID NO:908:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:
TGGCGGGCAC AG 12

(2) INFORMATION FOR SEQ ID NO:909:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:
TGGCGGGCAC A 11

(2) INFORMATION FOR SEQ ID NO:910:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:
TGGCGGGCAC 10

(2) INFORMATION FOR SEQ ID NO:911:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:
GGCGGGCACA GGCTGGGC 18

(2) INFORMATION FOR SEQ ID NO:912:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:
GGCGGGCACA GGCTGGG 17

(2) INFORMATION FOR SEQ ID NO:913:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

GGCGGGCACA GGCTGG 16

(2) INFORMATION FOR SEQ ID NO:914:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:
GGCGGGCACA GGCTG 15

(2) INFORMATION FOR SEQ ID NO:915:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:
GGCGGGCACA GGCT 14

(2) INFORMATION FOR SEQ ID NO:916:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:
GGCGGGCACA GGC 13

(2) INFORMATION FOR SEQ ID NO:917:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:
GGCGGGCACA GG 12

(2) INFORMATION FOR SEQ ID NO:918:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:
GGCGGGCACA G 11

(2) INFORMATION FOR SEQ ID NO:919:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:
GGCGGGCACA 10

(2) INFORMATION FOR SEQ ID NO:920:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:
GCGGGCACAG GCTGGGC 17

(2) INFORMATION FOR SEQ ID NO:921:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:
GCGGGCACAG GCTGGG 16

(2) INFORMATION FOR SEQ ID NO:922:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:
GCGGGCACAG GCTGG 15

(2) INFORMATION FOR SEQ ID NO:923:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:
GCGGGCACAG GCTG 14

(2) INFORMATION FOR SEQ ID NO:924:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:
GCGGGCACAG GCT 13

(2) INFORMATION FOR SEQ ID NO:925:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:
GCGGGCACAG GC 12

(2) INFORMATION FOR SEQ ID NO:926:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:
GCGGGCACAG G 11

(2) INFORMATION FOR SEQ ID NO:927:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:
GCGGGCACAG 10

(2) INFORMATION FOR SEQ ID NO:928:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:
CGGGCACAGG CTGGGC 16

(2) INFORMATION FOR SEQ ID NO:929:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:
GGGCACAGGC TGGG 14

(2) INFORMATION FOR SEQ ID NO:930:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:
CGGGCACAGG CTGG 14

(2) INFORMATION FOR SEQ ID NO:931:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:
CGGGCACAGG CTG 13

(2) INFORMATION FOR SEQ ID NO:932:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:
CGGGCACAGG CT 12

(2) INFORMATION FOR SEQ ID NO:933:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:
CGGGCACAGG C 11

(2) INFORMATION FOR SEQ ID NO:934:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:
CGGGCACAGG 10

(2) INFORMATION FOR SEQ ID NO:935:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:
GGGCACAGGC TGGGC 15

(2) INFORMATION FOR SEQ ID NO:936:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:
GGGCACAGGC TGGG 14

(2) INFORMATION FOR SEQ ID NO:937:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:
GGGCACAGGC TGG 13

(2) INFORMATION FOR SEQ ID NO:938:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:
GGGCACAGGC TG 12

(2) INFORMATION FOR SEQ ID NO:939:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:
GGGCACAGGC T 11

(2) INFORMATION FOR SEQ ID NO:940:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:
GGGCACAGGC 10

(2) INFORMATION FOR SEQ ID NO:941:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:
GGCACAGGCT GGGC 14

(2) INFORMATION FOR SEQ ID NO:942:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:
GGCACAGGCT GGG 13

(2) INFORMATION FOR SEQ ID NO:943:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:
GGCACAGGCT GG 12

(2) INFORMATION FOR SEQ ID NO:944:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:
GGCACAGGCT G 11

(2) INFORMATION FOR SEQ ID NO:945:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:
GGCACAGGCT 10

(2) INFORMATION FOR SEQ ID NO:946:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:
GCACAGGCTG GGC 13

(2) INFORMATION FOR SEQ ID NO:947:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:
GCACAGGCTG GG 12

(2) INFORMATION FOR SEQ ID NO:948:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:
GCACAGGCTG G 11

(2) INFORMATION FOR SEQ ID NO:949:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:
GCACAGGCTG 10

(2) INFORMATION FOR SEQ ID NO:950:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:
CACAGGCTGG GC 12

(2) INFORMATION FOR SEQ ID NO:951:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:
CACAGGCTGG G 11

(2) INFORMATION FOR SEQ ID NO:952:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:
CACAGGCTGG 10

(2) INFORMATION FOR SEQ ID NO:953:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:
ACAGGCTGGG C 11

(2) INFORMATION FOR SEQ ID NO:954:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:
ACAGGCTGGG 10

(2) INFORMATION FOR SEQ ID NO:955:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:
CAGGCTGGGC 10

(2) INFORMATION FOR SEQ ID NO:956:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:
TTTTCCTTCC TTTGTCTCTC TTC 23

(2) INFORMATION FOR SEQ ID NO:957:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:
GCTCCCGGCT GCCTG 15

(2) INFORMATION FOR SEQ ID NO:958:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:
CTCGGCCGTG CGGCTCTGTC GCTCCCGGT 29

(2) INFORMATION FOR SEQ ID NO:959:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:
CCGCCGCCCT CCGGGGGGTC 20

(2) INFORMATION FOR SEQ ID NO:960:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:
TGCTGCCGTT GGCTGCCC 18

(2) INFORMATION FOR SEQ ID NO:961:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:
CTTCTGCGGG TCGCCGG 17

(2) INFORMATION FOR SEQ ID NO:962:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:
TGCTGGGCTT GTGGC 15

(2) INFORMATION FOR SEQ ID NO:963:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:
GGCCTCTCTT CTGGG 15

(2) INFORMATION FOR SEQ ID NO:964:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:
CCTGGTCCCT CCGT 14

(2) INFORMATION FOR SEQ ID NO:965:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:
GGTGGCTCCT CTGC 14

(2) INFORMATION FOR SEQ ID NO:966:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:
GCTTGGTCCT GGGGCTGC 18

(2) INFORMATION FOR SEQ ID NO:967:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:
TGCTCTCCTC TCCTT 15

(2) INFORMATION FOR SEQ ID NO:968:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:
TGCTTTTCTT TTCTGGGCCT C 21

(2) INFORMATION FOR SEQ ID NO:969:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:
TGTGGTCTGT TTTTTTCTG 19

(2) INFORMATION FOR SEQ ID NO:970:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:
GCCCTGCTGG GGCGCTCTCC 20

(2) INFORMATION FOR SEQ ID NO:971:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:
GCCGCCCGCC TGGCTCCC 18

(2) INFORMATION FOR SEQ ID NO:972:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:
GGBGCCCBTG BTGGGCBTGC C 21

(2) INFORMATION FOR SEQ ID NO:973:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:
GTGGTTCTTG CCCTCCTTTG GCTG 24

(2) INFORMATION FOR SEQ ID NO:974:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:
CCGTGCCCGC TCCCCGGC 18

(2) INFORMATION FOR SEQ ID NO:975:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:
CTCCTGGCGG GTGGCCGTTG 20

(2) INFORMATION FOR SEQ ID NO:976:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:
GGCCCGTGTT CCCCTGGG 18

(2) INFORMATION FOR SEQ ID NO:977:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:
GCCTGGGGCT CCCTTCTCTC 20

(2) INFORMATION FOR SEQ ID NO:978:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:
GCCCTTCTTG CTGGGCCTC 19

(2) INFORMATION FOR SEQ ID NO:979:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:
TGCTGCTGCT GGTGCTGTGG CCCCC 25

(2) INFORMATION FOR SEQ ID NO:980:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:
GTACACCGAG GAGCCCATGA TGGGCATGCC ACAGACGACA GGC 43

(2) INFORMATION FOR SEQ ID NO:981:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:
GTBCBCCGBG GBGCCCBTGB TGGGCBTGCC BCBGBCGBCB GGC 43

(2) INFORMATION FOR SEQ ID NO:982:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:
GGCGCCGTGC CGCGTCTTGG TGGCGGCGG 29

(2) INFORMATION FOR SEQ ID NO:983:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:
GTTCGCGCCC GCGCGGGGCC CCTCCGGTCC 30

(2) INFORMATION FOR SEQ ID NO:984:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:
GTTCGCGCCC GCGCGGGGCC CCTCCGGTCC 30

(2) INFORMATION FOR SEQ ID NO:985:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:
CGGGTCGGGG CCCCCCGCGG CC 22

(2) INFORMATION FOR SEQ ID NO:986:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:
GCCTCGGGGC TGGGGCGCTG GTGGCCGGG 29

(2) INFORMATION FOR SEQ ID NO:987:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:
CCGCGCCTCC GCCTGCCGCT TCTG 24

(2) INFORMATION FOR SEQ ID NO:988:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:
GCTGGGCCCC GGGCGCCCCC T 21

(2) INFORMATION FOR SEQ ID NO:989:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:
CCCCTCTTGC TCGGGTCCCC GTG 23

(2) INFORMATION FOR SEQ ID NO:990:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:
ACAGCGCGTC CTGTGTCTCC AGCAGCATGG CCGGGCCAGC TGGGCCCC 48

(2) INFORMATION FOR SEQ ID NO:991:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:
BCBGCGCGTC CTGTGTCTCC BGCBGCBTGG CCGGGCCBGC TGGGCCCC 48

(2) INFORMATION FOR SEQ ID NO:992:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:
ACAGAGCATG CTGTTGTTGG GCATCTTGCC TTCCCAGGG 39

(2) INFORMATION FOR SEQ ID NO:993:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:
BCBGBGCBTG CTGTTGTTGG GCBTCTTGCC TTCCCBGGG 39

(2) INFORMATION FOR SEQ ID NO:994:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:
CCCTTTTCTG GTGGGGTG 18

(2) INFORMATION FOR SEQ ID NO:995:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:
GTGCTGTTGT TGGGC 15

(2) INFORMATION FOR SEQ ID NO:996:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:
TTTCTTCTGT TCCC 14

(2) INFORMATION FOR SEQ ID NO:997:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:
CCCTTTTCTG GTGGGGTG 18

(2) INFORMATION FOR SEQ ID NO:998:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:
GTGCTGTTGT TGGGC 15

(2) INFORMATION FOR SEQ ID NO:999:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:
TTTCTTCTGT TCCC 14

(2) INFORMATION FOR SEQ ID NO:1000:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:
TTTCCCCTGG GTCTTCC 17

(2) INFORMATION FOR SEQ ID NO:1001:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:
CTCCTGCTCT TTTTTC 16

(2) INFORMATION FOR SEQ ID NO:1002:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:
ATTTGCTCTC CTATTACTTT CTGTGTCCAT TTTTTCATTA ACCGAGCTGT 50

(2) INFORMATION FOR SEQ ID NO:1003:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:
BTTTGCTCTC CTBTTBCTTT CTGTGTCCBT TTTTTCBTTB BCCGBGCTGT 50

(2) INFORMATION FOR SEQ ID NO:1004:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

GCCTGTGTCT GTCCTCCT 18

(2) INFORMATION FOR SEQ ID NO:1005:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:
GCTTCGTTCC TCTCGTTC 18

(2) INFORMATION FOR SEQ ID NO:1006:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:
CTGCTTGGTG CCCTTGCCG 19

(2) INFORMATION FOR SEQ ID NO:1007:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:
GTCCTGCTCC TCCGGGCTGT GG 22

(2) INFORMATION FOR SEQ ID NO:1008:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:
GTCGTGGCCC TGGCTCCGGC TGGTGGGCTC CCCTGG 36

(2) INFORMATION FOR SEQ ID NO:1009:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:
CCTTCGCTGG CTGGCGGCGT GC 22

(2) INFORMATION FOR SEQ ID NO:1010:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:
GGGTCTTGCT CTGGGCCTGG CTGT 24

(2) INFORMATION FOR SEQ ID NO:1011:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:
GGCCGTGGTT GGGGGTCTTC 20

(2) INFORMATION FOR SEQ ID NO:1012:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:
GCTGCCTCCG TTTGGGTGGC 20

(2) INFORMATION FOR SEQ ID NO:1013:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:
TCTCTGAATA TTGACCTTCC TCCATGGCGG TCCTGCTTGG ATTCTCCCGA 50

(2) INFORMATION FOR SEQ ID NO:1014:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:
TCTCTGBBTB TTGBCCTTCC TCCBTGGCGG TCCTGCTTGG BTTCTCCCGB 50

(2) INFORMATION FOR SEQ ID NO:1015:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:
GCCTTTCCTG GTTCTCTTGT TGTTTTTGGG GTTTGGCTT 39

(2) INFORMATION FOR SEQ ID NO:1016:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:
ACAGTAGAGT AGGGGATTCC ATGGCAGGAG CCATCTTCTT CATGGACTCC 50

(2) INFORMATION FOR SEQ ID NO:1017:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:
TTCAAGGAGA CCTTAGGTTT CTGAGGGACT GCTAACACGC CATCTGGAGC 50

(2) INFORMATION FOR SEQ ID NO:1018:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:
BCBGTBGBGT BGGGGBTTCC BTGGCBGGBG CCBTCTTCTT CBTGGBCTCC TTCBBGGBGB 60
CCTTBGGTTT CTGBGGG 77

(2) INFORMATION FOR SEQ ID NO:1019:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:
BCTGCTBBCB CGCCBTCTGG BGC 23

(2) INFORMATION FOR SEQ ID NO:1020:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:
GTTGTTTTTG GGGTTTGGCT T 21

(2) INFORMATION FOR SEQ ID NO:1021:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:
GCCTTTCCTG GTTCTCTT 18

(2) INFORMATION FOR SEQ ID NO:1022:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:
BCBGTBGBGT BGGGGBTTCC BTGGCBGGBG CCBTCTTCTT CBTGGBCTCC 50

(2) INFORMATION FOR SEQ ID NO:1023:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:
TTCBBGGBGB CCTTBGGTTT CTGBGGGBCT GCTBBCBCGC CBTCTGGBGC 50

(2) INFORMATION FOR SEQ ID NQ:1024:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:
GCCTGTGTCT GTCCTCCT 18

(2) INFORMATION FOR SEQ ID NO:1025:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:
GCTTCGTTCC TCTCGTTC 18

(2) INFORMATION FOR SEQ ID NO:1026:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:
CTGCTTGGTG CCCTTGCCG 19

(2) INFORMATION FOR SEQ ID NO:1027:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:
GTCCTGCTCC TCCGGGCTGT GG 22

(2) INFORMATION FOR SEQ ID NO:1028:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:
GTCCTCGCCC TGGCTCCGGC TGGTGGGCTC CCCTGG 36

(2) INFORMATION FOR SEQ ID NO:1029:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:
CCTTCGCTGG CTGGCGGCGT GC 22

(2) INFORMATION FOR SEQ ID NO:1030:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:
CCCBGBBCGB GBCCCGGBCC GBCB 24

(2) INFORMATION FOR SEQ ID NO:1031:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:
GGCCGTGGTT GGGGGTCTTC 20

(2) INFORMATION FOR SEQ ID NO:1032:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:
GCTGCCTCCG TTTGGGTGGC 20

(2) INFORMATION FOR SEQ ID NO:1033:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:
GBTCTCTGBB TBTTGBCCTT CCBTGGCGGT CCTGCTTGGB 40

(2) INFORMATION FOR SEQ ID NO:1034:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:
TCTCCCTTGG GCTCTGGCTC CTTCTC 26

(2) INFORMATION FOR SEQ ID NO:1035:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:
TCTCTCTCCC TCTCTCTCTG T 21

(2) INFORMATION FOR SEQ ID NO:1036:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:
CGCCTCCGCC CTGGCTGCTG GGGTGGTGGT GC 32

(2) INFORMATION FOR SEQ ID NO:1037:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:
TTTTGTTCTT CCTTGCTGCC 20

(2) INFORMATION FOR SEQ ID NO:1038:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:
GCCCCGCTGC TTGTCTTCCT CG 22

(2) INFORMATION FOR SEQ ID NO:1039:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:
CTCTGTCCCT CTCTCTCTGT BCTCCTCBGG CTCCBTCBTC TCCCTTGGGC 50

(2) INFORMATION FOR SEQ ID NO:1040:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:
CTTGCTCCTG GGGGCCTCCT G 21

(2) INFORMATION FOR SEQ ID NO:1041:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:
GTCCCTCCGG GTGTTCCCGG C 21

(2) INFORMATION FOR SEQ ID NO:1042:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:
GGGCCTGGCC TGGGGCBGGG GCCGCGTBGG CGCGGCTCGC CBGGBCGGGC BGCGCCBGCB 60
GCBGCBGBTT CBGCBTCCTG G 81

(2) INFORMATION FOR SEQ ID NO:1043:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:
CTTGCTCCTG GGGGCCTCCT G 21

(2) INFORMATION FOR SEQ ID NO:1044:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:
GTCCCTCTGG CTGTTCCCGG C 21

(2) INFORMATION FOR SEQ ID NO:1045:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

CCTGGBCTGG GGCBGGGGCC GCGTBGGCGC GGCTCGCCBG GBCGGGCBGC GCCBGCBGCB 60
GCBGGCTCBG CBTCCTGGCC BCGGBBTTCC 90

(2) INFORMATION FOR SEQ ID NO:1046:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

GGTGTGCGGG GCCTGGTGCC 20

(2) INFORMATION FOR SEQ ID NO:1047:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

CCTGGGCCTC GGGTGCTGCC TGT 23

(2) INFORMATION FOR SEQ ID NO:1048:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

GCGCTGCCTT CTTCTCCTGG 20

(2) INFORMATION FOR SEQ ID NO:1049:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

GTCCTCGCCG GGGCCCTTGC TGCCCTGGCT GT 32

(2) INFORMATION FOR SEQ ID NO:1050:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

GCCCTGGGGG TCTGGGTTCG GCTGT 25

(2) INFORMATION FOR SEQ ID NO:1051:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

CCCCBGCBGG BCCBGTCCCB TCCBCBGCGT GTGBTGBGTB GCCBTTCTCC TGCBGCCGBG 60

(2) INFORMATION FOR SEQ ID NO:1052:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

GGGCGCGGGC GBGCBTCGC 19

(2) INFORMATION FOR SEQ ID NO:1053:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:
TTTGGGCTTT TCTCCTTTGG TT 22

(2) INFORMATION FOR SEQ ID NO:1054:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:
TGBGCGCCBG GBCCGCGCBC BGCBGCBGGG CGCGGGCGBG CBTCGCBGCG GCGGGCBGGG 60

(2) INFORMATION FOR SEQ ID NO:1055:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:
GCCCTGCTGC TCTTTCTGCT 20

(2) INFORMATION FOR SEQ ID NO:1056:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:
TCCCTTGGTG GGTTGGGCC 19

(2) INFORMATION FOR SEQ ID NO:1057:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:
TTGCTGCCCC TTCTGTCCC 19

(2) INFORMATION FOR SEQ ID NO:1058:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:
TTGCTGCCCC TTCTGTCCC 19

(2) INFORMATION FOR SEQ ID NO:1059:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:
TGTTTGCTGG TGTCTGCGC 19

(2) INFORMATION FOR SEQ ID NO:1060:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:
CCCCBBCBGB BGBBGCBGBC BBBTTTGGGB BGTGBBCBGT TTTGGBBCCB TGTTTCCTGT 60

(2) INFORMATION FOR SEQ ID NO:1061:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:
GCGCTCGGCC TGGTCCCGG 19

(2) INFORMATION FOR SEQ ID NO:1062:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:
GGGTCTCCTC TTGTTGTTGC 20

(2) INFORMATION FOR SEQ ID NO:1063:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:
TTGCGCCTCC TGCTGGGGGT CC 22

(2) INFORMATION FOR SEQ ID NO:1064:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:
CTCTGTTCTT GTTTTGGGGG C 21

(2) INFORMATION FOR SEQ ID NO:1065:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:
GGGCCCGGCC GTTGTCTTG 19

(2) INFORMATION FOR SEQ ID NO:1066:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:
GTTTGGGGGT TTCCGTTG 18

(2) INFORMATION FOR SEQ ID NO:1067:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:
GGGTTCTCCT GGCCCGGGCC TTGCCC 26

(2) INFORMATION FOR SEQ ID NO:1068:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:
GGCCGTGGTC CCGGCTTCGT TGC 23

(2) INFORMATION FOR SEQ ID NO:1069:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:
CCTGTCTCCG TCTCGGCTCT TCTG 24

(2) INFORMATION FOR SEQ ID NO:1070:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:
GGGCCTTGCG CTGTCTTTGG TG 22

(2) INFORMATION FOR SEQ ID NO:1071:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:
GCBCCGTCCB GTGBTGGTGC GGTBCTTGTC GCTGCBGCGC TCGGCCTGGT CCCGGBGBGC 60

(2) INFORMATION FOR SEQ ID NO:1072:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:
GCGCGGGCCG GGGGCTGCTG GG 22

(2) INFORMATION FOR SEQ ID NO:1073:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:
GGTTGGCCCG GGGTGCCCC 19

(2) INFORMATION FOR SEQ ID NO:1074:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:
GCCGCTGGGT GCCCTCGTCC TCTGCGGTC 29

(2) INFORMATION FOR SEQ ID NO:1075:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:
GTGTCTCCTG GCTCTGGTTC CCC 23

(2) INFORMATION FOR SEQ ID NO:1076:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:
GCTGCGCCCG TTGTCCTCTG GGGTGGCCTT C 31

(2) INFORMATION FOR SEQ ID NO:1077:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

GCTCCCGGGT CTGGTTCTTG TGT 23

(2) INFORMATION FOR SEQ ID NO:1078:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:
TGGGGGTCCC TTTTTGGGCC TGTTGT 26

(2) INFORMATION FOR SEQ ID NO:1079:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:
GGCGTGGCTT GTGTGTTCGG TTTC 24

(2) INFORMATION FOR SEQ ID NO:1080:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:
TGCCCTGTCC TCCGGCGTCC C 21

(2) INFORMATION FOR SEQ ID NO:1081:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:
CGGBGCCTCC CCGGGGCBGG BTGBCTTTTG BGGGGGBCBC BGBTGTCTGG GCBTTGCCBG 60
GTCCTGGGBB CBGBGCCCCG BGCBGGBCCB GGBGTGCGGG CBGCGCGGGC CGGGGGCTGC 120
TGGGBGCCBT BGCGBGGCTG BG 142

(2) INFORMATION FOR SEQ ID NO:1082:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:
CCTCTTTTCT GTTTTTCCC 19

(2) INFORMATION FOR SEQ ID NO:1083:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:
CTCTGCCTTT GTTTGGGTTC G 21

(2) INFORMATION FOR SEQ ID NO:1084:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:
CTTCCTTTCT GCTTCTTCC 19

(2) INFORMATION FOR SEQ ID NO:1085:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

CTGTGTCTCC TGTCTCCGCT TTTTTCTTC 29

(2) INFORMATION FOR SEQ ID NO:1086:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:
GTCTTTGTTG TTTTCTCTTC CTTG 24

(2) INFORMATION FOR SEQ ID NO:1087:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:
CTGBGCBBGB TBTCTBGBTT CTGGGGTGGT CTCGBTTTTB BBBGCTTGBG BBGCTGCBBB 60
CBTTBTCCBB BGTBTBTTTG BGGCTCCBBG GBTCBCGBCC BTCTTCCCBG GCBTTTTBBG 120
TTGCTGTCGT 130

(2) INFORMATION FOR SEQ ID NO:1088:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:
GTTCTTGGCT TCTTCTGTC 19

(2) INFORMATION FOR SEQ ID NO:1089:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:
CGTTGGCTTC TCGTTGTCCC 20

(2) INFORMATION FOR SEQ ID NO:1090:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:
TGTGGGCTTC TCGTTGTCCC 20

(2) INFORMATION FOR SEQ ID NO:1091:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:
CCCTTCGGGG GCTGGTGG 18

(2) INFORMATION FOR SEQ ID NO:1092:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:
GGCTGGTGG 9

(2) INFORMATION FOR SEQ ID NO:1093:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

GGCCGTCCTT GCCTGCTGG 19

(2) INFORMATION FOR SEQ ID NO:1094:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:
TTTTCTCTTT CGCTTTCTTT TCGTCTCCTG TTCCTCCTTT T 41

(2) INFORMATION FOR SEQ ID NO:1095:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:
TTGCTGTTTT TTCTCCTTCT TCTCTCCTTT CTTTTC 36

(2) INFORMATION FOR SEQ ID NO:1096:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:
TTTTCTCTTT CGCTTTCTTT TCGTCTCCTG TTCCTCCTTT T 41

(2) INFORMATION FOR SEQ ID NO:1097:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:
TTGCTGTTTT TTCTCCTTCT TCTCTCCTTT CTTTTC 36

(2) INFORMATION FOR SEQ ID NO:1098:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:
CTCTGTCTTG TTCTGGTCCT TCGTGGGGCT CTG 33

(2) INFORMATION FOR SEQ ID NO:1099:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:
TGTCGCGTGG GTGCGGCCGT GGCC 24

(2) INFORMATION FOR SEQ ID NO:1100:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:
GGCGGBCCBG GBGTTGGBGC BGGBGCBGGB CGGGCBGGCG GCTCBTGTTT GGBTCGGCBG 60
GBGGCBCTC 69

(2) INFORMATION FOR SEQ ID NO:1101:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:
TCTGGGGTGT CCTG 14

(2) INFORMATION FOR SEQ ID NO:1102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:
GCCTTCGTGG TTCC 14

(2) INFORMATION FOR SEQ ID NO:1103:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:
TCTTCCTTCG TTTGC 15

(2) INFORMATION FOR SEQ ID NO:1104:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:
GGCTGCGCTC CTGCCCCGC 19

(2) INFORMATION FOR SEQ ID NO:1105:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:
GGCTGCGCTC CTGCCCCGC 19

(2) INFORMATION FOR SEQ ID NO:1106:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:
CTCTTTCCCG GGCTCTT 17

(2) INFORMATION FOR SEQ ID NO:1107:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:
GCGCTGGGGG GTGCTCC 17

(2) INFORMATION FOR SEQ ID NO:1108:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:
CGTGTGTTTG CGCCCTCCTC CTGGTCGC 28

(2) INFORMATION FOR SEQ ID NO:1109:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:
GCTTGTCGTT TTGG 14

(2) INFORMATION FOR SEQ ID NO:1110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:
GGCCGGCTTT GCCCGCCTCC C 21

(2) INFORMATION FOR SEQ ID NO:1111:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:
GGCGCCTGGC CCGGCC 16

(2) INFORMATION FOR SEQ ID NO:1112:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:
TTCCTGGGCT GCGTGCGC 18

(2) INFORMATION FOR SEQ ID NO:1113:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:
GTTCTGTTCT TCTTCCTGGC 20

(2) INFORMATION FOR SEQ ID NO:1114:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:
GCBGGBGBCB GGGCBGGGCG BTCBGGBGCB GCGTGBGCCB BBGGBGGBCC BTCGGGBBCG 60
CBGCTCCGGB BCGCBGGB 78

(2) INFORMATION FOR SEQ ID NO:1115:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:
CTCTGGTTGG CTTCCTTC 18

(2) INFORMATION FOR SEQ ID NO:1116:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:
GCCGGCBCBT GCTBGCBGGB BGBBCBGBGG GGGBBGCBGT TGGGBGGTGB GBCCCBTTBB 60
TBGGTGTCGB 70

(2) INFORMATION FOR SEQ ID NO:1117:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:
TCTGCGCGCC CCTGCTCC 18

(2) INFORMATION FOR SEQ ID NO:1118:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:
CGCCCGGCTT CTCT 14

(2) INFORMATION FOR SEQ ID NO:1119:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:
CGTGTGGGCT TCGG 14

(2) INFORMATION FOR SEQ ID NO:1120:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:
CCCCGCGCCT CCGTTGTTCT C 21

(2) INFORMATION FOR SEQ ID NO:1121:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:
TGCTCGCTGG GCTTG 15

(2) INFORMATION FOR SEQ ID NO:1122:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:
GGTTTCCTGG GGCCCTGGGT TTC 23

(2) INFORMATION FOR SEQ ID NO:1123:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:
TCTGCCGGGT CGTTTTC 17

(2) INFORMATION FOR SEQ ID NO:1124:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:
GGGTGCTGGC TGCG 14

(2) INFORMATION FOR SEQ ID NO:1125:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:
CTTGGTGCTG GGGCTCC 17

(2) INFORMATION FOR SEQ ID NO:1126:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:
GGCGGCTGCG GGCTGGGTTG GG 22

(2) INFORMATION FOR SEQ ID NO:1127:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:
CTTGGCTGGT TCCTGGCCTC GGG 23

(2) INFORMATION FOR SEQ ID NO:1128:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:
CCTCCTCCTC CTCCTCGCTC CCTTTTTCTT CCTCT 35

(2) INFORMATION FOR SEQ ID NO:1129:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:
TCCCTGCTGC TCTC 14

(2) INFORMATION FOR SEQ ID NO:1130:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:
TGCCCTCCCT TCCCTCCTGG 20

(2) INFORMATION FOR SEQ ID NO:1131:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:
GGTGCCTCCT TGGGCCCTGC 20

(2) INFORMATION FOR SEQ ID NO:1132:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:
GGCTGCTCCT TGCCCC 16

(2) INFORMATION FOR SEQ ID NO:1133:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:
CTCTGGGTCG GGCTGGC 17

(2) INFORMATION FOR SEQ ID NO:1134:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:
GGGGCGTCTC TGTGC 15

(2) INFORMATION FOR SEQ ID NO:1135:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:
CTGGCCTGGG TGCC 14

(2) INFORMATION FOR SEQ ID NO:1136:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:
GCCTCTCCTG GGGGGGTGGC TCCCTGTCC 29

(2) INFORMATION FOR SEQ ID NO:1137:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:
CCTTTTCCCC CGGCTCC 17

(2) INFORMATION FOR SEQ ID NO:1138:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:
GTGGGGGCTT TGGC 14

(2) INFORMATION FOR SEQ ID NO:1139:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:
GGGGGTCTGT GGCCTGCTCC TGGGG 25

(2) INFORMATION FOR SEQ ID NO:1140:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:
AGGGGTCTGG GGCCCTC 17

(2) INFORMATION FOR SEQ ID NO:1141:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:
TTTTGGGGGT CTGGCTTG 18

(2) INFORMATION FOR SEQ ID NO:1142:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:
GCCTGGCTGC CTTCC 15

(2) INFORMATION FOR SEQ ID NO:1143:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:
GGGGCCTGCC GTGGGGC 17

(2) INFORMATION FOR SEQ ID NO:1144:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:
TGTCCTCTGT TGCTCCCCTT 20

(2) INFORMATION FOR SEQ ID NO:1145:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:
TGCCTGCTGT CTGG 14

(2) INFORMATION FOR SEQ ID NO:1146:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:
GGTTCCCGCC TTCCCT 16

(2) INFORMATION FOR SEQ ID NO:1147:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:
GTTCCCAGAG CTTGCCACCT GCAGCAGGAC CAGGCAGCTC ACAGGGAACA GGAGCCCAGA 60
GCAAAGCCAC CCCATTGGGA GATGCCAAGG CACCAGGCTG 100

(2) INFORMATION FOR SEQ ID NO:1148:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:
GTTCCCBGBG CTTGCCBCCT GCBGCBGGBC CBGGCBGCTC BCBGGGBBCB GGBGCCCBGB 60
GCBBBGCCBC CCCBTTGGGB GBTGCCBBGG CBCCBGGCTG 100

(2) INFORMATION FOR SEQ ID NO:1149:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:
TCCCTGTTTC CCCCCTTT 18

(2) INFORMATION FOR SEQ ID NO:1150:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:
CGTTCTGCGT TTGCCTTTGG C 21

(2) INFORMATION FOR SEQ ID NO:1151:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:
GTTTTTTGTT TGTTTTCT 18

(2) INFORMATION FOR SEQ ID NO:1152:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:
CTCTCCGTCT TTCTTCTCC 19

(2) INFORMATION FOR SEQ ID NO:1153:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:
CCTCCTGCCT GTGTCCCTGC TCCCC 25

(2) INFORMATION FOR SEQ ID NO:1154:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:
GAGGGTTTCT GGCTTCCTCT CT 22

(2) INFORMATION FOR SEQ ID NO:1155:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:
TGTCTCTCTG TCCTTTTGTT 20

(2) INFORMATION FOR SEQ ID NO:1156:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:
TGTTGTGCGG CCTGGTGCTG CCCTGCCCCG GG 32

(2) INFORMATION FOR SEQ ID NO:1157:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:
GTGGGBBTTT CTGTGGGGBT GGCBTBCBCG TBGGCBGCTC CBBGBGCTBG CBBBCTCBBB 60
TGCBGBBGCB TCCTCBTGGC TCTGBBBCG 89

(2) INFORMATION FOR SEQ ID NO:1158:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:
GTGTGTCTTT GCTGT 15

(2) INFORMATION FOR SEQ ID NO:1159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:
TTCCTTTGCT CTTG 14

(2) INFORMATION FOR SEQ ID NO:1160:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:
GTGTGTCTTT GCTGT 15

(2) INFORMATION FOR SEQ ID NO:1161:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:
GCCCTGCCTC TCTGC 15

(2) INFORMATION FOR SEQ ID NO:1162:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:
GGGGGTGGCT TCCTGCC 17

(2) INFORMATION FOR SEQ ID NO:1163:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:
GCGTCTCTGG GCCGTCCC 18

(2) INFORMATION FOR SEQ ID NO:1164:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:
GTCCCTCGGC CCCGCGCCGC GCTCGGCTCC TCTCCC 36

(2) INFORMATION FOR SEQ ID NO:1165:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:
TCTGGCCCGG CTC 13

(2) INFORMATION FOR SEQ ID NO:1166:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:
GGGGCGGGGC GGGGCGGTGG GCGGGC 26

(2) INFORMATION FOR SEQ ID NO:1167:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:
GGCGCTGCCC TGCGC 15

(2) INFORMATION FOR SEQ ID NO:1168:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:
TGCTGGCCGT CGGCTGCGCG CTGCTGGCTG CCCT 34

(2) INFORMATION FOR SEQ ID NO:1169:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:
TGCTGGCCGT CGGCTGCGCG CTGCTGGCTG CCCT 34

(2) INFORMATION FOR SEQ ID NO:1170:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:
GCTGGCCGCG CCGGG 15

(2) INFORMATION FOR SEQ ID NO:1171:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:
GCCTGTCCGC CTCTGCGGG 19

(2) INFORMATION FOR SEQ ID NO:1172:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:
CGCTGTCTCC TGGC 14

(2) INFORMATION FOR SEQ ID NO:1173:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:
TTGTCTTCCG GCTCT 15

(2) INFORMATION FOR SEQ ID NO:1174:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:
TCTGCTGGGG TGGG 14

(2) INFORMATION FOR SEQ ID NO:1175:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

GCTGGGCGGC CGGCCCGGT 19

(2) INFORMATION FOR SEQ ID NO:1176:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:
GCTGGGGCTC CTCGGGGGG 19

(2) INFORMATION FOR SEQ ID NO:1177:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:
GGGGGCTCTT CCGG 14

(2) INFORMATION FOR SEQ ID NO:1178:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:
GCTGTCTCCC TCCGGG 16

(2) INFORMATION FOR SEQ ID NO:1179:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:
GCGGGGGTTT CTGGCC 16

(2) INFORMATION FOR SEQ ID NO:1180:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:
GTGGGGGTCT TGCC 14

(2) INFORMATION FOR SEQ ID NO:1181:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:
TGGCCTCCGG GCTCC 15

(2) INFORMATION FOR SEQ ID NO:1182:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:
TGCTTGTCTT GCCTTCCTTC 20

(2) INFORMATION FOR SEQ ID NO:1183:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:
TCTGGTCGGT TGTGGCTCG 19

(2) INFORMATION FOR SEQ ID NO:1184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:
GGGCTCCGTG GGTCCCTGGC 20

(2) INFORMATION FOR SEQ ID NO:1185:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:
GCCCGTTTGT GTTTTGTC 18

(2) INFORMATION FOR SEQ ID NO:1186:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:
TTTTCCCCTG GCGT 14

(2) INFORMATION FOR SEQ ID NO:1187:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:
CCCTGTGCCC CTCTCCTCTC CTTCCTCTGC TTCTC 35

(2) INFORMATION FOR SEQ ID NO:1188:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:
GCTCTCCTTT GTGGG 15

(2) INFORMATION FOR SEQ ID NO:1189:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:
GCCCTCCCTG CTGCT 15

(2) INFORMATION FOR SEQ ID NO:1190:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:
CTTGGTTTTG GGCT 14

(2) INFORMATION FOR SEQ ID NO:1191:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:
TTTTTTCTCT TCCTCCTTTT TC 22

(2) INFORMATION FOR SEQ ID NO:1192:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:
GTGCGTGGGC CTCC 14

(2) INFORMATION FOR SEQ ID NO:1193:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:
CCCGGCGC 8

(2) INFORMATION FOR SEQ ID NO:1194:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:
GCACGCCTCT TGCCACCTCC TGCGCAGGGC AGCGCCTTGG GGCCAGCGCC GCTCCCGGCG 60
CGGCCAGCAG GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCCT CCTCGGCTAC 120
CACTCCATGG TCCCGCAGAG GCGGACAGGC 150

(2) INFORMATION FOR SEQ ID NO:1195:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:
GGCCBGCBGG 10

(2) INFORMATION FOR SEQ ID NO:1196:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:
GCBCGCCTCT TGCCBCCTCC TGCGCBGGGC BGCGCCTTGG GGCCBGCGCC GCTCCCGGCG 60
CGGCCBGCBG GGCBGCCBGC BGCGCGCBGC CGBCGGCCBG CBTGCTTCCT CCTCGGCTBC 120
CBCTCCBTGG TCCCGCBGBG GCGGBCBGGC 150

(2) INFORMATION FOR SEQ ID NO:1197:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:
GCTTCTCTTT CGTTCCCGGT GGGCTCG 27

(2) INFORMATION FOR SEQ ID NO:1198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:
GTGGCTGTCT GTGTGGGGCG GCT 23

(2) INFORMATION FOR SEQ ID NO:1199:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:
GTGCCTCTTT GCTGCTTTC 19

(2) INFORMATION FOR SEQ ID NO:1200:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:
GATTCTTTGC CTTTTTCTGC 20

(2) INFORMATION FOR SEQ ID NO:1201:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201:
GCTTGTGTGC TCTGCTGTCT CT 22

(2) INFORMATION FOR SEQ ID NO:1202:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:
TGGTTCCTTC CGGTGGTTTC TTCCTGGCTC TTGTCCT 37

(2) INFORMATION FOR SEQ ID NO:1203:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:
TTCTCTTGGC CCTTGGC 17

(2) INFORMATION FOR SEQ ID NO:1204:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:
TGGTGGGGCT GGGGCTCCGG GGTCTCTGCC CCTCCGTGC 39

(2) INFORMATION FOR SEQ ID NO:1205:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:
CGCGTGGGGC CGCGCTCGCC GGCCCCCC 28

(2) INFORMATION FOR SEQ ID NO:1206:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:
CCTGCCGGGT GGGCTCCCGC CGCG 24

(2) INFORMATION FOR SEQ ID NO:1207:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:
CGCCGGCCTG CCGGCCCCTC 20

(2) INFORMATION FOR SEQ ID NO:1208:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:
GTGGGTCCTG CTGGCCGGGT CCGGGTCCCG GGGGTGGGG 39

(2) INFORMATION FOR SEQ ID NO:1209:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:
CGCGBGTCGG CGGCCGBGGG TC 22

(2) INFORMATION FOR SEQ ID NO:1210:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:
GGCCTCCBCC BGGGBCBTG 19

(2) INFORMATION FOR SEQ ID NO:1211:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:
GTCCTTCTTG TCCGCTGCC 19

(2) INFORMATION FOR SEQ ID NO:1212:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:
TCTCTGGGGT TTTCGGTCTG GGTGG 25

(2) INFORMATION FOR SEQ ID NO:1213:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:
GCTTTCCTCC TGGGGCTGCT GCTG 24

(2) INFORMATION FOR SEQ ID NO:1214:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:
GGCTCTTCTT TTTGTTTCTG GCCTGGTG 28

(2) INFORMATION FOR SEQ ID NO:1215:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:
CTCTCTCGTG CCCTTTCC 18

(2) INFORMATION FOR SEQ ID NO:1216:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:
CTTGGGTGTC TTGTTTTTGT 20

(2) INFORMATION FOR SEQ ID NO:1217:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:
GGCCTCCBCC BGGGBCBTG 19

(2) INFORMATION FOR SEQ ID NO:1218:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:
GTGGGGCCTG CTCTCCCGGC CTCCG 25

(2) INFORMATION FOR SEQ ID NO:1219:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:
TGTGTTGCTG GGTGTTTTCC CGTCTCTGG 29

(2) INFORMATION FOR SEQ ID NO:1220:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:
TCTGCCTTCG GGGGTCGT 18

(2) INFORMATION FOR SEQ ID NO:1221:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:
GGGTCCTCBT GGCTGGGG 18

(2) INFORMATION FOR SEQ ID NO:1222:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:
GCCTGGGCCT GCBGGGCC 18

(2) INFORMATION FOR SEQ ID NO:1223:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:
GCTCTTGCCT GGBGTGGCTC 20

(2) INFORMATION FOR SEQ ID NO:1224:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: lin ar
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:
GCCCBGBGTC TTCCCTGGT 19

(2) INFORMATION FOR SEQ ID NO:1225:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:
GGGTCCTCBT GGCTGGGGTC 20

(2) INFORMATION FOR SEQ ID NO:1226:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:
CCTCTCTCCC GTCCT 15

(2) INFORMATION FOR SEQ ID NO:1227:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:
GTCTTTGTTT CTGGGCTCGT GCC 23

(2) INFORMATION FOR SEQ ID NO:1228:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:
CCBTCCCGGC TTCTCTCTGG TTCC 24

(2) INFORMATION FOR SEQ ID NO:1229:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:
GTCCTCTGTG GTGTTTGG 18

(2) INFORMATION FOR SEQ ID NO:1230:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:
CCCTGCTTCC TTTTGCCTGT T 21

(2) INFORMATION FOR SEQ ID NO:1231:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:
GAGGGGGCAG CAGTTGGGCC CCAAAGGCCC TCTCGTTCAC CTTCTGGCAC GGAGTTGCAT 60
CCCCATAGTC AAACTCTGTG GTCGT 85

(2) INFORMATION FOR SEQ ID NO:1232:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:
GTCATAGTCC TCTGTGGTGT TTGGAGTTTC CATCCCGGCT TCTCTCTGGT TCCAAGGGA 59

(2) INFORMATION FOR SEQ ID NO:1233:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:
GBGGGGGCBG CBGTTGGGCC CCBBBGGCCC TCTCGTTCBC CTTCTGGCBC GGBGTTGCBT 60
CCCCBTBGTC BBBCTCTGTG GTCGTG 86

(2) INFORMATION FOR SEQ ID NO:1234:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:
TCBTBGTCCT CTGTGGTGTT TGGBGTTTCC BTCCCGGCTT CTCTCTGGTT CCBBGGGB 58

(2) INFORMATION FOR SEQ ID NO:1235:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:
GGGCBCGGGG CBGTGGGCGG GCBBTGTBGG CBBBGCBGCB GGGTGTGGTG TCCGBGGBBT 60
BTGGGGBGGC BGBTGCBGGB GCGC 84

(2) INFORMATION FOR SEQ ID NO:1236:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:
BGBGGGCBGT BGCBBTGBGG BTGBCBGCGB GGCGTGCCGC GGBGBCCTTC BTGGTBCCTG 60
TGGBGBGGCT GTCGGBGG 78

(2) INFORMATION FOR SEQ ID NO:1237:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:
GGGTGTGGTG TCCGCTTGGC GGTTCTTTCG GGTGTTTCTT CTCTGGGTTG GCCTGCTGCT 60
CGTCGTGGTC 70

(2) INFORMATION FOR SEQ ID NO:1238:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:
GCTCCGCTCC CGGGTTCGTC TCGCTCTGTC GCCCCTTCCT TCCTTGTCGT GTTCCTCCCT 60
TCCTTGCCTC T 71

(2) INFORMATION FOR SEQ ID NO:1239:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:
GGGTGTGGTG TCCG 14

(2) INFORMATION FOR SEQ ID NO:1240:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:
CTTGGCGGTT CTTTCGGGTG 20

(2) INFORMATION FOR SEQ ID NO:1241:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:
TTTCTTCTCT GGGTTGGC 18

(2) INFORMATION FOR SEQ ID NO:1242:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:
CTGCTGCTCG TCGTGGTC 18

(2) INFORMATION FOR SEQ ID NO:1243:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:
GCTCCGCTCC CGGGTTC 17

(2) INFORMATION FOR SEQ ID NO:1244:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:
GTCTCGCTCT GTCGCCC 17

(2) INFORMATION FOR SEQ ID NO:1245:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:
CTTCCTTCCT TGTC 14

(2) INFORMATION FOR SEQ ID NO:1246:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:
GTGTTCCTCC CTTCCTTGCC TCT 23

(2) INFORMATION FOR SEQ ID NO:1247:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:
GTTCBTGGTG GCTBGGTGGG GC 22

(2) INFORMATION FOR SEQ ID NO:1248:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:
GCTGCCCGGC GGGGTGTGCG CTTGGC 26

(2) INFORMATION FOR SEQ ID NO:1249:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:
GCTCCCGTGC TCGGTTCTCT GTCTCCCGGT 30

(2) INFORMATION FOR SEQ ID NO:1250:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:
CCCCCTTTGC CTGGCGTCTC GG 22

(2) INFORMATION FOR SEQ ID NO:1251:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:
GCCTTCGTCC TCTTCCTCTT CTTCCTTCC 29

(2) INFORMATION FOR SEQ ID NO:1252:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:
GCTCCGTGGG GGCTGCTTGG TGGGGGCCTG TGCCTCGGGG TCC 43

(2) INFORMATION FOR SEQ ID NO:1253:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:
CGGGGCTTCT GGCCCTTGCC 20

(2) INFORMATION FOR SEQ ID NO:1254:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:
GTTCATGGTG GCTAGGTGGG GC 22

(2) INFORMATION FOR SEQ ID NO:1255:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:
GGGGTGGGTB GGCCGTGTCT GGGG 24

(2) INFORMATION FOR SEQ ID NO:1256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:
GTTGGCCBTG TTGGTTGCC 19

(2) INFORMATION FOR SEQ ID NO:1257:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:
TCTTGGTGGT GCGCCGGGC 19

(2) INFORMATION FOR SEQ ID NO:1258:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:
GCGTCTTGGC TTTCTTCTCC TTCGGGCCCT CGGGCCGGTG CTTGTGG 47

(2) INFORMATION FOR SEQ ID NO:1259:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:
GCTCCTCCCG GGCGGCCTCC CCGGGCGGGG GCTTCTTG 38

(2) INFORMATION FOR SEQ ID NO:1260:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:
GCGCTGGCGG GGGGGCCTCC TCC 23

(2) INFORMATION FOR SEQ ID NO:1261:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:
GCTCTGTGGC TGGGCGTTCC TTGGTGTTCT GGGTGGC 37

(2) INFORMATION FOR SEQ ID NO:1262:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:
TGGCGGGCGT GGTGGCCTCT GTGGTGG 27

(2) INFORMATION FOR SEQ ID NO:1263:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:
GGGCCCGCGG CTGCBGGGG 19

(2) INFORMATION FOR SEQ ID NO:1264:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:
TTGCCTGTCT GCTTCGTC 18

(2) INFORMATION FOR SEQ ID NO:1265:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:
CTTTGCGCTC CCGGGCCGCC 20

(2) INFORMATION FOR SEQ ID NO:1266:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:
GGGGTGGGTA GGCCGTGTCT GGGG 24

(2) INFORMATION FOR SEQ ID NO:1267:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:
GTTGGCCATG TTGGTTGCC 19

(2) INFORMATION FOR SEQ ID NO:1268:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:
GGGCCCGCGG CTGCAGGGG 19

(2) INFORMATION FOR SEQ ID NO:1269:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:
CGGTTTCCTT TGCGGTC 17

(2) INFORMATION FOR SEQ ID NO:1270:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:
TTGGCCCGGG CTCCGGGTG 19

(2) INFORMATION FOR SEQ ID NO:1271:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:
CCCGCCCGCC CGCCGGCCGC CGC 23

(2) INFORMATION FOR SEQ ID NO:1272:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:
CCCGCCGGGC TGTCCCCGCC CCGCCCC 27

(2) INFORMATION FOR SEQ ID NO:1273:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:
GGCCCGGGGC GCGGGGG 17

(2) INFORMATION FOR SEQ ID NO:1274:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:
CGGCCCTCCC GCCCCTCTGG 20

(2) INFORMATION FOR SEQ ID NO:1275:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:
GCCGGCGCGG GCGTCGG 17

(2) INFORMATION FOR SEQ ID NO:1276:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:
CCGCTCGCGC CTGGGGTTCC CTCTCCTCCC CCTGTGC 37

(2) INFORMATION FOR SEQ ID NO:1277:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:
GCCTGCCTCT TGCTCTTC 18

(2) INFORMATION FOR SEQ ID NO:1278:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:
TGCGTCCGCT GCCTTCTCCC 20

(2) INFORMATION FOR SEQ ID NO:1279:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:
CTCTCCTCGG CCGTTGCCTG TGC 23

(2) INFORMATION FOR SEQ ID NO:1280:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: singl
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:
TGTCCGTCCT GTCGCCCTTC CGTGGTGC 28

(2) INFORMATION FOR SEQ ID NO:1281:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:
TGTTGTCTCT TCTGCCCTC 19

(2) INFORMATION FOR SEQ ID NO:1282:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:
GGTGTGCTGG TGCTGGTGGT GGTG 24

(2) INFORMATION FOR SEQ ID NO:1283:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:
CCTCTGCCCG TGCTCGCC 18

(2) INFORMATION FOR SEQ ID NO:1284:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:
CTGCCTGGGC TGGCCTCTTC GGGT 24

(2) INFORMATION FOR SEQ ID NO:1285:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:
GTGGCTTTGG GGCTCTCTTG GTTGCCCTTT 30

(2) INFORMATION FOR SEQ ID NO:1286:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:
CTTCTCGTGG TGCCTCTCCT CCCTGGCTTG GTCGT 35

(2) INFORMATION FOR SEQ ID NO:1287:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:
TGTCTGGGGT GGTGCTCCTC TCCC 24

(2) INFORMATION FOR SEQ ID NO:1288:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:
TTTCCCTGCT GGCCGTTTGT 20

(2) INFORMATION FOR SEQ ID NO:1289:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:
CCTGTTTTCT GTCTTCCTCT 20

(2) INFORMATION FOR SEQ ID NO:1290:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:
TTCCTCCTGT TTCTCCGT 18

(2) INFORMATION FOR SEQ ID NO:1291:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:
TTGGCTTGCT GCTTGCGGGG CTGTCTCC 28

(2) INFORMATION FOR SEQ ID NO:1292:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:
CTTGCCCCTG TGGGCTTTCC C 21

(2) INFORMATION FOR SEQ ID NO:1293:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:
TGGTCCGGTC TTCTCCTTGG GGGTC 25

(2) INFORMATION FOR SEQ ID NO:1294:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:
GCCCTTCTTG GTGGGCTG 18

(2) INFORMATION FOR SEQ ID NO:1295:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:
GCTCGTCTGT CTTTTTCCTT CC 22

(2) INFORMATION FOR SEQ ID NO:1296:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:
TGGGGGTGGC CGTTGTGGGC GGTGTGGTCC GCCT 34

(2) INFORMATION FOR SEQ ID NO:1297:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:
TGCCTCTGCT GGTCTTTC 18

(2) INFORMATION FOR SEQ ID NO:1298:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:
GTGCTCCGGT GGCTTTTT 18

(2) INFORMATION FOR SEQ ID NO:1299:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:
GCTTGTGTGC TCTGCTGTCT CTG 23

(2) INFORMATION FOR SEQ ID NO:1300:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:
TTCCTTCCGG TGGTTTCTTC CTGGCTCTTG TCCT 34

(2) INFORMATION FOR SEQ ID NO:1301:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:
TTCTCTTGGC CCTTGGCCC 19

(2) INFORMATION FOR SEQ ID NO:1302:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:
TGGCTCGGTG CTTCTGCCCC 20

(2) INFORMATION FOR SEQ ID NO:1303:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:
TGTTGTTGCG GCGCTC 16

(2) INFORMATION FOR SEQ ID NO:1304:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:
GGTTGGTGTG GCCCCTG 17

(2) INFORMATION FOR SEQ ID NO:1305:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:
TGGTGCTTCG TTTCC 15

(2) INFORMATION FOR SEQ ID NO:1306:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:
CCCTCTTTCT CTTTGTTC 18

(2) INFORMATION FOR SEQ ID NO:1307:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:
GGGGGTTCTT GTGGC 15

(2) INFORMATION FOR SEQ ID NO:1308:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:
GGGCTGCTTG TCTCGTTCC 19

(2) INFORMATION FOR SEQ ID NO:1309:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:
GGTCCBGCCB TGGGTCTGGG 20

(2) INFORMATION FOR SEQ ID NO:1310:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:
GGCTGGGCTG CBGGCTCCGG 20

(2) INFORMATION FOR SEQ ID NO:1311:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:
GCGGGCGGGT GCGGGCTGCG TGCTGGG 27

(2) INFORMATION FOR SEQ ID NO:1312:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:
GGCTGCCCCG CAGGCCCTGC 20

(2) INFORMATION FOR SEQ ID NO:1313:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Gen mic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:
GCBCCGCCTG GBGCCCTGGG GCCCCCCTGT CTTCTTGGGG BGCGCCTCCT CGGCCBGCTC 60

CBCGTCCCGG BTCBTGCTTT CBGTGCTCBT GGTGTCCTTT CCBGGGGBGB GBGGG 115

(2) INFORMATION FOR SEQ ID NO:1314:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:

```
GCTGGTCCTC TGCTGTCCTT GCTGGTGCTC BTGGTGTCCT TTCCGCCCTG GGGCCCCCCT    60
GTCTTCTTGG GGCCTCTTCC CTCTGGGGGC CGTCTCTCTC CCTCTCTTGC GTCTCTCTCT   120
TTCTCTCTCT CTCTTCCCCT TTCCCGCTCT TTCTGTCTCG GTGTCTGGTT TTCTCTCTCC   180
GCTGGCTGCC TGTCTGGCCT GCGCTCTTGG CCTGTGCTGT TCCTCCTCCG GTTCCTGTCC   240
TCTCTGTCTG TCGCCCCCTC TGGGGTCTCC CTCTGGCGTG GTGGTCTTGT TGCTTGGGCT   300
GGGCTCCGTG TCTCCBGTGC TCBTGGTGTC C                                  331
```

(2) INFORMATION FOR SEQ ID NO:1315:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

```
GCTGBGGGBG CGTCTGCTGG CGCTGGTCCT CTGCTGTCCT TGCTGGTGCT CBTGGTGTCC    60
TTTCCGCCCT GGGGCCCCCC TGTCTTCTTG GGGCCTCTTC CCTCTGGGGG CCGTCTCTCT   120
CCCTCTCTTG CGTCTCTCTC TTTCTCTCTC TCTCTTCCCC TTTCCCGCTC TTTCTGTCTC   180
GGTGTCTGGT TTTCTCTCTC CGCTGGCTGC CTGTCTGGCC TGCGCTCTTG GCCTGTGCTG   240
TTCCTCCTCC GGTTCCTGTC CTCTCTGTCT GTCGCCCCCT CTGGGGTCTC CCTCTGGCGT   300
GGTGGTCTTG TTGCTTGGGC TGGGCTCCGT GTCTCCBGTG CTCBTGGTGT CCGCTGBGGG   360
BGCGTCTGCT GGC                                                      373
```

(2) INFORMATION FOR SEQ ID NO:1316:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

```
GCCCCGTCTG CTGCTCCTCG TGCCG    25
```

(2) INFORMATION FOR SEQ ID NO:1317:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

```
CCTCGTCCTT CATGGTACCG TCGGTGTGGT GGC    33
```

(2) INFORMATION FOR SEQ ID NO:1318:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

```
CTCGGGTGGG CCGGTGGTG    19
```

(2) INFORMATION FOR SEQ ID NO:1319:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

```
GGGCGCGCGC GCTCGCGT    18
```

(2) INFORMATION FOR SEQ ID NO:1320:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:
GGCTCCGGCT CTTCTTTCCC GGCTCCGTCG GCCCGGGGGC CTTGGTCTC 49

(2) INFORMATION FOR SEQ ID NO:1321:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:
CCTCGTCCTT CBTGGTBCCG 20

(2) INFORMATION FOR SEQ ID NO:1322:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:
CCCGTTCGCC TGGCGC 16

(2) INFORMATION FOR SEQ ID NO:1323:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:
GCGCTGCGGG TTCCTC 16

(2) INFORMATION FOR SEQ ID NO:1324:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:
GTGGGTTTCT CCCCGCCGTT CTC 23

(2) INFORMATION FOR SEQ ID NO:1325:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:
CGGTCTGTTG CCTTTGTGGG 20

(2) INFORMATION FOR SEQ ID NO:1326:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:
CTTCTTGTCT TTTTGGCT 18

(2) INFORMATION FOR SEQ ID NO:1327:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:
GTTCTTTTCC TGCTTGGC 18

(2) INFORMATION FOR SEQ ID NO:1328:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:
GTCTTTTCCT TTCTT 15

(2) INFORMATION FOR SEQ ID NO:1329:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:
TGTGCTCGGT TGTGGGTC 18

(2) INFORMATION FOR SEQ ID NO:1330:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:
CGCTGGTCCT TTGCC 15

(2) INFORMATION FOR SEQ ID NO:1331:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:
CTGTGTGTTT CTGCTG 16

(2) INFORMATION FOR SEQ ID NO:1332:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:
CCCGTTCGCC TGGCGC 16

(2) INFORMATION FOR SEQ ID NO:1333:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:
GCGCTGCGGG TTCCTC 16

(2) INFORMATION FOR SEQ ID NO:1334:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:
GTGGGTTTCT CCCCGCCGTT CTC 23

(2) INFORMATION FOR SEQ ID NO:1335:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:
CGGTCTGTTG CCTTTGTGGG 20

(2) INFORMATION FOR SEQ ID NO:1336:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: singl
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:
CTTCTTGTCT TTTTGGCT 18

(2) INFORMATION FOR SEQ ID NO:1337:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:
GTTCTTTTCC TGCTTGGC 18

(2) INFORMATION FOR SEQ ID NO:1338:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:
GTCTTTTCCT TTCTT 15

(2) INFORMATION FOR SEQ ID NO:1339:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:
TGTGCTCGGT TGTGGGTC 18

(2) INFORMATION FOR SEQ ID NO:1340:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:
CGCTGGTCCT TTGCC 15

(2) INFORMATION FOR SEQ ID NO:1341:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:
CTGTGTGTTT CTGCTG 16

(2) INFORMATION FOR SEQ ID NO:1342:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:
GCGTCCGGTG GCCGCCGC 18

(2) INFORMATION FOR SEQ ID NO:1343:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:
GCCTCTCTCC TCTCCCC 17

(2) INFORMATION FOR SEQ ID NO:1344:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:
GTGGCCCTGT CGGGCGGG 18

(2) INFORMATION FOR SEQ ID NO:1345:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:
TCCTGCCGTC CTGTCTCCTT T 21

(2) INFORMATION FOR SEQ ID NO:1346:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:
TCTTTTGCTG TCTTGT 16

(2) INFORMATION FOR SEQ ID NO:1347:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:
CTTCCCGTCT CTGCTTT 17

(2) INFORMATION FOR SEQ ID NO:1348:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:
GTCTGTCCTC CCCGTCTCCT CCC 23

(2) INFORMATION FOR SEQ ID NO:1349:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:
ACTGCTTCTC CCGGGG 16

(2) INFORMATION FOR SEQ ID NO:1350:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:
GCTTCCCCGG CTTC 14

(2) INFORMATION FOR SEQ ID NO:1351:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:
GGGTGGCCGG TGTCCCGGGC TCCGGCGCGG CGGC 34

(2) INFORMATION FOR SEQ ID NO:1352:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:
GGCTTCGGCT GC 12

(2) INFORMATION FOR SEQ ID NO:1353:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:
GGGTGGGTGG CGCGG 15

(2) INFORMATION FOR SEQ ID NO:1354:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:
GCTGCCGGGT CCGCGCGGCG CCTGGGCC 28

(2) INFORMATION FOR SEQ ID NO:1355:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:
CTTGTGCTGC TTTT 14

(2) INFORMATION FOR SEQ ID NO:1356:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:
TGCTTGTTCC GTTC 14

(2) INFORMATION FOR SEQ ID NO:1357:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:
TGGCTGCTCC GGTCTGTGTT GTGGTTGTTT TG 32

(2) INFORMATION FOR SEQ ID NO:1358:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:
TTTCTTCTTG GGTGTGGG 18

(2) INFORMATION FOR SEQ ID NO:1359:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:
CCTTGCGGTT TTGG 14

(2) INFORMATION FOR SEQ ID NO:1360:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:
CTGTGGGCCC TTTG 14

(2) INFORMATION FOR SEQ ID NO:1361:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:
GGGCCTTGGC TTCTGGCTC 19

(2) INFORMATION FOR SEQ ID NO:1362:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: lin ar
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

```
CATCCACATG ATTGCTTAGA TTTGTGCTGT ATCTCTCAGG ATTATCACTG ATTACACATC    60
CAACCAGTGC CAGCCAAAAG GATGCCCTGA GGCAAAGGGT TTCCATCTTG AGGCAAATTT   120
GAGGA                                                               125
```

(2) INFORMATION FOR SEQ ID NO:1363:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

```
CBTCCBCBTG BTTGCTTBGB TTTGTGCTGT BTCTCTCBGG BTTBTCBCTG BTTBCBCBTC    60
CBBCCBGTGC CBGCCBBBBG GBTGCCCTGB GGCBBBGGGT TTCCBTCTTG BGGCBBBTTT   120
GBGGB                                                               125
```

(2) INFORMATION FOR SEQ ID NO:1364:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:

```
CGTGGTCGCT CCGC    14
```

(2) INFORMATION FOR SEQ ID NO:1365:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:

```
GTTTCTCTGG TTCCTCCG    18
```

(2) INFORMATION FOR SEQ ID NO:1366:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:

```
GTCCCGCGGG GTGCTG    16
```

(2) INFORMATION FOR SEQ ID NO:1367:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:

```
TCTGGTCGCT GTCGT    15
```

(2) INFORMATION FOR SEQ ID NO:1368:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:

```
GGCTTGGGTC TCCGGGCG    18
```

(2) INFORMATION FOR SEQ ID NO:1369:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:

```
GTTTCCTTCC TTTTCCGC    18
```

(2) INFORMATION FOR SEQ ID NO:1370:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:
GTCCTGTCGT GGCGCCTGGG GCTC 24

(2) INFORMATION FOR SEQ ID NO:1371:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:
TTCTTTTGTG GGCT 14

(2) INFORMATION FOR SEQ ID NO:1372:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:
CTTTGGTGGC TGTGGCTG 18

(2) INFORMATION FOR SEQ ID NO:1373:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:
TGGTCTCTGT GGTTG 15

(2) INFORMATION FOR SEQ ID NO:1374:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:
CTGCCCTGGG TCTGG 15

(2) INFORMATION FOR SEQ ID NO:1375:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:
GGGTGTGGCC TTGGGGCCGT CCTCTGGCTC CTCCTCGTGG GCCCCC 46

(2) INFORMATION FOR SEQ ID NO:1376:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:
GGGCTAAGAT GATCCACATC ACTACCACGT TGCCCACCAC AGAGGTCACC ACAATGACCG 60
TGTAGGCAGC TGCCCAAAGG ACAATTTGCC AGGCTGGTTG CACGAACTGA TTGGGTTCCG 120
AGGTGTTAGT GGAGATGTTT GGGGAGAGGT CTGAGTCCAC CGGGAGGACG TTATCCATTT 180
CGAAGCTAGG CGGTAAAGCC CTACTATCTG TACACAACCC CCCTCTGCAG CAGAGTCCTG 240
TCGTGGCGCC TGGGGCTCAG GGTCC 265

(2) INFORMATION FOR SEQ ID NO:1377:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

GGGCTBBGBT GBTCCBCBTC BCTBCCBCGT TGCCCBCCBC BGBGGTCBCC BCBBTGBCCG 60
TGTBGGCBGC TGCCCBBBGG BCBBTTTGCC BGGCTGGTTG CBCGBBCTGB TTGGGTTCCG 120
BGGTGTTBGT GGBGBTGTTT GGGGBGBGGT CTGBGTCCBC CGGGBGGBCG TTBTCCBTTT 180
CGBBGCTBGG CGGTBBBGCC CTBCTBTCTG TBCBCBBCCC CCCTCTGCBG CBGBGTCCTG 240
TCGTGGCGCC TGGGGCTCBG GGTCC 265

(2) INFORMATION FOR SEQ ID NO:1378:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:
CGTTTTCTTC TCTC 14

(2) INFORMATION FOR SEQ ID NO:1379:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:
GCTGGTTTTC CTTTCC 16

(2) INFORMATION FOR SEQ ID NO:1380:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:
TGGCAGTGGG TGGGGGTGGG GGTGGGGTGG C 31

(2) INFORMATION FOR SEQ ID NO:1381:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:
TTCCTTGTTC CTGGGGGTGT CCT 23

(2) INFORMATION FOR SEQ ID NO:1382:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:
CTTGCTCTGG GCTTTTCT 18

(2) INFORMATION FOR SEQ ID NO:1383:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:
CCCCTTTTCC TTCC 14

(2) INFORMATION FOR SEQ ID NO:1384:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:
TGTCTGTTTT CCTGGGG 17

(2) INFORMATION FOR SEQ ID NO:1385:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:
CTCTCCTCTG TCTCTGTGT 19

(2) INFORMATION FOR SEQ ID NO:1386:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:
CCTTGCCCTG GCCC 14

(2) INFORMATION FOR SEQ ID NO:1387:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:
TCTTCCCTCT CCTGTCTCCT GT 22

(2) INFORMATION FOR SEQ ID NO:1388:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:
CCCTGTGTTC CGCCC 15

(2) INFORMATION FOR SEQ ID NO:1389:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:
GTCTTCCCTC TCCTG 15

(2) INFORMATION FOR SEQ ID NO:1390:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:
ACCTCCTTTT CCTCCG 16

(2) INFORMATION FOR SEQ ID NO:1391:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:
CTGGGTGGGG CCCTG 15

(2) INFORMATION FOR SEQ ID NO:1392:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:
CCTGTTCTCT GCTCCC 16

(2) INFORMATION FOR SEQ ID NO:1393:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:
TGGCTTGGGG TTTCTTCTG 19

(2) INFORMATION FOR SEQ ID NO:1394:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:
TGTGTCTTCT TCCTCTGTT 19

(2) INFORMATION FOR SEQ ID NO:1395:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:
GGCTGGCTTT CTCCTTC 17

(2) INFORMATION FOR SEQ ID NO:1396:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:
TTTTGTCTTC CTGGG 15

(2) INFORMATION FOR SEQ ID NO:1397:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397:
TGCCCCTTCT TCCTTTCTTG GG 22

(2) INFORMATION FOR SEQ ID NO:1398:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:
TCCTTGGTGC TTGGGCTGGG 20

(2) INFORMATION FOR SEQ ID NO:1399:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:
CTGTGCGTCC GTCTGCTGG 19

(2) INFORMATION FOR SEQ ID NO:1400:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:
GGGGCCGGGG TGGCTGGGCC CTGCTTGCCG C 31

(2) INFORMATION FOR SEQ ID NO:1401:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:
ACGACCCCGG GCCGACCCGA G 21

(2) INFORMATION FOR SEQ ID NO:1402:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:
GCTCGGGGGG CTGTGTTCTG GCGCTGGTGG G 31

(2) INFORMATION FOR SEQ ID NO:1403:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:
CTTGGGCCCC TCTGGGGGCT GGGTT 25

(2) INFORMATION FOR SEQ ID NO:1404:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:
TCCTGCTGCG CCTGGGCGCT G 21

(2) INFORMATION FOR SEQ ID NO:1405:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:
GCGTCTTGGG GTGC 14

(2) INFORMATION FOR SEQ ID NO:1406:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:
GGGGCCGGGG GGCCGGGGG 19

(2) INFORMATION FOR SEQ ID NO:1407:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:
GCCGCTGTTC GTGGGCCTGG G 21

(2) INFORMATION FOR SEQ ID NO:1408:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:
GGTGCCTGTG GCTGCC 16

(2) INFORMATION FOR SEQ ID NO:1409:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:
GGTTGCCCCG GTTGGTGGC 19

(2) INFORMATION FOR SEQ ID NO:1410:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:
GCCGTCCTGC TGCCGGT 17

(2) INFORMATION FOR SEQ ID NO:1411:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:
CGTTGGCTGG GTCCCCCCGC 20

(2) INFORMATION FOR SEQ ID NO:1412:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:
CCGTTTCCTG GGGTCC 16

(2) INFORMATION FOR SEQ ID NO:1413:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:
GCGTGGGGTG CTCC 14

(2) INFORMATION FOR SEQ ID NO:1414:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:
GGTTCCTCGT GCCG 14

(2) INFORMATION FOR SEQ ID NO:1415:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:
CTGCTGCCTT GTCTTTCC 18

(2) INFORMATION FOR SEQ ID NO:1416:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:
GGCCGTGGCG GCGTGGTGGT CC 22

(2) INFORMATION FOR SEQ ID NO:1417:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:
GCCCCCCCTG GCCTTCTGCT C 21

(2) INFORMATION FOR SEQ ID NO:1418:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:
GGGGTCTGGC TGGT 14

(2) INFORMATION FOR SEQ ID NO:1419:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:
TGCCGGTGCC CTTGGCGGC 19

(2) INFORMATION FOR SEQ ID NO:1420:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:
GGTCTTCTTC CTGGTG 16

(2) INFORMATION FOR SEQ ID NO:1421:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:
GCTCTGGGCC CGGCCGGTCT CGG 23

(2) INFORMATION FOR SEQ ID NO:1422:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:
GCGTCTCGTG TTCG 14

(2) INFORMATION FOR SEQ ID NO:1423:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:
CTCTTGTGCT GTTCCGGCCG 20

(2) INFORMATION FOR SEQ ID NO:1424:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:
CTCCTTCCTC TTCCGCCGCC 20

(2) INFORMATION FOR SEQ ID NO:1425:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:
GCCGCTCCCC GCCC 14

(2) INFORMATION FOR SEQ ID NO:1426:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:
GCTCGTCGCC CTGGCCC 17

(2) INFORMATION FOR SEQ ID NO:1427:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:
GGCCTCCTCC TGGCCGC 17

(2) INFORMATION FOR SEQ ID NO:1428:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:
TGTCTCGGGC GGCGGCCTTG GC 22

(2) INFORMATION FOR SEQ ID NO:1429:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:
GCTCCGTTTG GGGCTG 16

(2) INFORMATION FOR SEQ ID NO:1430:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:
CCTCTGGCGC TTCC 14

(2) INFORMATION FOR SEQ ID NO:1431:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:
GGCCCTCGGC CTGGGCGCTC 20

(2) INFORMATION FOR SEQ ID NO:1432:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:
TCTTCCGCCT GTGC 14

(2) INFORMATION FOR SEQ ID NO:1433:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:
TGGTGGCCCT CGTGG 15

(2) INFORMATION FOR SEQ ID NO:1434:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:
GCCCCTCCTG GCCTCCGGTG TCC 23

(2) INFORMATION FOR SEQ ID NO:1435:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:
TGTGGTCCCC CGGCTGGT 18

(2) INFORMATION FOR SEQ ID NO:1436:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:
GGCCGGGCCG GTTGGGCGGG C 21

(2) INFORMATION FOR SEQ ID NO:1437:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:
GTGGGCGCCG GCGGGTCCTC C 21

(2) INFORMATION FOR SEQ ID NO:1438:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:
GGGCTGCCCT TCTCC 15

(2) INFORMATION FOR SEQ ID NO:1439:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:
GCCGGGGGTC CCGC 14

(2) INFORMATION FOR SEQ ID NO:1440:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:
GCTCCTGCTG TTCCCTGGGC TCTTCTGCC 29

(2) INFORMATION FOR SEQ ID NO:1441:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:
TCTCTCCTGG GTGGGTGCTG GGTGCCG 27

(2) INFORMATION FOR SEQ ID NO:1442:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:
GGGTCTCCGG GCTTG 15

(2) INFORMATION FOR SEQ ID NO:1443:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:
CCCCGCGCTG CTGGGCGTTC TGC 23

(2) INFORMATION FOR SEQ ID NO:1444:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:
GGTCTTGGGG TTGTC 15

(2) INFORMATION FOR SEQ ID NO:1445:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:
TGTGGCCCCG CTCG 14

(2) INFORMATION FOR SEQ ID NO:1446:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:
TGTCGCCCTC CGTCGCC 17

(2) INFORMATION FOR SEQ ID NO:1447:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:
CGTCGCCGGC CTCGTCC 17

(2) INFORMATION FOR SEQ ID NO:1448:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:
CCTCCTGGGT GCGC 14

(2) INFORMATION FOR SEQ ID NO:1449:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:
GGCGGGCTGG TCCT 14

(2) INFORMATION FOR SEQ ID NO:1450:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:
GGCGTTTTGC TCCTTCCTGG 20

(2) INFORMATION FOR SEQ ID NO:1451:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: lin ar
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:
CTGCCTCCCC GGGGT 15

(2) INFORMATION FOR SEQ ID NO:1452:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: singl
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:
TTCTGCTGCT TGCTG 15

(2) INFORMATION FOR SEQ ID NO:1453:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:
CTTCTTTCCC GTCTCC 16

(2) INFORMATION FOR SEQ ID NO:1454:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:
CTTCTTTCCC GTCTCC 16

(2) INFORMATION FOR SEQ ID NO:1455:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:
TTTTTGCCTC TTTG 14

(2) INFORMATION FOR SEQ ID NO:1456:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:
GGTTCCTGTT GTTTCT 16

(2) INFORMATION FOR SEQ ID NO:1457:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:
GGCCTGCTTG GTGGCG 16

(2) INFORMATION FOR SEQ ID NO:1458:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:
GCTTGTGCGT TTCC 14

(2) INFORMATION FOR SEQ ID NO:1459:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:
TCTCTCTTCT CTTGGGTCTC CGCTTCTCGT CCTGCC 36

(2) INFORMATION FOR SEQ ID NO:1460:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:
TTTTCCTGTC TCTGTCGC 18

(2) INFORMATION FOR SEQ ID NO:1461:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:
GCCGTTCCTC CTCC 14

(2) INFORMATION FOR SEQ ID NO:1462:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:
GGCGTCCTCC TGCCC 15

(2) INFORMATION FOR SEQ ID NO:1463:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:
TGTGCTGTTT GCCTCGG 17

(2) INFORMATION FOR SEQ ID NO:1464:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:
GTGGTGCGGG TCCC 14

(2) INFORMATION FOR SEQ ID NO:1465:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:
GGTGCTCCCC CGGC 14

(2) INFORMATION FOR SEQ ID NO:1466:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:
GGGCCGGCTG GTTGCCTGGG C 21

(2) INFORMATION FOR SEQ ID NO:1467:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:
CTGTCTGGTG GGGTGTGGGG CC 22

(2) INFORMATION FOR SEQ ID NO:1468:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: singl
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:
GCTGGGTTGG GGGTGTGGTG 20

(2) INFORMATION FOR SEQ ID NO:1469:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:
GGCTCTTCTG TGGCC 15

(2) INFORMATION FOR SEQ ID NO:1470:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:
TGTGGGGCTG TTGGTG 16

(2) INFORMATION FOR SEQ ID NO:1471:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:
TCTCTGTGGG CGTGTG 16

(2) INFORMATION FOR SEQ ID NO:1472:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:
CTGGGTCTTG GGGCTTC 17

(2) INFORMATION FOR SEQ ID NO:1473:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:
CTCCCTTGTG CTGGG 15

(2) INFORMATION FOR SEQ ID NO:1474:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:
TGCGGCCTCC CCGC 14

(2) INFORMATION FOR SEQ ID NO:1475:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:
CCCCCTTCTG GGCC 14

(2) INFORMATION FOR SEQ ID NO:1476:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:
GGTGGCCTGG CTCCTTGTGG 20

(2) INFORMATION FOR SEQ ID NO:1477:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:
GCGCTTCTGG CTCTTG 16

(2) INFORMATION FOR SEQ ID NO:1478:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:
CCCTGTCCTT CTTCGCCTCG T 21

(2) INFORMATION FOR SEQ ID NO:1479:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:
GGCTGCTGGG CTGC 14

(2) INFORMATION FOR SEQ ID NO:1480:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:
GTTGGGCTTG GCCGGGG 17

(2) INFORMATION FOR SEQ ID NO:1481:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:
CTGCCCGGTG CCTCC 15

(2) INFORMATION FOR SEQ ID NO:1482:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:
TCTTGGCTGG TCCCTCGT 18

(2) INFORMATION FOR SEQ ID NO:1483:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:
TGTCCTTGGG CCCC 14

(2) INFORMATION FOR SEQ ID NO:1484:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:
GCTCCCGCTG CTCGGCCTCC GT 22

(2) INFORMATION FOR SEQ ID NO:1485:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:
GTTCTTTGGC CTCTTGCTCC 20

(2) INFORMATION FOR SEQ ID NO:1486:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:
GCCTGCTGTC TTGTCC 16

(2) INFORMATION FOR SEQ ID NO:1487:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:
CGTCCCCTCC TCGCTTGCGT TTC 23

(2) INFORMATION FOR SEQ ID NO:1488:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:
CCTCTTCCTT GTCTTCCA 18

(2) INFORMATION FOR SEQ ID NO:1489:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:
GGCCTTCCTC CGCTTCCGCT GC 22

(2) INFORMATION FOR SEQ ID NO:1490:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:
TGGGGCCCGC GCCGG 15

(2) INFORMATION FOR SEQ ID NO:1491:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:
GGGGGCGCTC GGCTCCGCGG CTTCCTCCCC GG 32

(2) INFORMATION FOR SEQ ID NO:1492:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:
CTGGGGGGTC CTGG 14

(2) INFORMATION FOR SEQ ID NO:1493:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:
TCTCCGGGGC CTGCGGCTCG C 21

(2) INFORMATION FOR SEQ ID NO:1494:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:
GGGCTCGGGG CTGCGTGCGC C 21

(2) INFORMATION FOR SEQ ID NO:1495:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:
GCGCGCGGCG TCCGCGGTG 19

(2) INFORMATION FOR SEQ ID NO:1496:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:
GGTGGCGCTG TCCCGCC 17

(2) INFORMATION FOR SEQ ID NO:1497:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:
GTGGTGTGTC TCCGTTCTCG TCCTGCGCCG TC 32

(2) INFORMATION FOR SEQ ID NO:1498:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:
CTGGTCTGCC CGTGG 15

(2) INFORMATION FOR SEQ ID NO:1499:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:
GGTCCTGGGC GTGGTGG 17

(2) INFORMATION FOR SEQ ID NO:1500:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:
GGGGCGTCTG GTGC 14

(2) INFORMATION FOR SEQ ID NO:1501:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:
CTCGTCTGCC CCGTG 15

(2) INFORMATION FOR SEQ ID NO:1502:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:
GGGCTTCGGG CTCGG 15

(2) INFORMATION FOR SEQ ID NO:1503:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503:
GGCTGTTCGT CCCCCCTGCC GCTCTGTGGC CTCC 34

(2) INFORMATION FOR SEQ ID NO:1504:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504:
GGGGCTCCTC GTTTTC 16

(2) INFORMATION FOR SEQ ID NO:1505:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505:
GCTGCTTCGG GTGTCCTTCT C 21

(2) INFORMATION FOR SEQ ID NO:1506:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506:
GGCGTGTGGC CCCGG 15

(2) INFORMATION FOR SEQ ID NO:1507:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507:
GTCCCGGCCC TGCTGGGCTG GGCGGGGTC 29

(2) INFORMATION FOR SEQ ID NO:1508:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508:
GCTGCCCTGG GCTTCTGGCC CGTCT 25

(2) INFORMATION FOR SEQ ID NO:1509:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509:
GGTTGTCTGT CGGT 14

(2) INFORMATION FOR SEQ ID NO:1510:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510:
GCTTGTCTCG GGTTTCTGG 19

(2) INFORMATION FOR SEQ ID NO:1511:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511:
CCTCTGTGCT GGGC 14

(2) INFORMATION FOR SEQ ID NO:1512:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512:
GCTTCTCTGC CTCCTGCTCC 20

(2) INFORMATION FOR SEQ ID NO:1513:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513:
GCCCTCCTGG TGGCTC 16

(2) INFORMATION FOR SEQ ID NO:1514:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514:
GGCTGGGGGT GCCCGTGCG 19

(2) INFORMATION FOR SEQ ID NO:1515:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515:
GGGGTGGGTG TGGGGTGTT 19

(2) INFORMATION FOR SEQ ID NO:1516:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516:
TTCGGGGTCC TCCCCTTCCC 20

(2) INFORMATION FOR SEQ ID NO:1517:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517:
GTTTCATCTT GGCTTTATCC 20

(2) INFORMATION FOR SEQ ID NO:1518:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518:
TCTCCCCTTG TTCCTCCCC 19

(2) INFORMATION FOR SEQ ID NO:1519:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519:
TCTCCTGCTC TGGRGTCTCC TC 22

(2) INFORMATION FOR SEQ ID NO:1520:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520:
TTCCCTCCCT CCCCTGCC 18

(2) INFORMATION FOR SEQ ID NO:1521:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521:
GTGTTGTCTG TGGGTGTCC 19

(2) INFORMATION FOR SEQ ID NO:1522:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522:
GTTTCGCTCT TGTTGCCC 18

(2) INFORMATION FOR SEQ ID NO:1523:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523:
TGGGCCCTTC CCTGCTGG 18

(2) INFORMATION FOR SEQ ID NO:1524:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524:
GGGGGAGTTT CATCTTGG 18

(2) INFORMATION FOR SEQ ID NO:1525:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525:
GGGGGBGTTT CBTCTTGGCT TT 22

(2) INFORMATION FOR SEQ ID NO:1526:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526:
GGGGGBGTTT CBTCTTGGCT T 21

(2) INFORMATION FOR SEQ ID NO:1527:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1527:
GGGGGBGTTT CBTCTTGGCT 20

(2) INFORMATION FOR SEQ ID NO:1528:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1528:
GGGGGBGTTT CBTCTTGGC 19

(2) INFORMATION FOR SEQ ID NO:1529:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1529:
GGGGGBGTTT CBTCTTGG 18

(2) INFORMATION FOR SEQ ID NO:1530:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530:
GGGGGBGTTT CBTCTTG 17

(2) INFORMATION FOR SEQ ID NO:1531:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531:
GGGGGBGTTT CBTCTT 16

(2) INFORMATION FOR SEQ ID NO:1532:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532:
GGGGGBGTTT CBTCT 15

(2) INFORMATION FOR SEQ ID NO:1533:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533:
GGGGGBGTTT CBTC 14

(2) INFORMATION FOR SEQ ID NO:1534:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: lin ar
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1534:
GGGGGBGTTT CBT 13

(2) INFORMATION FOR SEQ ID NO:1535:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1535:
GGGGGBGTTT CB 12

(2) INFORMATION FOR SEQ ID NO:1536:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1536:
GGGGBGTTTC BTCTTGGCTT T 21

(2) INFORMATION FOR SEQ ID NO:1537:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537:
GGGGBGTTTC BTCTTGGCTT 20

(2) INFORMATION FOR SEQ ID NO:1538:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538:
GGGGBGTTTC BTCTTGGCT 19

(2) INFORMATION FOR SEQ ID NO:1539:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539:
GGGGBGTTTC BTCTTGGC 18

(2) INFORMATION FOR SEQ ID NO:1540:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540:
GGGGBGTTTC BTCTTGG 17

(2) INFORMATION FOR SEQ ID NO:1541:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541:
GGGGBGTTTC BTCTTG 16

(2) INFORMATION FOR SEQ ID NO:1542:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542:
GGGGBGTTTC BTCTT 15

(2) INFORMATION FOR SEQ ID NO:1543:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543:
GGGGBGTTTC BTCT 14

(2) INFORMATION FOR SEQ ID NO:1544:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544:
GGGGBGTTTC BTC 13

(2) INFORMATION FOR SEQ ID NO:1545:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1545:
GGGGBGTTTC BT 12

(2) INFORMATION FOR SEQ ID NO:1546:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1546:
GGGBGTTTCB TCTTGGCTTT 20

(2) INFORMATION FOR SEQ ID NO:1547:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1547:
GGGBGTTTCB TCTTGGCTT 19

(2) INFORMATION FOR SEQ ID NO:1548:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548:
GGGBGTTTCB TCTTGGCT 18

(2) INFORMATION FOR SEQ ID NO:1549:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1549:
GGGBGTTTCB TCTTGGC 17

(2) INFORMATION FOR SEQ ID NO:1550:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550:
GGGBGTTTCB TCTTGG 16

(2) INFORMATION FOR SEQ ID NO:1551:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551:
GGGBGTTTCB TCTTG 15

(2) INFORMATION FOR SEQ ID NO:1552:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1552:
GGGBGTTTCB TCTT 14

(2) INFORMATION FOR SEQ ID NO:1553:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553:
GGGBGTTTCB TCT 13

(2) INFORMATION FOR SEQ ID NO:1554:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554:
GGGBGTTTCB TC 12

(2) INFORMATION FOR SEQ ID NO:1555:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1555:
GGBGTTTCBT CTTGGCTTT 19

(2) INFORMATION FOR SEQ ID NO:1556:
(i) SEQUENCE CHARACTERISTICS:
(A)- LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1556:
GGBGTTTCBT CTTGGCTT 18

(2) INFORMATION FOR SEQ ID NO:1557:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557:
GGBGTTTCBT CTTGGCT 17

(2) INFORMATION FOR SEQ ID NO:1558:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558:
GGBGTTTCBT CTTGGC 16

(2) INFORMATION FOR SEQ ID NO:1559:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559:
GGBGTTTCBT CTTGG 15

(2) INFORMATION FOR SEQ ID NO:1560:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560:
GGBGTTTCBT CTTG 14

(2) INFORMATION FOR SEQ ID NO:1561:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561:
GGBGTTTCBT CTT 13

(2) INFORMATION FOR SEQ ID NO:1562:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562:
GGBGTTTCBT CT 12

(2) INFORMATION FOR SEQ ID NO:1563:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1563:
GBGTTTCBTC TTGGCTTT 18

(2) INFORMATION FOR SEQ ID NO:1564:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564:
GBGTTTCBTC TTGGCTT 17

(2) INFORMATION FOR SEQ ID NO:1565:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565:
GBGTTTCBTC TTGGCT 16

(2) INFORMATION FOR SEQ ID NO:1566:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566:
GBGTTTCBTC TTGGC 15

(2) INFORMATION FOR SEQ ID NO:1567:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567:
GBGTTTCBTC TTGG 14

(2) INFORMATION FOR SEQ ID NO:1568:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568:
GBGTTTCBTC TTG 13

(2) INFORMATION FOR SEQ ID NO:1569:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569:
GBGTTTCBTC TT 12

(2) INFORMATION FOR SEQ ID NO:1570:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570:
BGTTTCBTCT TGGCTTT 17

(2) INFORMATION FOR SEQ ID NO:1571:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1571:
BGTTTCBTCT TGGCTT 16

(2) INFORMATION FOR SEQ ID NO:1572:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1572:
BGTTTCBTCT TGGCTT 16

(2) INFORMATION FOR SEQ ID NO:1573:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1573:
BGTTTCBTCT TGGCT 15

(2) INFORMATION FOR SEQ ID NO:1574:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: lin ar
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1574:
BGTTTCBTCT TGGC 14

(2) INFORMATION FOR SEQ ID NO:1575:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1575:
BGTTTCBTCT TGG 13

(2) INFORMATION FOR SEQ ID NO:1576:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576:
BGTTTCBTCT TG 12

(2) INFORMATION FOR SEQ ID NO:1577:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577:
GTTTCBTCTT GGCTTT 16

(2) INFORMATION FOR SEQ ID NO:1578:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578:
GTTTCBTCTT GGCTT 15

(2) INFORMATION FOR SEQ ID NO:1579:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579:
GTTTCBTCTT GGCT 14

(2) INFORMATION FOR SEQ ID NO:1580:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580:
GTTTCBTCTT GGC 13

(2) INFORMATION FOR SEQ ID NO:1581:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1581:
GTTTCBTCTT GG 12

(2) INFORMATION FOR SEQ ID NO:1582:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582:
TTTCBTCTTG GCTTT 15

(2) INFORMATION FOR SEQ ID NO:1583:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1583:
TTTCBTCTTG GCTT 14

(2) INFORMATION FOR SEQ ID NO:1584:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584:
TTTCBTCTTG GCT 13

(2) INFORMATION FOR SEQ ID NO:1585:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1585:
TTTCBTCTTG GC 12

(2) INFORMATION FOR SEQ ID NO:1586:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1586:
TTCBTCTTGG CTTT 14

(2) INFORMATION FOR SEQ ID NO:1587:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587:
TTCBTCTTGG CTT 13

(2) INFORMATION FOR SEQ ID NO:1588:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588:
TTCBTCTTGG CT 12

(2) INFORMATION FOR SEQ ID NO:1589:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589:
TCBTCTTGGC TTT 13

(2) INFORMATION FOR SEQ ID NO:1590:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1590:
TCBTCTTGGC TT 12

(2) INFORMATION FOR SEQ ID NO:1591:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1591:
GGGGGBGTTT CBTCTTGGCT TT 22

(2) INFORMATION FOR SEQ ID NO:1592:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592:
GGGGBGTTTC BTCTTGGCTT T 21

(2) INFORMATION FOR SEQ ID NO:1593:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593:
GGGBGTTTCB TCTTGGCTTT 20

(2) INFORMATION FOR SEQ ID NO:1594:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594:
GGBGTTTCBT CTTGGCTTT 19

(2) INFORMATION FOR SEQ ID NO:1595:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595:
GBGTTTCBTC TTGGCTTT 18

(2) INFORMATION FOR SEQ ID NO:1596:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596:
BGTTTCBTCT TGGCTTT 17

(2) INFORMATION FOR SEQ ID NO:1597:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597:
GTTTCBTCTT GGCTTT 16

(2) INFORMATION FOR SEQ ID NO:1598:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598:
TTTCBTCTTG GCTTT 15

(2) INFORMATION FOR SEQ ID NO:1599:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599:
TTCBTCTTGG CTTT 14

(2) INFORMATION FOR SEQ ID NO:1600:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600:
TCBTCTTGGC TTT 13

(2) INFORMATION FOR SEQ ID NO:1601:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601:
CBTCTTGGCT TT 12

(2) INFORMATION FOR SEQ ID NO:1602:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602:
GGGGGBGTTT CBTCTTGGCT T 21

(2) INFORMATION FOR SEQ ID NO:1603:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603:
GGGGBGTTTC BTCTTGGCTT 20

(2) INFORMATION FOR SEQ ID NO:1604:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604:
GGGBGTTTCB TCTTGGCTT 19

(2) INFORMATION FOR SEQ ID NO:1605:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1605:
GGBGTTTCBT CTTGGCTT 18

(2) INFORMATION FOR SEQ ID NO:1606:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606:
GBGTTTCBTC TTGGCTT 17

(2) INFORMATION FOR SEQ ID NO:1607:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607:
BGTTTCBTCT TGGCTT 16

(2) INFORMATION FOR SEQ ID NO:1608:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608:
GTTTCBTCTT GGCTT 15

(2) INFORMATION FOR SEQ ID NO:1609:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1609:
TTTCBTCTTG GCTT 14

(2) INFORMATION FOR SEQ ID NO:1610:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610:
TTCBTCTTGG CTT 13

(2) INFORMATION FOR SEQ ID NO:1611:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611:
TCBTCTTGGC TT 12

(2) INFORMATION FOR SEQ ID NO:1612:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612:
GGGGGBGTTT CBTCTTGGCT 20

(2) INFORMATION FOR SEQ ID NO:1613:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1613:
GGGGBGTTTC BTCTTGGCT 19

(2) INFORMATION FOR SEQ ID NO:1614:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614:
GGGBGTTTCB TCTTGGCT 18

(2) INFORMATION FOR SEQ ID NO:1615:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615:
GGBGTTTCBT CTTGGCT 17

(2) INFORMATION FOR SEQ ID NO:1616:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616:
GBGTTTCBTC TTGGCT 16

(2) INFORMATION FOR SEQ ID NO:1617:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617:
BGTTTCBTCT TGGCT 15

(2) INFORMATION FOR SEQ ID NO:1618:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1618:
GTTTCBTCTT GGCT 14

(2) INFORMATION FOR SEQ ID NO:1619:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1619:
TTTCBTCTTG GCT 13

(2) INFORMATION FOR SEQ ID NO:1620:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620:
TTCBTCTTGG CT 12

(2) INFORMATION FOR SEQ ID NO:1621:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621:
GGGGGBGTTT CBTCTTGGC 19

(2) INFORMATION FOR SEQ ID NO:1622:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622:
GGGGBGTTTC BTCTTGGC 18

(2) INFORMATION FOR SEQ ID NO:1623:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1623:
GGGBGTTTCB TCTTGGC 17

(2) INFORMATION FOR SEQ ID NO:1624:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1624:
GGBGTTTCBT CTTGGC 16

(2) INFORMATION FOR SEQ ID NO:1625:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1625:
GBGTTTCBTC TTGGC 15

(2) INFORMATION FOR SEQ ID NO:1626:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1626:
BGTTTCBTCT TGGC 14

(2) INFORMATION FOR SEQ ID NO:1627:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627:
GTTTCBTCTT GGC 13

(2) INFORMATION FOR SEQ ID NO:1628:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1628:
TTTCBTCTTG GC 12

(2) INFORMATION FOR SEQ ID NO:1629:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1629:
GGGGGBGTTT CBTCTTGG 18

(2) INFORMATION FOR SEQ ID NO:1630:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630:
GGGGBGTTTC BTCTTGG 17

(2) INFORMATION FOR SEQ ID NO:1631:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1631:
GGGBGTTTCB TCTTGG 16

(2) INFORMATION FOR SEQ ID NO:1632:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632:
GGBGTTTCBT CTTGG 15

(2) INFORMATION FOR SEQ ID NO:1633:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1633:
GBGTTTCBTC TTGG 14

(2) INFORMATION FOR SEQ ID NO:1634:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634:
BGTTTCBTCT TGG 13

(2) INFORMATION FOR SEQ ID NO:1635:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635:
GTTTCBTCTT GG 12

(2) INFORMATION FOR SEQ ID NO:1636:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636:
GGGGGBGTTT CBTCTTG 17

(2) INFORMATION FOR SEQ ID NO:1637:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637:
GGGGBGTTTC BTCTTG 16

(2) INFORMATION FOR SEQ ID NO:1638:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638:
GGGBGTTTCB TCTTG 15

(2) INFORMATION FOR SEQ ID NO:1639:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639:
GGBGTTTCBT CTTG 14

(2) INFORMATION FOR SEQ ID NO:1640:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1640:
GBGTTTCBTC TTG 13

(2) INFORMATION FOR SEQ ID NO:1641:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641:
BGTTTCBTCT TG 12

(2) INFORMATION FOR SEQ ID NO:1642:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642:
GGGGGBGTTT CBTCTT 16

(2) INFORMATION FOR SEQ ID NO:1643:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1643:
GGGGBGTTTC BTCTT 15

(2) INFORMATION FOR SEQ ID NO:1644:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1644:
GGGBGTTTCB TCTT 14

(2) INFORMATION FOR SEQ ID NO:1645:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1645:
GGGBGTTTCB TCTT 14

(2) INFORMATION FOR SEQ ID NO:1646:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1646:
GGBGTTTCBT CTT 13

(2) INFORMATION FOR SEQ ID NO:1647:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1647:
GBGTTTCBTC TT 12

(2) INFORMATION FOR SEQ ID NO:1648:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1648:
GGGGGBGTTT CBTCT 15

(2) INFORMATION FOR SEQ ID NO:1649:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1649:
GGGGBGTTTC BTCT 14

(2) INFORMATION FOR SEQ ID NO:1650:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1650:
GGGBGTTTCB TCT 13

(2) INFORMATION FOR SEQ ID NO:1651:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1651:
GGBGTTTCBT CT 12

(2) INFORMATION FOR SEQ ID NO:1652:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1652:
GGGGGBGTTT CBTC 14

(2) INFORMATION FOR SEQ ID NO:1653:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1653:
GGGGBGTTTC BTC 13

(2) INFORMATION FOR SEQ ID NO:1654:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1654:
GGGBGTTTCB TC 12

(2) INFORMATION FOR SEQ ID NO:1655:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1655:
GGGGGBGTTT CBT 13

(2) INFORMATION FOR SEQ ID NO:1656:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1656:
GGGGBGTTTC BT 12

(2) INFORMATION FOR SEQ ID NO:1657:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1657:
GGGGGBGTTT CB 12

(2) INFORMATION FOR SEQ ID NO:1658:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1658:
TCTCCCCTTG TTCCTCCCC 19

(2) INFORMATION FOR SEQ ID NO:1659:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659:
TCTCCTGCTC TGGTGTCTCC TC 22

(2) INFORMATION FOR SEQ ID NO:1660:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1660:
TTCCCTCCCT CCCCTGCC 18

(2) INFORMATION FOR SEQ ID NO:1661:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661:
GTGTTGTCTG TGGGTGTCC 19

(2) INFORMATION FOR SEQ ID NO:1662:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1662:
GTTTCGCTCT TGTTGCCC 18

(2) INFORMATION FOR SEQ ID NO:1663:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663:
TGGGCCCTTC CCTGCTGG 18

(2) INFORMATION FOR SEQ ID NO:1664:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1664:
GCTGGTCCTC TGCTGTCCTT GCTG 24

(2) INFORMATION FOR SEQ ID NO:1665:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665:
GTGCTCBTGG TGTCCTTTCC 20

(2) INFORMATION FOR SEQ ID NO:1666:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1666:
GCCCTGGGGC CCCCCTGTCT TCTTGGGG 28

(2) INFORMATION FOR SEQ ID NO:1667:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667:
CCTCTTCCCT CTGGGGGCCG 20

(2) INFORMATION FOR SEQ ID NO:1668:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1668:
TCTCTCTCCC TCTCTTGCGT CTCTC 25

(2) INFORMATION FOR SEQ ID NO:1669:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669:
TCTTTCTCTC TCTCTCTTCC CC 22

(2) INFORMATION FOR SEQ ID NO:1670:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670:
TTTCCCGCTC TTTCTGTCTC 20

(2) INFORMATION FOR SEQ ID NO:1671:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671:
GGTGTCTGGT TTTCTCTCTC C 21

(2) INFORMATION FOR SEQ ID NO:1672:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672:
GCTGGCTGCC TGTCTGGCCT GCGCTCTT 28

(2) INFORMATION FOR SEQ ID NO:1673:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673:
GGCCTGTGCT GTTCCTCC 18

(2) INFORMATION FOR SEQ ID NO:1674:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674:
TCCGGTTCCT GTCCTCTCTG TCTGTC 26

(2) INFORMATION FOR SEQ ID NO:1675:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675:
GCCCCCTCTG GGGTCTCCCT CTGGC 25

(2) INFORMATION FOR SEQ ID NO:1676:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676:
GTGGTGGTCT TGTTGCTT 18

(2) INFORMATION FOR SEQ ID NO:1677:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677:
GGGCTGGGCT CCGTGTCTC 19

(2) INFORMATION FOR SEQ ID NO:1678:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678:
CBGTGCTCBT GGTGTCC 17

(2) INFORMATION FOR SEQ ID NO:1679:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679:
GCTGBGGGBG CGTCTGCTGG C 21

(2) INFORMATION FOR SEQ ID NO:1680:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680:
TGCTTTTCTT TTCTGGGCCT CTGTGGTCTG TTTTTTTCTG GCCCTGCTGG GGCGCTCTCC 60
GCCGCCCGCC TGGCTCCCGG BGCCCBTGBT GGGCBTGCCG TGGTTCTTGC CCTCCTTTGG 120
CTGCCGTGCC CGCTCCCCGG CCTCCTGGCG GGTGGCCGTT GGGCCCGTGT TCCCCTGGGG 180
CCTGGGGCTC CCTTCTCTCG CCCTTCTTGC TGGGCCTCTG CTGCTGCTGG TGCTGTGGCC 240
CCCGTACACC GAGGAGCCCA TGATGGGCAT GCCACAGACG ACAGGCGTBC BCCGBGGBGC 300
CCBTGBTGGG CBTGCCBCBG BCGBCBGGC 329

(2) INFORMATION FOR SEQ ID NO:1681:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681:
CTGGGCCTC 9

(2) INFORMATION FOR SEQ ID NO:1682:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1682:
GCCGCCCGCC TG 12

(2) INFORMATION FOR SEQ ID NO:1683:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1683:
GCCCGCTCCC CGGC 14

(2) INFORMATION FOR SEQ ID NO:1684:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684:
CBCCGBGGBG CCC 13

(2) INFORMATION FOR SEQ ID NO:1685:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1685:
GGCGCCGTGC CGCGTCTTGG TGGCGGCGGG TTCGCGCCCG CGCGGGGCCC CTCCGGTCCG 60
TTCGCGCCCG CGCGGGGCCC CTCCGGTCCC GGGTCGGGGC CCCCCGCGGC CGCCTCGGGG 120
CTGGGGCGCT GGTGGCCGGG CCGCGCCTCC GCCTGCCGCT TCTGGCTGGG CCCCGGGCGC 180
CCCCTCCCCT CTTGCTCGGG TCCCCGTGAC AGCGCGTCCT GTGTCTCCAG CAGCATGGCC 240
GGGCCAGCTG GGCCCCBCBG CGCGTCCTGT GTCTCCBGCB GCBTGGCCGG GCCBGCTGGG 300
CCCC 304

(2) INFORMATION FOR SEQ ID NO:1686:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:
GCGCGTCCTG 10

(2) INFORMATION FOR SEQ ID NO:1687:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687:
GCTGGGCCCC GG 12

(2) INFORMATION FOR SEQ ID NO:1688:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688:
CGGGTCGGGG CCCCCC 16

(2) INFORMATION FOR SEQ ID NO:1689:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689:
CGCGCCCGCG 10

(2) INFORMATION FOR SEQ ID NO:1690:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690:
ACAGAGCAGT GCTGTTGTTG GGCATCTTGC CTTCCCAGGG BCBGBGCBTG CTGTTGTTGG 60
GCBTCTTGCC TTCCCBGGGC CCTTTTCTGG TGGGGTGGTG CTGTTGTTGG GCTTTCTTCT 120
GTTCCCBCBG BGCBGTGCTG TTGTTGGGCB TCTTGCCTTC CCBGGGCCCT TTTCTGGTGG 180
GGTGGTGCTG TTGTTGGGCT TTCTTCTGTT CCC 213

(2) INFORMATION FOR SEQ ID NO:1691:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691:
GBGCBTGC 8

(2) INFORMATION FOR SEQ ID NO:1692:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692:
TTGTTGGGC 9

(2) INFORMATION FOR SEQ ID NO:1693:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693:
TGCCTTCCCB GGG 13

(2) INFORMATION FOR SEQ ID NO:1694:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694:
TTTCCCCTGG GTCTTCCCTC CTGCTCTTTT TTCATTTGCT CTCCTATTAC TTTCTGTGTC 60
CATTTTTTCA TTAACCGAGC TGTBTTTGCT CTCCTBTTBC TTTCTGTGTC CBTTTTTTCB 120
TTBBCCGBGC TGT 133

(2) INFORMATION FOR SEQ ID NO:1695:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695:
CCCCTGGG 8

(2) INFORMATION FOR SEQ ID NO:1696:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696:
GCTCTCCTBT T 11

(2) INFORMATION FOR SEQ ID NO:1697:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697:
CBTTBBCCGB GCTG 14

(2) INFORMATION FOR SEQ ID NO:1698:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1698:
GCCTGTGTCT GTCCTCCTGC TTCGTTCCTC TCGTTCCTGC TTGGTGCCCT TGCCGGTCCT 60
GCTCCTCCGG GCTGTGGGTC GTGGCCCTGG CTCCGGCTGG TGGGCTCCCC TGGCCTTCGC 120

TGGCTGGCGG CGTGCGGGTC TTGCTCTGGG CCTGGCTGTG GCCGTGGTTG GGGGTCTTCG 180
CTGCCTCCGT TTGGGTGGCT CTCTGAATAT TGACCTTCCT CCATGGCGGT CCTGCTTGGA 240
TTCTCCCGAT CTCTGBBTBT TGBCCTTCCT CCBTGGCGGT CCTGCTTGGB TTCTCCCGB 299

(2) INFORMATION FOR SEQ ID NO:1699:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699:
GTCCTCCT 8

(2) INFORMATION FOR SEQ ID NO:1700:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700:
TGTGTCTGTC CTCC 14

(2) INFORMATION FOR SEQ ID NO:1701:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701:
GTGGCCCTGG C 11

(2) INFORMATION FOR SEQ ID NO:1702:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1702:
CGTGGTTGGG G 11

(2) INFORMATION FOR SEQ ID NO:1703:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1703:
TCTCTGBBTB TTGBCC 16

(2) INFORMATION FOR SEQ ID NO:1704:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704:
GCCTTTCCTG GTTCTCTTGT TGTTTTTGGG GTTTGGCTTA CAGTAGAGTA GGGGATTCCA 60
TGGCAGGAGC CATCTTCTTC ATGGACTCCT TCAAGGAGAC CTTAGGTTTC TGAGGGACTG 120
CTAACACGCC ATCTGGAGCB CBGTBGBGTB GGGGBTTCCB TGGCBGGBGC CBTCTTCTTC 180
BTGGBCTCCT TCBBGGBGBC CTTBGGTTTC TGBGGGBCTG CTBBCBCGCC BTCTGGBGCG 240
TTGTTTTTGG GGTTTGGCTT GCCTTTCCTG GTTCTCTTBC BGTBGBGTBG GGGBTTCCBT 300
GGCBGGBGCC BTCTTCTTCB TGGBCTCCTT CBBGGBGBCC TTBGGTTTCT GBGGGBCTGC 360
TBBCBCGCCB TCTGGBGC 378

(2) INFORMATION FOR SEQ ID NO:1705:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705:
TGGBCTCC 8

(2) INFORMATION FOR SEQ ID NO:1706:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706:
CCBTCTGGB 9

(2) INFORMATION FOR SEQ ID NO:1707:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1707:
CTGCTBBCBC G 11

(2) INFORMATION FOR SEQ ID NO:1708:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708:
GTTTTTGGGG TTTG 14

(2) INFORMATION FOR SEQ ID NO:1709:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1709:
GCCTGTGTCT GTCCTCCTGC TTCGTTCCTC TCGTTCCTGC TTGGTGCCCT TGCCGGTCCT 60
GCTCCTCCGG GCTGTGGGTC CTCGCCCTGG CTCCGGCTGG TGGGCTCCCC TGGCCTTCGC 120
TGGCTGGCGG CGTGCCCCBG BBCGBGBCCC GGBCCGBCBG GCCGTGGTTG GGGGTCTTCG 180
CTGCCTCCGT TTGGGTGGCG ATCTCTGAAT ATTGACCTTC CATGGCGGTC CTGCTTGGAG 240
BTCTCTGBBT BTTGBCCTTC CBTGGCGGTC CTGCTTGGB 279

(2) INFORMATION FOR SEQ ID NO:1710:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710:
GCCTGTGTCT GTCCTCCTGC TTCGTTCCTC TCGTTCCTGC TTGGTGCCCT TGCCGGTCCT 60
GCTCCTCCGG GCTGTGGGTC CTCGCCCTGG CTCCGGCTGG TGGGCTCCCC TGGCCTTCGC 120
TGGCTGGCGG CGTGCCCCBG BBCGBGBCCC GGBCCGBCBG GCCGTGGTTG GGGGTCTTCG 180
CTGCCTCCGT TTGGGTGGCG ATCTCTGAAT ATTGACCTTC CATGGCGGTC CTGCTTGGAG 240
BTCTCTGBBT BTTGBCCTTC CBTGGCGGTC CTGCTTGGBT CGTTCCTCTC G 291

(2) INFORMATION FOR SEQ ID NO:1711:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1711:
BGBBCGBGBC 10

(2) INFORMATION FOR SEQ ID NO:1712:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1712:
TGBBTBTTGB 10

(2) INFORMATION FOR SEQ ID NO:1713:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713:
TCTCCCTTGG GCTCTGGCTC CTTCTCTCTC TCTCCCTCTC TCTCTGTCGC CTCCGCCCTG 60
GCTGCTGGGG TGGTGGTGCT TTTGTTCTTC CTTGCTGCCG CCCCGCTGCT TGTCTTCCTC 120
GCTCTGTCCC TCTCTCTCTG TBCTCCTCBG GCTCCBTCBT CTCCCTTGGG C 171

(2) INFORMATION FOR SEQ ID NO:1714:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714:
GGCTCTGGC 9

(2) INFORMATION FOR SEQ ID NO:1715:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1715:
CCCTTGG 7

(2) INFORMATION FOR SEQ ID NO:1716:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1716:
TTTGTTCTTC C 11

(2) INFORMATION FOR SEQ ID NO:1717:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1717:
CTTGCTCCTG GGGGCCTCCT GGTCCCTCCG GGTGTTCCCG GCGGGCCTGG CCTGGGGCBG 60
GGGCCGCGTB GGCGCGGCTC GCCBGGBCGG GCBGCGCCBG CBGCBGCBGB TTCBGCBTCC 120
TGG 123

(2) INFORMATION FOR SEQ ID NO:1718:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1718:
GCTCCTGGGG GCCT 14

(2) INFORMATION FOR SEQ ID NO:1719:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1719:
CGTBGGCGC 9

(2) INFORMATION FOR SEQ ID NO:1720:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720:
TGGCCTGGGG 10

(2) INFORMATION FOR SEQ ID NO:1721:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721:

CTTGCTCCTG GGGGCCTCCT GGTCCCTCTG GCTGTTCCCG GCCCTGGBCT GGGGCBGGGG 60
CCGCGTBGGC GCGGCTCGCC BGGBCGGGCB GCGCCBGCBG CBGCBGGCTC BGCBTCCTGG 120
CCBCGGBBTT CC 132

(2) INFORMATION FOR SEQ ID NO:1722:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722:

CTCCTGGGGG CCTCCTG 17

(2) INFORMATION FOR SEQ ID NO:1723:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723:

BTCCTGGCCB CGGBBTTCC 19

(2) INFORMATION FOR SEQ ID NO:1724:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724:

GTCCCTC 7

(2) INFORMATION FOR SEQ ID NO:1725:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725:

GGTGTGCGGG GCCTGGTGCC CCTGGGCCTC GGGTGCTGCC TGTGCGCTGC CTTCTTCTCC 60
TGGGTCCTCG CCGGGGCCCT TGCTGCCCTG GCTGTGCCCT GGGGGTCTGG GTTCGGCTGT 120
CCCCBGCBGG BCCBGTCCCB TCCBCBGCGT GTGBTGBGTB GCCBTTCTCC TGCBGCCGBG 180

(2) INFORMATION FOR SEQ ID NO:1726:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1726:

TTCTCCTGCB GCCGBG 16

(2) INFORMATION FOR SEQ ID NO:1727:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1727:

CTTGCTGCCC TGGCTGT 17

(2) INFORMATION FOR SEQ ID NO:1728:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728:

TCTTCTCCTG G 11

(2) INFORMATION FOR SEQ ID NO:1729:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729:
GGGCGCGGGC GBGCBTCGCT TTGGGCTTTT CTCCTTTGGT TTGBGCGCCB GGBCCGCGCB 60
CBGCBGCBGG GCGCGGGCGB GCBTCGCBGC GGCGGGCBGG G 101

(2) INFORMATION FOR SEQ ID NO:1730:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730:
GGCBGGG 7

(2) INFORMATION FOR SEQ ID NO:1731:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731:
TCCTTTGGTT 10

(2) INFORMATION FOR SEQ ID NO:1732:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732:
CCTCCTTCCT GGTCTGTCTG CCBGBCBBBT TTGGGBBGTG BBCBGTTTTG GBBCCBTGTT 60
TCCCBGTCTC TGBGCTGTGG C 81

(2) INFORMATION FOR SEQ ID NO:1733:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733:
TTCTCCTTTG GTT 13

(2) INFORMATION FOR SEQ ID NO:1734:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734:
TTTCTCCTTT GGTT 14

(2) INFORMATION FOR SEQ ID NO:1735:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735:
GCCCTGCTGC TCTTTCTGCT TCCCTTGGTG GGTTGGGCCG CTGGTTGTTC TGGGGTTCTT 60
GCTGCCCCTT CTGTCCCTGT TTGCTGGTGT CTGCGCCCCC BBCBGBBGBB GCBGBCBBBT 120
TTGGGBBGTG BBCBGTTTTG GBBCCBTGTT TCCTGT 156

(2) INFORMATION FOR SEQ ID NO:1736:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736:
TTCCTGT 7

(2) INFORMATION FOR SEQ ID NO:1737:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737:
CTCTTTCTGC T 11

(2) INFORMATION FOR SEQ ID NO:1738:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738:
CCCCTTCTGT CCC 13

(2) INFORMATION FOR SEQ ID NO:1739:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739:
GCGCTCGGCC TGGTCCCGGG GGTCTCCTCT TGTTGTTGCT TGCGCCTCCT GCTGGGGGTC 60
CCTCTGTTCT TGTTTTGGGG GCGGGCCCGG CCGTTGTCTT GGTTTGGGGG TTTCCGTTGG 120
GGTTCTCCTG GCCCGGGCCT TGCCCGGCCG TGGTCCCGGC TTCGTTCCTG TCTCCGTCTC 180
GGCTCTTCTG GGGCCTTGCG CTGTCTTTGG TGGCBCCGTC CBGTGBTGGT GCGGTBCTTG 240
TCGCTGCBGC GCTCGGCCTG GTCCCGGBGB GC 272

(2) INFORMATION FOR SEQ ID NO:1740:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1740:
TCGGCCTGGT CCCGG 15

(2) INFORMATION FOR SEQ ID NO:1741:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1741:
TGGGGGTTTC CGTTG 15

(2) INFORMATION FOR SEQ ID NO:1742:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1742:
TGGTCCCGGB GBGC 14

(2) INFORMATION FOR SEQ ID NO:1743:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743:
GCGCGGGCCG GGGGCTGCTG GGGGTTGGCC CGGGGTGCCC CGCCGCTGGG TGCCCTCGTC 60
CTCTGCGGTC GTGTCTCCTG GCTCTGGTTC CCCGCTGCGC CCGTTGTCCT CTGGGGTGGC 120
CTTCGCTCCC GGGTCTGGTT CTTGTGTTGG GGGTCCCTTT TTGGGCCTGT TGTGGCGTGG 180
CTTGTGTGTT CGGTTTCTGC CCTGTCCTCC GGCGTCCCCG GBGCCTCCCC GGGGCBGGBT 240
GBCTTTTGBG GGGGBCBCBG BTGTCTGGGC BTTGCCBGGT CCTGGGBBCB GBGCCCCGBG 300
CBGGBCCBGG BGTGCGGGCB GCGCGGGCCG GGGGCTGCTG GGBGCCBTBG CGBGGCTGBG 360

(2) INFORMATION FOR SEQ ID NO:1744:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744:
GGGGGCTGCT GGG 13

(2) INFORMATION FOR SEQ ID NO:1745:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745:
TGTCCTCCGG CGTCCC 16

(2) INFORMATION FOR SEQ ID NO:1746:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746:
GCCBTBGCGB GGCTGBG 17

(2) INFORMATION FOR SEQ ID NO:1747:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747:
CTCTGGGGTG GCCTTC 16

(2) INFORMATION FOR SEQ ID NO:1748:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748:
CCTCTTTTCT GTTTTTCCCC TCTGCCTTTG TTTGGGTTCG CTTCCTTTCT GCTTCTTCCC 60
TGTGTCTCCT GTCTCCGCTT TTTTCTTCGT CTTTGTTGTT TTCTCTTCCT TGCTGBGCBB 120
GBTBTCTBGB TTCTGGGGTG GTCTCGBTTT TBBBBGCTTG BGBBGCTGCB BBCBTTBTCC 180
BBBGTBTBTT TGBGGCTCCB BGGBTCBCGB CCBTCTTCCC BGGCBTTTTB BGTTGCTGTC 240
GT 242

(2) INFORMATION FOR SEQ ID NO:1749:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749:
CTGTCGT 7

(2) INFORMATION FOR SEQ ID NO:1750:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750:
TGCTTCTTCC 10

(2) INFORMATION FOR SEQ ID NO:1751:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751:
BBGTGBGBGC TGBGBGBBBC TGTGBBGCBB TCBTGBCTTC BBGBGTTCTT TTCBCCCGTT 60
CTTGGCTTCT TCTGTCCGTT GGCTTCTCGT TGTCCCTGTG GGCTTCTCGT TGTCCCCCCT 120
TCGGGGGCTG GTGGGGCCGT CCTTGCCTGC TGGGTTCTTG GCTTCTTCTG TCCGTTGGCT 180
TCTCGTTGTC CCTGTGGGCT TCTCGTTGTC CCCCCTTCGG GGGCTGGTGG GGCCGTCCTT 240
GCCTGCTGG 249

(2) INFORMATION FOR SEQ ID NO:1752:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1752:
CCTTGCCTGC TGG 13

(2) INFORMATION FOR SEQ ID NO:1753:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753:
GTTGTCCC 8

(2) INFORMATION FOR SEQ ID NO:1754:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754:
TTTTCTCTTT CGCTTTCTTT TCGTCTCCTG TTCCTCCTTT TTTGCTGTTT TTTCTCCTTC 60
TTCTCTCCTT TCTTTTC 77

(2) INFORMATION FOR SEQ ID NO:1755:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1755:
TCCTTTCTTT TC 12

(2) INFORMATION FOR SEQ ID NO:1756:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756:
CTCCTTTT 8

(2) INFORMATION FOR SEQ ID NO:1757:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1757:
TTTTCTCTTT CGCTTTCTTT TCGTCTCCTG TTCCTCCTTT TTTGCTGTTT TTTCTCCTTC 60
TTCTCTCCTT TCTTTTC 77

(2) INFORMATION FOR SEQ ID NO:1758:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758:
CCTTTCTTTT C 11

(2) INFORMATION FOR SEQ ID NO:1759:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: lin ar
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759:
CTGTTCCTCC TTTT 14

(2) INFORMATION FOR SEQ ID NO:1760:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760:
CTCTGTCTTG TTCTGGTCCT TCGTGGGGCT CTGTGTCGCG TGGGTGCGGC CGTGGCCGGC 60
GGBCCBGGBG TTGGBGCBGG BGCBGGBCGG GCBGGCGGCT CBTGTTTGGB TCGGCBGGBG 120
GCBCTC 126

(2) INFORMATION FOR SEQ ID NO:1761:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761:
GGBGGCBCTC 10

(2) INFORMATION FOR SEQ ID NO:1762:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1762:
GTGGGGCTCT G 11

(2) INFORMATION FOR SEQ ID NO:1763:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 648 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1763:
TCTGGGGTGT CCTGGCCTTC GTGGTTCCTC TTCCTTCGTT TGCCGTCCGC GGGGGCCCCC 60
GGGCCTGGCT GCGCTCCTGC CCCGCCTCTT TCCCGGGCTC TTGCGCTGGG GGGTGCTCCC 120
GTGTGTTTGC GCCCTCCTCC TGGTCGCGCT TGTCGTTTTG GGGCCGGCTT TGCCCGCCTC 180
CCGGCGCCTG GCCCGGCCTT CCTGGGCTGC GTGCGCGTTC TGTTCTTCTT CCTGGCTCTG 240
GGGTGTCCTG GCCTTCGTGG TTCCTCTTCC TTCGTTTGCC GTCCGCGGGG GCCCCCGGGC 300
CTGGCTGCGC TCCTGCCCCG CCTCTTTCCC GGGCTCTTGC GCTGGGGGGT GCTCCCGTGT 360
GTTTGCGCCC TCCTCCTGGT CGCGCTTGTC GTTTTGGGGC CGGCTTTGCC CGCCTCCCGG 420
CGCCTGGCCC GGCCTTCCTG GGCTGCGTGC GCGTTCTGTT CTTCTTCCTG GCGCAGGAGA 480
CAGGGCAGGG CGATCAGGAG CAGCGTGAGC CAAAGGAGGA CCATCGGGAA CGCAGCTCCG 540
GAACGCAGGA CAGAGGTGCC GCBGGBGBCB GGGCBGGGCG BTCBGGBGCB GCGTGBGCCB 600
BBGGBGGBCC BTCGGGBBCG CBGCTCCGGB BCGCBGGBCB GBGGTGCC 648

(2) INFORMATION FOR SEQ ID NO:1764:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764:
GBGGTGCC 8

(2) INFORMATION FOR SEQ ID NO:1765:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765:
GCCCCGC 7

(2) INFORMATION FOR SEQ ID NO:1766:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766:
CTCTGGTTGG CTTCCTTCGC CGGCBCBTGC TBGCBGGBBG BBCBGBGGGG GBBGCBGTTG 60
GGBGGTGBGB CCCBTTBBTB GGTGTCGB 88

(2) INFORMATION FOR SEQ ID NO:1767:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767:
GCCGGCBCB 9

(2) INFORMATION FOR SEQ ID NO:1768:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1768:
TTCCTTC 7

(2) INFORMATION FOR SEQ ID NO:1769:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 562 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1769:
TCTGCCCTGT CCGCCGGCTC TTCGGTGGCT CGGCCCCGCT CCTTGTCTTG CCGCGGGTTG 60
GTTCCTGGGC CTGGTTCTTG CGGGCGTTTC GGTCTGCTGG CTGGTCTGGG CCCGCGGTGC 120
GGCGGGTGGC TTGCTGTTCT GCCTGGGCTC TCCCCTCTCC TCCTTTTCTC CCTTCCTCTG 180
TCTTGCCTCC TTCCTCTGGG TCCTCTTGGC CTGGGCGCTC TTCCCCTCGG GCGGCTGCGG 240
GCGCTCGTGC TGCCTGGTCC GCTCCCTGGG GGTGCTCCTT CCCTTTCCCC GCTCGTGGGG 300
TTTGCGGGGC TGGGCTGCCC TGGGGGGTCT GGGCCTTTTG GGGTCGGCTG GCTGCTGCTT 360
CGGGCCGCCT GGGCTTCCCT GTGCCCCTTT CCTCTGCTGG GTCCCCCTCC CGTTCCAAGC 420
TGCACCGCAC AGACCGGCGC TACAGGACAG AGCCAGGCAA GCACCCATGG GGATCCAGGC 480
CCAGCTGTTC CBBGCTGCBC CGCBCBGBCC GGCGCTBCBG GBCBGBGCCB GGCBBGCBCC 540
CBTGGGGBTC CBGGCCCBGC TG 562

(2) INFORMATION FOR SEQ ID NO:1770:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1770:
TCTGCGC 7

(2) INFORMATION FOR SEQ ID NO:1771:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1771:
CCTGCTCCTG GGG 13

(2) INFORMATION FOR SEQ ID NO:1772:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1772:
TCCCTGTTTC CCCCCTTTCG TTCTGCGTTT GCCTTTGGCG TTTTTTGTTT GTTTTCTCTC 60
TCCGTCTTTC TTCTCCCCTG TGGGBBTTTC TGTGGGGBTG GCBTBCBCGT BGGCBGCTCC 120
BBGBGCTBGC BBBCTCBBBT GCBGBBGCBT CCTCBTGGCT CTGBBBCGGT GGGAATTTCT 180
GTGGGGBTGG CATACACGTA GGCAGCTCCA AGAGCTAGCA AACTCAAATG CAGAAGCATC 240
CTCATGGCTC TGAAACG 257

(2) INFORMATION FOR SEQ ID NO:1773:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1773:
GCCCCGGG 8

(2) INFORMATION FOR SEQ ID NO:1774:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1774:
GGGTTTCT 8

(2) INFORMATION FOR SEQ ID NO:1775:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1775:
GTGGGGBTGG C 11

(2) INFORMATION FOR SEQ ID NO:1776:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1776:
CCBBGBGCTB GC 12

(2) INFORMATION FOR SEQ ID NO:1777:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1777:
GTGGGAATTT CTGTGGGGBT GGCATACACG TAGGCAGCTC CAAGAGCTAG CAAACTCAAA 60
TGCAGAAGCA TCCTCATGGC TCTGAAACG 89

(2) INFORMATION FOR SEQ ID NO:1778:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1778:
CTCAGTGGCC CCCAAAAGGA TGAGTAATAC ATGCGCCACG ATGATCATAT CCTTTTTACT 60
ATGAGGCCGT GTCTGTCGTG TCTTTCCTTT GCTCTTGGTG TGTCTTTGCT GTGCCCTGCC 120
TCTCTGCCCG TGTCTGTCGT GTCTTTCCTT TGCTCTTGGT GTGTCTTTGC TGTGCCCTGC 180
CTCTCTGCCC GTGTCTGTCG TGTCTTTCCT TTGCTCTTGG TGTGTCTTTG CTGTGCCCTG 240
CCTCTCTGC 249

(2) INFORMATION FOR SEQ ID NO:1779:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1779:
CCGTGTC 7

(2) INFORMATION FOR SEQ ID NO:1780:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1780:
GCCCTGCC 8

(2) INFORMATION FOR SEQ ID NO:1781:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1781:
CTCBGTGGCC CCCBBBBGGB TGBGTBBTBC BTGCGCCBCG BTGBTCBTBT CCTTTTTBCT 60
BTGBGG 66

(2) INFORMATION FOR SEQ ID NO:1782:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 869 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1782:
GGGGGTGGCT TCCTGCCGCG TCTCTGGGCC GTCCCGTCCC TCGGCCCCGC GCCGCGCTCG 60
GCTCCTCTCC CTCTGGCCCG GCTCGGGGCG GGGCGGGGCG GTGGGCGGGC GGCGCTGCCC 120
TGCGCGCGGC GCTGGCCCCT GCTGGCCGTC GGCTGCGCGC TGCTGGCTGC CCTGCTGGCC 180
GCGCCGGGGC CTGTCCGCCT CTGCGGGCGC TGTCTCCTGG CTTGTCTTCC GGCTCTTCTG 240
CTGGGGTGGG GCTGGGCGGC CGGCCCGGTG CTGGGGCTCC TCGGGGGGGG GGGCTCTTCC 300
GGGCTGTCTC CCTCCGGGGC GGGGGTTTCT GGCCGTGGGG GTCTTGCCTG GCCTCCGGGC 360
TCCTGCTTGT CTTGCCTTCC TTCTCTGGTC GGTTGTGGCT CGGGGCTCCG TGGGTCCCTG 420
GCGCCCGTTT GTGTTTTGTC TTTTCCCCTG GCGTCCCTGT GCCCCTCTCC TCTCCTTCCT 480
CTGCTTCTCG CTCTCCTTTG TGGGGCCCTC CCTGCTGCTC TTGGTTTTGG GCTTTTTTTC 540
TCTTCCTCCT TTTTCGTGCG TGGGCCTCCG CACGCCTCTT GCCACCTCCT GCGCAGGGCA 600
GCGCCTTGGG GCCAGCGCCG CTCCCGGCGC GGCCAGCAGG GCAGCCAGCA GCGCGCAGCC 660
GACGGCCAGC ATGCTTCCTC CTCGGCTACC ACTCCATGGT CCCGCAGAGG CGGACAGGCG 720
CBCGCCTCTT GCCBCCTCCT GCGCBGGGCB GCGCCTTGGG GCCBGCGCCG CTCCCGGCGC 780
GGCCBGCBGG GCBGCCBGCB GCGCGCBGCC GBCGGCCBGC BTGCTTCCTC CTCGGCTBCC 840
BCTCCBTGGT CCCGCBGBGG CGGBCBGGC 869

(2) INFORMATION FOR SEQ ID NO:1783:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1783:
GCBGCCBGCB GCG 13

(2) INFORMATION FOR SEQ ID NO:1784:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1784:
CGCBGCCGBC GGCC 14

(2) INFORMATION FOR SEQ ID NO:1785:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 869 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1785:
GGGGGTGGCT TCCTGCCGCG TCTCTGGGCC GTCCCGTCCC TCGGCCCCGC GCCGCGCTCG 60
GCTCCTCTCC CTCTGGCCCG GCTCGGGGCG GGGCGGGGCG GTGGGCGGGC GGCGCTGCCC 120
TGCGCGCGGC GCTGGCCCCT GCTGGCCGTC GGCTGCGCGC TGCTGGCTGC CCTGCTGGCC 180
GCGCCGGGGC CTGTCCGCCT CTGCGGGCGC TGTCTCCTGG CTTGTCTTCC GGCTCTTCTG 240
CTGGGGTGGG GCTGGGCGGC CGGCCCGGTG CTGGGGCTCC TCGGGGGGGG GGGCTCTTCC 300
GGGCTGTCTC CCTCCGGGGC GGGGGTTTCT GGCCGTGGGG GTCTTGCCTG GCCTCCGGGC 360
TCCTGCTTGT CTTGCCTTCC TTCTCTGGTC GGTTGTGGCT CGGGGCTCCG TGGGTCCCTG 420
GCGCCCGTTT GTGTTTTGTC TTTTCCCCTG GCGTCCCTGT GCCCCTCTCC TCTCCTTCCT 480
CTGCTTCTCG CTCTCCTTTG TGGGGCCCTC CCTGCTGCTC TTGGTTTTGG GCTTTTTTTC 540
TCTTCCTCCT TTTTCGTGCG TGGGCCTCCG CACGCCTCTT GCCACCTCCT GCGCAGGGCA 600
GCGCCTTGGG GCCAGCGCCG CTCCCGGCGC GGCCAGCAGG GCAGCCAGCA GCGCGCAGCC 660
GACGGCCAGC ATGCTTCCTC CTCGGCTACC ACTCCATGGT CCCGCAGAGG CGGACAGGCG 720
CBCGCCTCTT GCCBCCTCCT GCGCBGGGCB GCGCCTTGGG GCCBGCGCCG CTCCCGGCGC 780
GGCCBGCBGG GCBGCCBGCB GCGCGCBGCC GBCGGCCBGC BTGCTTCCTC CTCGGCTBCC 840
BCTCCBTGGT CCCGCBGBGG CGGBCBGGC 869

(2) INFORMATION FOR SEQ ID NO:1786:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1786:

GGGGCBGG 8

(2) INFORMATION FOR SEQ ID NO:1787:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1787:
GBBGGCBGCB GGC 13

(2) INFORMATION FOR SEQ ID NO:1788:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1788:
CCBGGBGCBG CCCC 14

(2) INFORMATION FOR SEQ ID NO:1789:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1789:
BGGGBGBBGG CBBC 14

(2) INFORMATION FOR SEQ ID NO:1790:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1790:
CTCCTGGGGG TBCTGGGGCB GGGBBGGCBG CBGGCBBCBC CBGGBGCBGC CCCBGGGBGB 60
BGGCBBCTGG BCCGBBGGCG CTTGTGGBGB BGGBGTTCBT BGCTGGGCTC CTGGBGGGGB 120
GBTBGBGC 128

(2) INFORMATION FOR SEQ ID NO:1791:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1791:
GGGGTGGBBB GGTTTGGBGT BTGTCTTTBT GCBCTGBCBT CTBBGTTCTT TBGCBCTCCT 60
TGGCBBBBCT GCBCCTTCBC BCBGBGCTGC BGBBBTCBGG BBGGCTGCCB BGBGBGCCBC 120
GGCCBGCTTG GBBGTCBTGT TTBCBCBCBG TGBGBTGGTT CCTTCCGGGC TTGTGTGCTC 180
TGCTGTCTCT TGGTTCCTTC CGGTGGTTTC TTCCTGGCTC TTGTCCTTTC TCTTGGCCCT 240
TGGC 244

(2) INFORMATION FOR SEQ ID NO:1792:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1792:
GGBGTBTG 8

(2) INFORMATION FOR SEQ ID NO:1793:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1793:
GCBCTGBCBT CT 12

(2) INFORMATION FOR SEQ ID NO:1794:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1794:
CCGGTGG 7

(2) INFORMATION FOR SEQ ID NO:1795:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1795:
GGCCCTTGGC 10

(2) INFORMATION FOR SEQ ID NO:1796:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1796:
GGGGTGGBBB GGTTTGGBGT BTGTCTTTBT GCBCTGBCBT CTBBGTTCTT TBGCBCTCCT 60
TGGCBBBBCT GCBCCTTCBC BCBGBGC 87

(2) INFORMATION FOR SEQ ID NO:1797:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1797:
GGGCTCCCGC CGCGBGBGGT TBTGGGCTCC CBGGBCCBCC CGCBCCGCGC GGBCGTTTBC 60
BTTCGCCBCG CBGTGCGCGG CCGBCBTGBC GBBGTTGGGC GCBBTCBGGG TGGCGCCGCB 120
GBBGTGGCCT CCGCGCBGCT GCBGGGBCBC CBTGBBGGGC CBCGCGTGGG GCCGCGCTCG 180
CCGGCCCCCC BCBBTCTCCG BGGCCBGCGC GGTGCCCCCC BGCBGCBBGG CCGGCBGGBC 240
BCBGGCGBGG BGBCBCGCGB GTCGGCGGCC GBGGGTCBTG GTGGGGCTGG GGCTCCGGGG 300
TCTCTGCCCC TCCGTGCTGG TGGGGCTGGG GCTCCGGGGT CTCTGCCCCT CCGTGCCGCG 360
TGGGGCCGCG CTCGCCGGCC CCCCCCTGCC GGGTGGGCTC CCGCCGCGCG CCGGCCTGCC 420
GGCCCCTCGT GGGTCCTGCT GGCCGGGTCC GGGTCCCGGG GGTGGGGCGC GBGTCGGCGG 480
CCGBGGGTC 489

(2) INFORMATION FOR SEQ ID NO:1798:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1798:
GGTGGGGC 8

(2) INFORMATION FOR SEQ ID NO:1799:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1799:
GGGGCCG 7

(2) INFORMATION FOR SEQ ID NO:1800:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1800:
GGCCGGGTCC GGG 13

(2) INFORMATION FOR SEQ ID NO:1801:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1801:

```
GGGCTCCCGC CGCGBGBGGT TBTGGGCTCC CBGGBCCBCC CGCBCCGCGC GGBCGTTTBC    60
BTTCGCCBCG CBGTGCGCGG CCGBCBTGBC GBBGTTGGGC GCBBTCBGGG TGGCGCCGCB   120
GBBGTGGCCT CCGCGCBGCT GCBGGGBCBC CBTGBBGGGC CBCGCGTGGG GCCGCGCTCG   180
CCGGCCCCCC BCBBTCTCCG BGGCCBGCGC GGTGCCCCCC BGCBGCBBGG CCGGCBGGBC   240
BCBGGCGBGG BGBCBCGCGB GTCGGCGGCC GBGGGTCBTG GTGGGGCTGG GGCTCCGGGG   300
TCTCTGCCCC TCCGTGC                                                  317
```

(2) INFORMATION FOR SEQ ID NO:1802:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1802:

```
CGGGBGTGGG GGTCCTGGBC GGCBCTGBBG GCBTCCBGGG CTCCCTTCCB GTCCTTCTTG    60
TCCGCTGCCB GCBCCCCTTC BTTCCBGBGG CTGBTGGCCT CCBCCBGGGB CBTGBTTBGG   120
TBGBBBCTBG GBGGCCGGCC TCCBCCBGGG BCBTGGTCCT TCTTGTCCGC TGCCTCTCTG   180
GGGTTTTCGG TCTGGGTGGG CTTTCCTCCT GGGGCTGCTG CTGGGCTCTT CTTTTTGTTT   240
CTGGCCTGGT GCTCTCTCGT GCCCTTTCCC TTGGGTGTCT TGTTTTTGTG GCCTCCBCCB   300
GGGBCBTG                                                            308
```

(2) INFORMATION FOR SEQ ID NO:1803:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1803:

```
CGGGBGTGGG GG                                                        12
```

(2) INFORMATION FOR SEQ ID NO:1804:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1804:

```
GCCBGCBCCC C                                                         11
```

(2) INFORMATION FOR SEQ ID NO:1805:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1805:

```
CCBCCBG                                                               7
```

(2) INFORMATION FOR SEQ ID NO:1806:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1806:

```
CGGGBGTGGG GGTCCTGGBC GGCBCTGBBG GCBTCCBGGG CTCCCTTCCB GTCCTTCTTG    60
TCCGCTGCCB GCBCCCCTTC BTTCCBGBGG CTGBTGGCCT CCBCCBGGGB CBTGBTTBGG   120
TBGBBBCTBG GBGGCC                                                   136
```

(2) INFORMATION FOR SEQ ID NO:1807:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1807:

```
CCCTCCBCBT CTGCTCTGBC CTGCTGGBCT CTGGBTCTGB BGBTBCGCCB TGTBGGGGCG    60
GGBGTGGGGC CTGCTCTCCC GGCCTCCGBT GBTCTCCCCT GCCTCBGCCC CBGTGGGTBG   120
GBGBBBGGCC BGCBGBBGCB GGBGTGGCTG CBTCTTTCCT GGTGGGGCCT GCTCTCCCGG   180
CCTCCGTGTG TTGCTGGGTG TTTTCCCGTC TCTGGTCTGC CTTCGGGGGT CGT          233
```

(2) INFORMATION FOR SEQ ID NO:1808:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1808:
GBBGBTBCGC C 11

(2) INFORMATION FOR SEQ ID NO:1809:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1809:
CBGCCCCBG 9

(2) INFORMATION FOR SEQ ID NO:1810:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1810:
TCCCGTCTCT GG 12

(2) INFORMATION FOR SEQ ID NO:1811:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1811:
CCCTCCBCBT CTGCTCTGBC CTGCTGGBCT CTGGBTCTGB BGBTBCGCCB TGTBGGGGCG 60
GGBGTGGGGC CTGCTCTCCC GGCCTCCGBT GBTCTCCCCT GCCTCBGCCC CBGTGGGTBG 120
GBGBBBGGCC BGCBGBBGCB GGBGTGGCTG 150

(2) INFORMATION FOR SEQ ID NO:1812:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1812:
CCGGGGCTGC BGCBBCCTCB TCBGCTCTTG CCTGGBGTGG CTCBGCCTGG GCCTGCBGGG 60
CCBCCBGGBG BBTGGCBGCB BGGBTGGCGB GGGTCCTCBT GGCTGGGGTC BCBGBTCCTC 120
TBGCTBGGCB GGGTGBCCBG BGBGGGCGGG TCCTCBTGGC TGGGGGCCTG GGCCTGCBGG 180
GCCGCTCTTG CCTGGBGTGG CTCGCCCBGB GTCTTCCCTG GT 222

(2) INFORMATION FOR SEQ ID NO:1813:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1813:
CCGGGGC 7

(2) INFORMATION FOR SEQ ID NO:1814:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1814:
GGGCCTGCBG GGCC 14

(2) INFORMATION FOR SEQ ID NO:1815:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1815:
GGCBGCBBGG 10

(2) INFORMATION FOR SEQ ID NO:1816:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1816:

CCGGGGCTGC BGCBBCCTCB TCBGCTCTTG CCTGGBGTGG CTCBGCCTGG GCCTGCBGGG 60
CCBCCBGGBG BBTGGCBGCB BGGBTGGCGB GGGTCCTCBT GGCTGGGGTC BCBGBTCCTC 120
TBGCTBGGCB GGGTGBCCBG BGBGGGC 147

(2) INFORMATION FOR SEQ ID NO:1817:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1817:

CGCTGCBBTC TGCTCCGGGG CTGCBGCBBC CTCBTCBGCT CTTGCCTGGB GTGGCTCBGC 60
CTGGGCCTGC BGGGCCBCCB GGBGBBTGGC BGCBBGGBTG GCGBGGGTCC TCBTGGCTGG 120
GGTCBCCTGG BGGBGGGBGB GCBGGGGGTC CTCBTGGCTG GGGTCCCTCT CTCCCGTCCT 180

(2) INFORMATION FOR SEQ ID NO:1818:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1818:

GGCBGCBBGG 10

(2) INFORMATION FOR SEQ ID NO:1819:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1819:

GGCTGGGG 8

(2) INFORMATION FOR SEQ ID NO:1820:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1820:

GGGGTCBCC 9

(2) INFORMATION FOR SEQ ID NO:1821:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1821:

CGCTGCBBTC TGCTCCGGGG CTGCBGCBBC CTCBTCBGCT CTTGCCTGGB GTGGCTCBGC 60
CTGGGCCTGC BGGGCCBCCB GGBGBBTGGC BGCBBGGBTG GCGBGGGTCC TCBTGGCTGG 120
GGTCBCCTGG BGGBGGGBGB GCBGG 145

(2) INFORMATION FOR SEQ ID NO:1822:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1822:

GTCTTTGTTT CTGGGCTCGT GCCCCBTCCC GGCTTCTCTC TGGTTCCGTC CTCTGTGGTG 60
TTTGGCCCTG CTTCCTTTTG CCTGTTGAGG GGGCAGCAGT TGGGCCCCAA AGGCCCTCTC 120
GTTCACCTTC TGGCACGGAG TTGCATCCCC ATAGTCAAAC TCTGTGGTCG TGTCATAGTC 180
CTCTGTGGTG TTTGGAGTTT CCATCCCGGC TTCTCTCTGG TTCCAAGGGA GBGGGGGCBG 240
CBGTTGGGCC CCBBBGGCCC TCTCGTTCBC CTTCTGGCBC GGBGTTGCBT CCCCBTBGTC 300
BBBCTCTGTG GTCGTGTCBT BGTCCTCTGT GGTGTTTGGB GTTTCCBTCC CGGCTTCTCT 360
CTGGTTCCBB GGGB 374

(2) INFORMATION FOR SEQ ID NO:1823:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1823:
GGGCCCC 7

(2) INFORMATION FOR SEQ ID NO:1824:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1824:
GGGGGCBGC 9

(2) INFORMATION FOR SEQ ID NO:1825:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1825:
CCCGGCTTC 9

(2) INFORMATION FOR SEQ ID NO:1826:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1826:
GGGCBCGGGG CBGTGGGCGG GCBBTGTBGG CBBBGCBGCB GGGTGTGGTG TCCGBGGBBT 60
BTGGGGBGGC BGBTGCBGGB GCGCBGBGGG CBGTBGCBBT GBGGBTGBCB GCGBGGCGTG 120
CCGCGGBGBC CTTCBTGGTB CCTGTGGBGB GGCTGTCGGB GGGGGTGTGG TGTCCGCTTG 180
GCGGTTCTTT CGGGTGTTTC TTCTCTGGGT TGGCCTGCTG CTCGTCGTGG TCGCTCCGCT 240
CCCGGGTTCG TCTCGCTCTG TCGCCCCTTC CTTCCTTGTC GTGTTCCTCC CTTCCTTGCC 300
TCT 303

(2) INFORMATION FOR SEQ ID NO:1827:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1827:
GGGTTGGC 8

(2) INFORMATION FOR SEQ ID NO:1828:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1828:
CGGGGCBG 8

(2) INFORMATION FOR SEQ ID NO:1829:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1829:
CCCGGGTTCG 10

(2) INFORMATION FOR SEQ ID NO:1830:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1830:

GGGTGTGGTG 10

(2) INFORMATION FOR SEQ ID NO:1831:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1831:
GGGCBCGGGG CBGTGGGCGG GCBBTGTBGG CBBBGCBGCB GGGTGTGGTG TCCGBGGBBT 60
BTGGGGBGGC BGBTGCBGGB GCGCBGBGGG CBGTBGCBBT GBGGBTGBCB GCGBGGCGTG 120
CCGCGGBGBC CTTCBTGGTB CCTGTGGBGB GGCTGTCGGB GG 162

(2) INFORMATION FOR SEQ ID NO:1832:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1832:
GCTGCCCGGC GGGGTGTGCG CTTGGCGCTC CCGTGCTCGG TTCTCTGTCT CCCGGTCCCC 60
CTTGCCTGGC GTCTCGGGCC TTCGTCCTCT TCCTCTTCTT CCTTCCGCTC CGTGGGGGCT 120
GCTTGGTGGG GGCCTGTGCC TCGGGGTCCC GGGGCTTCTG GCCCTTGCCG TTCATGGTGG 180
CTAGGTGGGG CGTTCBTGGT GGCTBGGTGG GGC 213

(2) INFORMATION FOR SEQ ID NO:1833:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1833:
GGTGGGGC 8

(2) INFORMATION FOR SEQ ID NO:1834:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1834:
GCCCGGCGGG G 11

(2) INFORMATION FOR SEQ ID NO:1835:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1835:
CGGGGCTTCT GGCCC 15

(2) INFORMATION FOR SEQ ID NO:1836:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1836:
GGGGTGGGTB GGCCGTGTCT GGGGGTTGGC CBTGTTGGTT GCCTCTTGGT GGTGCGCCGG 60
GCGCGTCTTG GCTTTCTTCT CCTTCGGGCC CTCGGGCCGG TGCTTGTGGG CTCCTCCCGG 120
GCGGCCTCCC CGGGCGGGGG CTTCTTGGCG CTGGCGGGGG GGCCTCCTGC TCTGTGGCTG 180
GGCGTTCCTT GGTGTTCTGG GTGGTGGCGG GCGTGGTGGC CTCTGTGGGG GCCCGCGGCT 240
GCBGGGGTTG CCTGTCTGCT TCGTCCTTTG CGCTCCCGGG CCGCCGGGGT GGGTAGGCCG 300
TGTCTGGGGG TTGGCCATGT TGGTTGCCGG GCCCGCGGCT GCAGGGG 347

(2) INFORMATION FOR SEQ ID NO:1837:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1837:
CCCGGGCGG 9

(2) INFORMATION FOR SEQ ID NO:1838:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: lin ar
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1838:
GGCGGGGGGG CC 12

(2) INFORMATION FOR SEQ ID NO:1839:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1839:
CCCGGGCCGC C 11

(2) INFORMATION FOR SEQ ID NO:1840:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1840:
GGCCGTGT 8

(2) INFORMATION FOR SEQ ID NO:1841:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 664 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1841:
CGGTTTCCTT TGCGGTCTTG GCCCGGGCTC CGGGTGCCCG CCCGCCCGCC GGCCGCCGCC 60
CCGCCGGGCT GTCCCCGCCC CGCCCCGGCC CGGGGCGCGG GGGCGGCCCT CCCGCCCCTC 120
TGGGCCGGCG CGGGCGTCGG CCGCTCGCGC CTGGGGTTCC CTCTCCTCCC CCTGTGCGCC 180
TGCCTCTTGC TCTTCTGCGT CCGCTGCCTT CTCCCCTCTC CTCGGCCGTT GCCTGTGCTG 240
TCCGTCCTGT CGCCCTTCCG TGGTGCTGTT GTCTCTTCTG CCCTCGGTGT GCTGGTGCTG 300
GTGGTGGTGC CTCTGCCCGT GCTCGCCCTG CCTGGGCTGG CCTCTTCGGG TGTGGCTTTG 360
GGGCTCTCTT GGTTGCCCTT TCTTCTCGTG GTGCCTCTCC TCCCTGGCTT GGTCGTTGTC 420
TGGGGTGGTG CTCCTCTCCC TTTCCCTGCT GGCCGTTTGT CCTGTTTTCT GTCTTCCTCT 480
TTCCTCCTGT TTCTCCGTTT GGCTTGCTGC TTGCGGGGCT GTCTCCCTTG CCCCTGTGGG 540
CTTTCCCTGG TCCGGTCTTC TCCTTGGGGG TCGCCCTTCT TGGTGGGCTG GCTCGTCTGT 600
CTTTTTCCTT CCTGGGGGTG GCCGTTGTGG GCGGTGTGGT CCGCCTTGCC TCTGCTGGTC 660
TTTC 664

(2) INFORMATION FOR SEQ ID NO:1842:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1842:
GGCCCGGGC 9

(2) INFORMATION FOR SEQ ID NO:1843:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1843:
GCCGGCGCGG GCG 13

(2) INFORMATION FOR SEQ ID NO:1844:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1844:
GCCTGGGCTG GCC 13

(2) INFORMATION FOR SEQ ID NO:1845:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1845:
GGGGGTGGCC G 11

(2) INFORMATION FOR SEQ ID NO:1846:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1846:
GGGGGTGGCC GTTGTGGGCG G 21

(2) INFORMATION FOR SEQ ID NO:1847:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1847:

GBTGTTTGTT BCCBBBGCBT CBBGBBTBGC TTTGCTBTCT BBGGBTCBCB TTTBGBCBTB 60
GGBBBBCGCT GTBGGTCBGB BBGBTGTGCT TBCCTTCBCB CBGBGCTGCB GBBBTCBGGB 120
BGGCTGCCBB GBGBGCCBCG GCCBGCTTGG BGTCBTGTTT BCBCBCBGTG BGGTGCTCCG 180
GTGGCTTTTT GCTTGTGTGC TCTGCTGTCT CTGTTCCTTC CGGTGGTTTC TTCCTGGCTC 240
TTGTCCTTTC TCTTGGCCCT TGGCCC 266

(2) INFORMATION FOR SEQ ID NO:1848:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1848:
GCTCCGG 7

(2) INFORMATION FOR SEQ ID NO:1849:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1849:
CBBGBBTBGC 10

(2) INFORMATION FOR SEQ ID NO:1850:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1850:
CBCBCBGTGB GGTGC 15

(2) INFORMATION FOR SEQ ID NO:1851:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1851:
BCCBBBGCBT CBBGBBTBGC 20

(2) INFORMATION FOR SEQ ID NO:1852:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1852:
GCCBBGBGBG CCBCGGCCBG C 21

(2) INFORMATION FOR SEQ ID NO:1853:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1853:
GBTGTTTGTT BCCBBBGCBT CBBGBBTBGC TTTGCTBTCT BBGGBTCBCB TTTBGBCBTB 60
GGBBBBCGCT GTBGGTCBGB BBGBTGTGCT TBCCTTCBCB CBGBGCTGCB GBBBTCBGGB 120
BGGCTGCCBB GBGBGCCBCG GCCBGCTTGG BGTCBTGTTT BCBCBCBGTG BGGTGCTCCG 180
GTGGCTTTTT GCTTGT 196

(2) INFORMATION FOR SEQ ID NO:1854:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1854:
ACAGGGGCTG TAATCTTCAT CTGCAGGTGG CATGCCAGTG AAATTTAGAT CATCAAAATC 60
CCACATCTGT GGATCTGTAA TATTTGACAT GTCCTCTTCA GTTTCAGCAA TGGTTTGATC 120
TAACTGAAGC ACCGGCCAGG BCBGGGGCTG TBBTCTTCBT CTGCBGGTGG CBTGCCBGTG 180
BBBTTTBGBT CBTCBBBBTC CCBCBTCTGT GGBTCTGTBB TBTTTGBCBT GTCCTCTTCB 240
GTTTCBGCBB TGGTTTGBTC TBBCTGBBGC BCCGGCCBGG TGGCTCGGTG CTTCTGCCCC 300
TGTTGTTGCG GCGCTCGGTT GGTGTGGCCC CTGTGGTGCT TCGTTTCCCC CTCTTTCTCT 360
TTGTTCGGGG GTTCTTGTGG CGGGCTGCTT GTCTCGTTCC 400

(2) INFORMATION FOR SEQ ID NO:1855:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1855:
CBGGGGC 7

(2) INFORMATION FOR SEQ ID NO:1856:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1856:
GCBGGTGGC 9

(2) INFORMATION FOR SEQ ID NO:1857:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1857:
GCGGCGCTC 9

(2) INFORMATION FOR SEQ ID NO:1858:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1858:
ACAGGGGCTG TAATCTTCAT CTGCAGGTGG CATGCCAGTG AAATTTAGAT CATCAAAATC 60
CCACATCTGT GGATCTGTAA TATTTGACAT GTCCTCTTCA GTTTCAGCAA TGGTTTGATC 120
TAACTGAAGC ACCGGCCAGG 140

(2) INFORMATION FOR SEQ ID NO:1859:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1859:
BCBGGGGCTG TBBTCTTCBT CTGCBGGTGG CBTGCCBGTG BBBTTTBGBT CBTCBBBBTC 60
CCBCBTCTGT GGBTCTGTBB TBTTTGBCBT GTCCTCTTCB GTTTCBGCBB TGGTTTGBTC 120

TBBCTGBBGC BCCGGCCBGG 140

(2) INFORMATION FOR SEQ ID NO:1860:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1860:

```
CTTGBGCBGG BBGCTCTGGG GCBGGGBGCT GGCBGGGCCC BGGGGGGTGG CTTCCTGCBC   60
TGTCCBGBGT GCBCTGTGCC BCBGCBGCBG CTGCBGGGCC BTCBGCTTCB TGGGGCTCTG  120
GGTGGCBGGT CCBGCCBTGG GTCTGGGTGG GGCTGGGCTG CBGGCTCCGG GCGGTCCBGC  180
CBTGGGTCTG GGGGCTGGGC TGCBGGCTCC GGGCGGGCGG GTGCGGGCTG CGTGCTGGGG  240
GCTGCCCCGC AGGCCCTGCG GTCCBGCCBT GGGTCTGGGG GCTGGGCTGC BGGCTCCGGG  300
CGGGCGGGTG CGGGCTGCGT GCTGGGGGCT GCCCCGCAGG CCCTGC                346
```

(2) INFORMATION FOR SEQ ID NO:1861:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1861:

```
GBGCBGGBBG                                                         10
```

(2) INFORMATION FOR SEQ ID NO:1862:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1862:

```
GCCBCBGCBG CBGC                                                    14
```

(2) INFORMATION FOR SEQ ID NO:1863:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1863:

```
GGGTGCGGGC                                                         10
```

(2) INFORMATION FOR SEQ ID NO:1864:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1864:

```
CTTGBGCBGG BBGCTCTGGG GCBGGGBGCT GGCBGGGCCC BGGGGGGTGG CTTCCTGCBC   60
TGTCCBGBGT GCBCTGTGCC BCBGCBGCBG CTGCBGGGCC BTCBGCTTCB TGGGGCTCTG  120
GGTGGCBGGT CCBGCCBTGG GTCTGGGTGG GGCTGGGCTG CBGGCTCCGG GC         172
```

(2) INFORMATION FOR SEQ ID NO:1865:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 818 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1865:

```
GCBCCGCCTG GBGCCCTGGG GCCCCCCTGT CTTCTTGGGG BGCGCCTCCT CGGCCBGCTC   60
CBCGTCCCGG BTCBTGCTTT CBGTGCTCBT GGTGTCCTTT CCBGGGGBGB GBGGGGCTGG  120
TCCTCTGCTG TCCTTGCTGG TGCTCBTGGT GTCCTTTCCG CCCTGGGGCC CCCCTGTCTT  180
CTTGGGGCCT CTTCCCTCTG GGGGCCGTCT CTCTCCCTCT CTTGCGTCTC TCTCTTTCTC  240
TCTCTCTCTT CCCCTTTCCC GCTCTTTCTG TCTCGGTGTC TGGTTTTCTC TCTCCGCTGG  300
CTGCCTGTCT GGCCTGCGCT CTTGGCCTGT GCTGTTCCTC CTCCGGTTCC TGTCCTCTCT  360
GTCTGTCGCC CCCTCTGGGG TCTCCCTCTG GGTGGTGGTC TTGTTGCTTG GGCTGGGCTC  420
CGTGTCTCCB GTGCTCBTGG TGTCCGCTGB GGGBGCGTCT GCTGGCGCTG GTCCTCTGCT  480
GTCCTTGCTG GTGCTCBTGG TGTCCTTTCC GCCCTGGGGC CCCCCTGTCT TCTTGGGGCC  540
TCTTCCCTCT GGGGGCCGTC TCTCTCCCTC TCTTGCGTCT CTCTCTTTCT CTCTCTCTCT  600
TCCCCTTTCC CGCTCTTTCT GTCTCGGTGT CTGGTTTTCT CTCTCCGCTG GCTGCCTGTC  660
TGGCCTGCGC TCTTGGCCTG TGCTGTTCCT CCTCCGGTTC CTGTCCTCTC TGTCTGTCGC  720
CCCCTCTGGG GTCTCCCTCT GGCGTGGTGG TCTTGTTGCT TGGGCTGGGC TCCGTGTCTC  780
CBGTGCTCBT GGTGTCCGCT GBGGGBGCGT CTGCTGGC                         818
```